

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:15:30 ; Search time 46.2295 Seconds
(without alignments)
47.521 Million cell updates/sec

Title: US-10-808-538-1
Perfect score: 34
Sequence: 1 NYWMT 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	5	2	Aaw23429 CDR-1 of
2	34	100.0	5	8	Adu81132 MAB 289-V
3	34	100.0	10	4	Aab35294 Murine PS
4	34	100.0	122	2	Aaw23432 rW12 heav
5	34	100.0	122	2	Aaw23437 Modified
6	34	100.0	122	2	Aaw23441 hW12 heav
7	34	100.0	122	2	Aaw23438 Modified
8	34	100.0	151	4	Aau76696 Mouse hea
9	34	100.0	151	4	Aau76692 Murine PS
10	34	100.0	249	5	Abp44963 Human Bly
11	34	100.0	249	7	Adg95790 Single ch
12	34	100.0	489	7	Adh87596 Enterococ
13	34	100.0	1314	5	Abb92290 Herbicida
14	31	91.2	226	4	Aau62804 Murine PS
15	31	91.2	226	6	Abm59323 Propionib
16	31	91.2	233	6	Abu33375 Protein e
17	31	91.2	241	8	Adl05135 M. catarr
18	31	91.2	454	5	Abp73979 Candida a
19	31	91.2	489	6	Abu39334 Protein e
20	31	91.2	504	6	Abm68236 Photorhab
21	31	91.2	511	6	Abu30485 Protein e
22	31	91.2	520	9	Aeb41540 L. pneumo
23	31	91.2	525	9	Aeb38256 L. pneumo
24	31	91.2	539	4	Abb72015 Drosophil

25	31	91.2	762	3	AAW90977	Aaw90977 N. denitr
26	31	91.2	781	6	ADA55068	Ada55068 Human pro
27	31	91.2	789	5	AAO19309	Aao19309 Human chl
28	31	91.2	803	5	ABB85024	Abb85024 Pain regu
29	31	91.2	803	5	ABB85025	Abb85025 Pain regu
30	31	91.2	803	5	AAO19308	Aao19308 Rat chlor
31	31	91.2	803	6	AGF79649	Agf79649 Murine CL
32	31	91.2	803	7	ADF60665	Adf60665 Rat CLC-7
33	31	91.2	803	7	ADF60667	Adf60667 Mouse CLC
34	31	91.2	805	4	AAW38696	Aaw38696 Human pol
35	31	91.2	805	5	ABB85023	Abb85023 Pain regu
36	31	91.2	805	7	ADF60663	Adf60663 Human CLC
37	31	91.2	805	7	ADJ70009	Adj70009 Human hea
38	31	91.2	805	8	ADQ18241	Adq18241 Human sof
39	31	91.2	805	8	ABM81693	Abm81693 Tumour-as
40	31	91.2	816	4	AAW40482	Aaw40482 Human pol
41	31	91.2	816	4	ABG19474	Abg19474 Novel hum
42	31	91.2	823	8	ADK70509	Adk70509 Respirato
43	31	91.2	925	8	ABM82606	Abm82606 Human dia
44	31	91.2	926	8	ABM82607	Abm82607 Human dia
45	31	91.2	926	8	ABM82605	Abm82605 Human dia
46	31	91.2	1097	4	ABB11833	Abb11833 Human Cl
47	31	91.2	1217	9	ADW26751	Adw26751 Fructo-ol
48	31	91.2	1229	4	ABG19475	Abg19475 Novel hum
49	31	91.2	1872	9	ADY26847	Ady26847 S. pulver
50	31	91.2	1880	9	ADY26830	Ady26830 S. pulver
51	31	91.2	3272	6	ABM68319	Abm68319 Photorhab
52	30	88.2	5	5	AAO17609	Aao17609 Human PAP
53	30	88.2	5	9	ADW10770	Adw10770 Heavy cha
54	30	88.2	56	4	AAW15741	Aaw15741 Peptide #
55	30	88.2	56	4	ABB34740	Abb34740 Peptide #
56	30	88.2	56	4	AAW28250	Aaw28250 Peptide #
57	30	88.2	56	4	ABB29560	Abb29560 Peptide #
58	30	88.2	56	4	ABB20153	Abb20153 Protein #
59	30	88.2	56	4	AAW67924	Aaw67924 Human bon
60	30	88.2	56	4	AAW55540	Aaw55540 Human bra
61	30	88.2	56	4	ABG49567	Abg49567 Human liv
62	30	88.2	56	4	AAW03475	Aaw03475 Peptide #
63	30	88.2	56	5	ABG37458	Abg37458 Human pep
64	30	88.2	61	4	AAU66091	Aau66091 Propionib
65	30	88.2	61	6	ABM62610	Abm62610 Propionib
66	30	88.2	100	4	AAE69973	Aae69973 Mouse ger
67	30	88.2	100	8	ADQ89258	Adq89258 Mouse imm
68	30	88.2	100	9	ABO9531	Abo9531 Murine ge
69	30	88.2	113	8	ADS16509	Ads16509 Human ant
70	30	88.2	128	8	ADP29923	Adp29923 Human sec
71	30	88.2	134	5	AAO14049	Aao14049 Human ant
72	30	88.2	142	7	ADD27361	Add27361 Human adi
73	30	88.2	156	8	ADS16615	Ads16615 Human ant
74	30	88.2	178	5	ABP42506	Abp42506 Human ova
75	30	88.2	214	7	ADD26847	Add26847 Human adi
76	30	88.2	234	3	AAG29510	Aag29510 Arabidops
77	30	88.2	234	3	ADY77503	Ady77503 Paraquat
78	30	88.2	237	3	AAG29509	Aag29509 Arabidops
79	30	88.2	247	5	ABP46092	Abp46092 Human Bly
80	30	88.2	247	7	ADG96919	Adg96919 Single ch
81	30	88.2	252	8	ABO13324	Abo13324 scFv F1TC
82	30	88.2	262	5	AAO14058	Aao14058 Anti-PAPA
83	30	88.2	262	8	ADP30072	Adp30072 Human sec
84	30	88.2	271	3	AAG29508	Aag29508 Arabidops
85	30	88.2	299	4	AAW50425	Aaw50425 Mouse ant
86	30	88.2	309	5	ABP30227	Abp30227 Streptoco
87	30	88.2	309	8	ADV89864	Adv89864 Streptoco
88	30	88.2	309	8	ADV83254	Adv83254 Streptoco
89	30	88.2	309	8	ADV81117	Adv81117 Streptoco
90	30	88.2	319	5	ABP28163	Abp28163 Streptoco
91	30	88.2	327	8	ADN23989	Adn23989 Bacterial
92	30	88.2	362	8	ADN23989	Adn23989 Bacterial
93	30	88.2	377	4	ABB61559	Abb61559 Drosophil
94	30	88.2	394	9	ADX66523	Adx66523 Cyclin-de
95	30	88.2	397	6	ABU70790	Abu70790 Human adi
96	30	88.2	406	4	AAE58268	Aae58268 Lung canc
97	30	88.2	406	4	AAE05077	Aae05077 Drosophil

98	30	88.2	449	7	ADP72635	Adf72635	B. burgdo	171	29	85.3	10	8	ADQ90780	Adg90780	Mouse com
99	30	88.2	461	7	ADD26748	Add26748	Human adi	172	29	85.3	10	8	ADU67908	Adu67908	Mouse ant
100	30	88.2	461	7	ADD27710	Add27710	Human adi	173	29	85.3	10	9	ADW95741	Adw95741	Anti-hil-
101	30	88.2	492	6	ADB25873	Adb25873	DNA encod	174	29	85.3	10	9	ADX15746	Adx15746	Mouse ant
102	30	88.2	492	7	ADF71806	Adf71806	Fragment	175	29	85.3	34	6	ADA95237	Ada95237	Protein d
103	30	88.2	494	5	ADP29724	Adp29724	Streptoco	176	29	85.3	34	6	ADA95218	Ada95218	Protein d
104	30	88.2	494	5	ABP26391	Abp26391	Streptoco	177	29	85.3	43	4	ABB41636	Abb41636	Peptide #
105	30	88.2	494	8	ADV88813	Adv88813	Streptoco	178	29	85.3	43	4	ABM35430	Abm35430	Peptide #
106	30	88.2	494	8	ADV82202	Adv82202	Streptoco	179	29	85.3	43	4	AAW75317	Aaw75317	Human bon
107	30	88.2	494	8	ADV80066	Adv80066	Streptoco	180	29	85.3	43	4	AAW62508	Aaw62508	Human bra
108	30	88.2	506	1	AAP94858	Aap94858	Expressio	181	29	85.3	43	4	ABG57076	Abg57076	Human liv
109	30	88.2	554	5	ABB91106	Abb91106	Herbicida	182	29	85.3	43	5	ABG44944	Abg44944	Human pep
110	30	88.2	555	1	AAP94857	Aap94857	Expressio	183	29	85.3	59	8	AAV64781	Aav64781	Human 5'
111	30	88.2	567	3	AAW58734	Aaw58734	Breast an	184	29	85.3	59	8	ADU72345	Adu72345	Signal pe
112	30	88.2	567	3	ADH09629	Adh09629	Human hos	185	29	85.3	59	9	ADZ73336	Adz73336	Human inc
113	30	88.2	604	5	ABB05593	Abb05593	Mitotic c	186	29	85.3	67	7	ADC95420	Adc95420	E. faeciu
114	30	88.2	609	6	ABU26106	Abu26106	Protein e	187	29	85.3	71	5	ABM79629	Abm79629	Human ORF
115	30	88.2	623	6	ABU24603	Abu24603	Protein e	188	29	85.3	75	8	ABW79629	Abw79629	E coli Cy
116	30	88.2	673	6	ADA55457	Ada55457	Human pro	189	29	85.3	96	3	AAV56647	Aav56647	Partial p
117	30	88.2	688	6	ABU62734	Abu62734	Alpha-ami	190	29	85.3	97	2	AAR89475	Aar89475	Salmonell
118	30	88.2	693	1	AAP94856	Aap94856	Expressio	191	29	85.3	97	3	ADOS8553	Ados8553	GANP gene
119	30	88.2	696	7	AAR75366	Aar75366	Adhesin.	192	29	85.3	101	7	ADC96428	Adc96428	E. faeciu
120	30	88.2	696	7	ADC00149	Adc00149	Enterohae	193	29	85.3	105	2	AAV55735	Aav55735	FKHL2 for
121	30	88.2	776	2	AAR06400	Aar06400	Lambda gt	194	29	85.3	106	2	AAV55736	Aav55736	FKHL3 for
122	30	88.2	853	2	AAR10322	Aar10322	Type A al	195	29	85.3	106	2	AAV55734	Aav55734	FKHL4 for
123	30	88.2	853	2	AAR06426	Aar06426	Protein e	196	29	85.3	111	2	AAW35907	Aaw35907	Streptoco
124	30	88.2	853	2	AAR11110	Aar11110	Rat C-ter	197	29	85.3	111	9	ADW10186	Adw10186	Thy-1 bas
125	30	88.2	866	2	AAR06379	Aar06379	Lambda gt	198	29	85.3	113	2	AAW93480	Aaw93480	mAb TTC8
126	30	88.2	872	4	AAW51684	Aaw51684	PAM. 1/20	199	29	85.3	113	4	ABU53097	Abu53097	Human nuc
127	30	88.2	875	1	AAP94854	Aap94854	C-termina	200	29	85.3	114	2	AAR25410	Aar25410	Heavy cha
128	30	88.2	875	2	AAR73053	Aar73053	Peptidyl	201	29	85.3	114	2	AAR28748	Aar28748	Heavy cha
129	30	88.2	887	9	ADY19540	Ady19540	PRO polyp	202	29	85.3	114	3	AAV90816	Aav90816	113F1 hyb
130	30	88.2	906	2	AAR20028	Aar20028	C-termina	203	29	85.3	115	2	AAW34018	Aaw34018	BW 835 VH
131	30	88.2	912	4	ABG24743	Abg24743	Novel hum	204	29	85.3	115	4	AAE03748	Aae03748	Murine PS
132	30	88.2	935	2	AAR20112	Aar20112	AE-III (p	205	29	85.3	116	6	ABO10728	Abol0728	Consensus
133	30	88.2	944	2	AAR10323	Aar10323	Type B al	206	29	85.3	116	6	ABO10734	Abol0734	Variable
134	30	88.2	944	2	AAR06427	Aar06427	Protein e	207	29	85.3	116	6	ABO10726	Abol0726	Variable
135	30	88.2	953	2	AAR20027	Aar20027	C-termina	208	29	85.3	116	6	ABO10732	Abol0732	Variable
136	30	88.2	954	2	AAR29770	Aar29770	Porcine p	209	29	85.3	116	6	ABO10733	Abol0733	Variable
137	30	88.2	971	7	ADJ68335	Adj68335	Human hea	210	29	85.3	116	6	ABR44676	Abr44676	Murine J4
138	30	88.2	973	2	AAR20026	Aar20026	C-termina	211	29	85.3	116	6	ABR44672	Abr44672	Murine J4
139	30	88.2	974	2	AAR06399	Aar06399	Lambda gt	212	29	85.3	116	6	ABR44670	Abr44670	Murine J4
140	30	88.2	974	7	ADE62711	Ade62711	Human pro	213	29	85.3	116	6	ABR44678	Abr44678	Murine J4
141	30	88.2	974	7	ADES58482	Ades58482	Human pro	214	29	85.3	116	6	ABR44677	Abr44677	Murine J4
142	30	88.2	974	7	ADES6520	Ades6520	Human pro	215	29	85.3	116	8	ABR44677	Abr44677	Murine J4
143	30	88.2	974	7	ADD47406	Add47406	Human pro	216	29	85.3	116	8	ABR44677	Abr44677	Murine J4
144	30	88.2	974	7	ADD47410	Add47410	Human pro	217	29	85.3	116	8	ADQ90798	Adq90798	Mouse J41
145	30	88.2	974	9	ADY14759	Ady14759	PRO polyp	218	29	85.3	116	8	ADQ90800	Adq90800	Deimmunis
146	30	88.2	976	7	ADW47404	Adw47404	Rat Prote	219	29	85.3	116	8	ADU67926	Adu67926	Mouse ant
147	30	88.2	976	7	ADES6480	Ades6480	Rat Prote	220	29	85.3	116	8	ADU67928	Adu67928	Mouse ant
148	30	88.2	976	7	ADE62710	Ade62710	Rat Prote	221	29	85.3	116	8	ADU67939	Adu67939	Mouse ant
149	30	88.2	976	7	ADES6518	Ades6518	Rat Prote	222	29	85.3	116	8	ADU67940	Adu67940	Mouse ant
150	30	88.2	976	7	ADD47408	Add47408	Rat Prote	223	29	85.3	116	8	ADU67938	Adu67938	Female mo
151	30	88.2	980	1	AAP93323	Aap93323	Bovine pe	224	29	85.3	117	8	ADM80355	Adm80355	Murine ho
152	30	88.2	980	2	AAR11113	Aar11113	Equine C-	225	29	85.3	117	8	ADQ90812	Adq90812	Deimmunis
153	30	88.2	1020	2	AAR20025	Aar20025	C-termina	226	29	85.3	117	8	ADR19296	Adr19296	Mucin 1 r
154	30	88.2	1305	4	ABB67631	Abb67631	Drosophil	227	29	85.3	117	8	AAE03753	Aae03753	Murine PS
155	30	88.2	1305	4	ABW74931	Abw74931	H-CDR-1 o	228	29	85.3	118	4	ADQ90811	Adq90811	Deimmunis
156	30	88.2	1684	2	AAR14948	Aar14948	Bacterial	229	29	85.3	118	8	ADQ90811	Adq90811	Human bre
157	29	85.3	5	2	AAW93474	Aaw93474	mAb TTC8	230	29	85.3	118	9	ADZ45473	Adz45473	Murine fa
158	29	85.3	5	8	ADP84873	Adp84873	Complemen	231	29	85.3	119	2	AAW01588	Aaw01588	Lead bind
159	29	85.3	5	8	ADR19265	Adr19265	Glycosyla	232	29	85.3	119	2	AAW46958	Aaw46958	Amino aci
160	29	85.3	5	9	ADW95744	Adw95744	Anti-hil-	233	29	85.3	119	2	AAW26798	Aaw26798	Anti-gp54
161	29	85.3	5	9	ADX15749	Adx15749	Mouse ant	234	29	85.3	119	2	AAW71240	Aaw71240	Heavy cha
162	29	85.3	5	9	ADZ45474	Adz45474	Murine fa	235	29	85.3	119	8	ADE25822	Ade25822	Anti-alpha
163	29	85.3	7	2	AAR90418	Aar90418	Antibody	236	29	85.3	119	8	ADQ90810	Adq90810	Deimmunis
164	29	85.3	7	2	AAV55145	Aav55145	Anti CD34	237	29	85.3	120	2	AAW01589	Aaw01589	Lead bind
165	29	85.3	7	3	AAV86891	Aav86891	Human hae	238	29	85.3	120	2	AAW41465	Aaw41465	MAb 25D2
166	29	85.3	8	2	AAR90424	Aar90424	Antibody	239	29	85.3	121	2	AAW41465	Aaw41465	Immunoglo
167	29	85.3	8	2	AAV55151	Aav55151	Anti CD34	240	29	85.3	121	2	AAW41465	Aaw41465	Anti-idio
168	29	85.3	8	3	AAV86897	Aav86897	Human hae	241	29	85.3	121	2	AAW41465	Aaw41465	Anti-idio
169	29	85.3	10	6	ABO10708	Abol0708	Murine J4	242	29	85.3	122	3	AAV90812	Aav90812	2G3 hybri
170	29	85.3	10	6	ABR44652	Abr44652	Murine J4	243	29	85.3	122	9	ADW95740	Adw95740	Mouse ant

244	29	85.3	122	9	ADX15745	Adx15745 Mouse ant	317	29	85.3	262	8	ADRI9315	Adri9315 Mucin 1 a
245	29	85.3	123	4	AAW93184	AAW93184 Human pol	318	29	85.3	263	8	ADRI9314	Adri9314 Mucin 1 a
246	29	85.3	123	6	ABO10742	Variable	319	29	85.3	264	8	ADRI9313	Adri9313 Mucin 1 a
247	29	85.3	123	6	ABO10743	Consensus	320	29	85.3	265	8	ADRI9312	Adri9312 Mucin 1 a
248	29	85.3	123	6	ABR44686	Murine Mu	321	29	85.3	266	5	ABG31024	Abg31024 Synthetic
249	29	85.3	123	6	ABR44687	Murine J4	322	29	85.3	267	7	ADD25453	Add25453 Binding d
250	29	85.3	123	8	ADL30519	Human pro	323	29	85.3	268	7	ADM42728	Adm42728 Synthetic
251	29	85.3	123	8	ADQ90820	Kabat sub	324	29	85.3	269	9	ABE95396	Abe95396 Mouse G28
252	29	85.3	123	8	ADQ90821	Kabat sub	325	29	85.3	270	9	ABE94430	Abe94430 Mouse ant
253	29	85.3	123	8	ADU67949	Mouse ant	326	29	85.3	271	5	ABB48031	Abb48031 Listeria
254	29	85.3	123	8	ADU67948	Mouse Kab	327	29	85.3	272	7	ADRI19311	Adri19311 Mucin 1 a
255	29	85.3	124	8	ADI26706	Human ant	328	29	85.3	273	7	ABO63669	AbO63669 Klebsiell
256	29	85.3	124	9	ADM10184	Human ant	329	29	85.3	274	4	AGS98964	AgS98964 E. coli 9
257	29	85.3	125	2	RAY27074	Monoclonal	330	29	85.3	275	4	AGS98964	AgS98964 E. coli 9
258	29	85.3	131	2	AAE63128	Anti-Inte	331	29	85.3	276	6	AAAY75708	AaY75708 Neisseria
259	29	85.3	133	6	ABO10730	Variable	332	29	85.3	277	6	ABP77852	Abp77852 N. gonorr
260	29	85.3	133	6	ABR44674	Murine J4	333	29	85.3	278	6	AAU37579	Aau37579 Protein e
261	29	85.3	133	8	ADQ90805	Deimmunis	334	29	85.3	279	3	AAU375710	Aau375710 Neisseria
262	29	85.3	133	8	ADU67933	Mouse ant	335	29	85.3	280	3	AAU375173	Aau375173 Neisseria
263	29	85.3	137	8	ADJ57305	MAG-1 ant	336	29	85.3	281	6	ABU37937	Abu37937 Protein e
264	29	85.3	140	2	AAAR41469	MAB 25D2	337	29	85.3	282	6	ADA35792	Ada35792 Acinetoba
265	29	85.3	140	2	AAAR89480	Anti-huma	338	29	85.3	283	6	ABP77912	Abp77912 N. gonorr
266	29	85.3	140	3	AAAY56712	Amino aci	339	29	85.3	284	6	ABU37874	Abu37874 Protein e
267	29	85.3	140	4	AAW74791	Anti-CA12	340	29	85.3	285	6	ABU37235	Abu37235 Protein e
268	29	85.3	142	2	AAW06212	MAB Br-3	341	29	85.3	286	7	ADU53220	Adu53220 Human met
269	29	85.3	142	2	AAW85059	Mouse Br-	342	29	85.3	287	7	ADU53220	Adu53220 Human met
270	29	85.3	142	6	ABU58893	Mouse ant	343	29	85.3	288	6	ADN72281	Adn72281 Thale cre
271	29	85.3	143	2	AAAR09423	Br-3 Heav	344	29	85.3	289	6	AAE16965	Aea16965 Arabidops
272	29	85.3	151	7	ADM26313	Hyperther	345	29	85.3	290	5	AAAG92853	Aag92853 C glutami
273	29	85.3	159	3	ABAB1853	Human ORF	346	29	85.3	291	8	AAE14678	Aae14678 Human tra
274	29	85.3	167	5	AAU97209	Portion o	347	29	85.3	292	8	ADX90526	Adx90526 Plant ful
275	29	85.3	167	6	ABU08334	Corn suga	348	29	85.3	293	6	ABJ38686	Abj38686 Human nuc
276	29	85.3	167	8	ADG47922	Corr Beta	349	29	85.3	294	5	ABP51313	Abp51313 Human MDD
277	29	85.3	185	5	ABW78646	Rat OST32	350	29	85.3	295	6	ABU21917	Abu21917 Protein e
278	29	85.3	194	7	ADC96941	E. faeciu	351	29	85.3	296	7	ABO82339	AbO82339 Pseudomon
279	29	85.3	200	6	ABU40985	Protein e	352	29	85.3	297	8	ADK52137	Adk52137 Mouse ato
280	29	85.3	214	5	ABU05547	M. tuberc	353	29	85.3	298	5	ABP54691	Abp54691 Metastati
281	29	85.3	226	7	ADP03979	Bacterial	354	29	85.3	299	4	ADL70231	Adl70231 Colon can
282	29	85.3	234	2	AAAY22171	Drosophil	355	29	85.3	300	8	ADN59623	Adn59623 Human DIT
283	29	85.3	234	4	ABW66468	Drosophil	356	29	85.3	301	4	ABR41158	AbR41158 Human DIT
284	29	85.3	236	5	ABP26618	Streptoco	357	29	85.3	302	8	ADX79987	Adx79987 Plant ful
285	29	85.3	236	5	ABW53386	Lactococc	358	29	85.3	303	6	ABU42300	Abu42300 Protein e
286	29	85.3	240	2	AAW71243	scfV comp	359	29	85.3	304	6	ABM72077	Abm72077 Staphyloc
287	29	85.3	241	5	ABP45921	Human Bly	360	29	85.3	305	8	ADV81075	Adv81075 Streptoco
288	29	85.3	241	5	ABP46043	Human Bly	361	29	85.3	306	8	ADV81075	Adv81075 Streptoco
289	29	85.3	241	7	ADG96870	Single ch	362	29	85.3	307	4	AAE09781	Aae09781 Escherich
290	29	85.3	241	7	ADG96748	Single ch	363	29	85.3	308	7	ADD47621	Add47621 Rat Prote
291	29	85.3	243	5	ABP45898	Human Bly	364	29	85.3	309	8	ADRI9326	Adri9326 Murine Ig
292	29	85.3	243	5	ABP46040	Human Bly	365	29	85.3	310	8	ADRI9328	Adri9328 Chimeric
293	29	85.3	243	5	ABP45905	Human Bly	366	29	85.3	311	5	AAW35906	Aaw35906 Streptoco
294	29	85.3	243	7	ADG96867	Single ch	367	29	85.3	312	5	ABP25686	Abp25686 Streptoco
295	29	85.3	243	7	ADG96725	Single ch	368	29	85.3	313	5	ABP25685	Abp25685 Streptoco
296	29	85.3	243	7	ADG96732	Single ch	369	29	85.3	314	6	ABU00966	Abu00966 S. pneumo
297	29	85.3	245	2	AAW26800	Anti-Sp54	370	29	85.3	315	6	ABU46835	Abu46835 Protein e
298	29	85.3	247	5	ABP46081	Human Bly	371	29	85.3	316	4	ABU45926	Abu45926 Protein e
299	29	85.3	247	7	ADG96908	Single ch	372	29	85.3	317	8	ADK46413	Adk46413 Streptoco
300	29	85.3	249	5	ABP46054	Human Bly	373	29	85.3	318	5	ABW55200	AbW55200 Lactococc
301	29	85.3	249	7	ADG96881	Single ch	374	29	85.3	319	8	ADR94736	Adr94736 Novel S.
302	29	85.3	251	4	AAW74793	Single ch	375	29	85.3	320	8	AEA58606	Aea58606 Streptoco
303	29	85.3	252	8	ABE01325	scfV SAI	376	29	85.3	321	9	ABB59467	Abb59467 Drosophil
304	29	85.3	253	4	ABW52930	Escherich	377	29	85.3	322	4	ADA32894	Ada32894 Acinetoba
305	29	85.3	253	4	ABW52964	Escherich	378	29	85.3	323	6	ABW66690	AbW66690 Drosophil
306	29	85.3	253	8	ADJ57281	MAG-1 ant	379	29	85.3	324	4	ABW66690	AbW66690 Drosophil
307	29	85.3	255	8	ADRI9322	Mucin 1 a	380	29	85.3	325	6	ABU44840	Abu44840 Protein e
308	29	85.3	255	8	ADY11103	Plant ful	381	29	85.3	326	4	AGS92649	AgS92649 C glutam
309	29	85.3	256	5	AAU72866	PS-3 sing	382	29	85.3	327	6	ABU28536	Abu28536 Protein e
310	29	85.3	256	8	ADRI9321	Mucin 1 a	383	29	85.3	328	6	ABU47007	Abu47007 Protein e
311	29	85.3	257	8	ADRI9320	Mucin 1 a	384	29	85.3	329	6	ABU50126	Abu50126 Protein e
312	29	85.3	258	4	AAW74794	Single ch	385	29	85.3	330	6	ABU47681	Abu47681 Protein e
313	29	85.3	258	8	ADRI9319	Mucin 1 a	386	29	85.3	331	6	ABU28132	Abu28132 Protein e
314	29	85.3	259	8	ADRI9318	Mucin 1 a	387	29	85.3	332	7	ADP70693	Adp70693 E. coli c
315	29	85.3	260	8	ADRI9317	Mucin 1 a	388	29	85.3	333	8	ABM79605	Abm79605 E. coli Cy
316	29	85.3	261	8	ADRI9316	Mucin 1 a	389	29	85.3	334	8	ADH96904	Adh96904 E. coli c

390	29	85.3	461	8	ADH96906	Adh96906	E. coli c	463	29	85.3	716	4	ABB58703	Abb58703	Drosophila
391	29	85.3	461	8	ADT98589	Adt98589	Escherich	464	29	85.3	724	2	AAW23406	Aaw23406	Actinoptera
392	29	85.3	461	9	AEC13261	Aec13261	Escherich	465	29	85.3	724	2	AAW76193	Aaw76193	Actinoptera
393	29	85.3	461	9	AEC13259	Aec13259	Escherich	466	29	85.3	724	5	AAW49563	Aam49563	Actinoptera
394	29	85.3	462	6	ABM70326	Abm70326	Photorehab	467	29	85.3	729	6	ABU25232	Abu25232	Protein e
395	29	85.3	463	6	ABU41064	Abu41064	Protein e	468	29	85.3	764	6	ABU02688	Abu02688	S. pneumoniae
396	29	85.3	463	6	ABU25904	Abu25904	Protein e	469	29	85.3	991	7	ADL23091	Adl23091	Streptomyces
397	29	85.3	463	4	AAU34291	Aau34291	Staphylococcus	470	29	85.3	1079	4	ABG28556	Abg28556	Novel human
398	29	85.3	465	6	ABU22845	Abu22845	Protein e	471	29	85.3	1098	4	ABG30367	Abg30367	Novel human
399	29	85.3	466	2	AAW22467	Aaw22467	Staphylococcus	472	29	85.3	1225	2	AAU34538	Aay34538	Porphyrin
400	29	85.3	466	2	AAW58529	Aaw58529	Staphylococcus	473	29	85.3	1226	2	AAU34537	Aay34537	Porphyrin
401	29	85.3	466	3	AAU91053	Aay91053	Staphylococcus	474	29	85.3	1248	5	ABG22291	Abg22291	Herbicidal
402	29	85.3	466	3	AAU43778	Aay43778	Protein e	475	29	85.3	1251	2	AAU34404	Aay34404	Herbicidal
403	29	85.3	467	2	AAU80617	Aar80617	Anti-human	476	29	85.3	1317	8	ADS22210	AdS22210	Bacterial
404	29	85.3	467	4	ABB68882	Abb68882	Drosophila	477	29	85.3	1450	4	ABG10837	Abg10837	Novel human
405	29	85.3	467	6	ABU16589	Abu16589	Protein e	478	29	85.3	1514	5	ABG22289	Abg22289	Herbicidal
406	29	85.3	469	7	ADU06783	Adf06783	Bacterial	479	29	85.3	1534	4	ABB60348	Abb60348	Drosophila
407	29	85.3	470	8	ADO25573	Ado25573	E. faecalis	480	29	85.3	1772	3	AAU52485	Aag52485	Arabidopsis
408	29	85.3	470	8	ADO25573	Ado25573	E. faecalis	481	29	85.3	1776	3	AAU52484	Aag52484	Arabidopsis
409	29	85.3	470	8	ADO25575	Ado25575	E. faecalis	482	29	85.3	1787	3	AAU58575	Aay58575	Sorangium
410	29	85.3	471	5	ABU49151	Abb49151	Listeria	483	29	85.3	1832	3	AAU17899	Aaw17899	Photorehab
411	29	85.3	471	6	ABU32797	Abu32797	Protein e	484	29	85.3	2516	2	AAU56572	Aaw56572	Toxin Tcd
412	29	85.3	471	7	ADU13202	Adi13202	C. glutamicum	485	29	85.3	2516	4	ABG72609	Abg72609	Photorehab
413	29	85.3	474	8	ADU59120	AdS9120	Anti-K88/	486	29	85.3	2516	5	ABG32651	Abg32651	P. luminescens
414	29	85.3	475	8	ADU11668	Ady11668	Plant full	487	29	85.3	2516	8	ADP18614	Adp18614	Photorehab
415	29	85.3	476	6	ABM72474	Abm72474	Staphylococcus	488	29	85.3	2516	8	ADP18614	Adp18614	Photorehab
416	29	85.3	477	6	ABP72344	Abp72344	Brain fac	489	29	85.3	2516	9	ADZ72157	Adz72157	P. luminescens
417	29	85.3	477	7	ADU80175	Adj80175	Novel human	490	29	85.3	2517	4	AAU372611	Aay372611	Modified
418	29	85.3	478	6	ABU28959	Abu28959	Protein e	491	29	85.3	2522	2	AAU373729	Aay373729	Photorehab
419	29	85.3	478	7	ADC95295	Adc95295	E. faecium	492	29	85.3	2522	6	ABM70229	Abm70229	Photorehab
420	29	85.3	478	7	ADH86827	Adh86827	Enterococcus	493	29	85.3	2537	8	ADP22426	Adp22426	Human ant
421	29	85.3	479	5	ABP39283	Abp39283	Staphylococcus	494	29	85.3	2537	8	ADP22426	Adp22426	Human ant
422	29	85.3	479	7	ABO66919	AbO66919	Klebsiella	495	28	82.4	10	7	ADP22426	Adp22426	Human ant
423	29	85.3	479	8	ADU06132	Adu06132	Staphylococcus	496	28	82.4	14	6	AAO26114	Aao26114	FC region
424	29	85.3	480	2	AAU44551	Adh44551	Brain fac	497	28	82.4	14	6	AAO26114	Aao26114	FC region
425	29	85.3	480	7	ADH26642	Adh26642	Granzyme	498	28	82.4	14	6	AAO26114	Aao26114	FC region
426	29	85.3	481	5	ABU57076	Abu57076	Mouse isc	499	28	82.4	14	8	ADU50781	Aau50781	Human ser
427	29	85.3	485	6	ADA35504	Ada35504	Acinetobacter	500	28	82.4	14	8	ADU50781	Aau50781	Human ser
428	29	85.3	489	8	ADU19922	Adu19922	Human sof	501	28	82.4	17	4	AAE11110	Aae11110	Tryptic p
429	29	85.3	491	6	ABU20159	Abu20159	Protein e	502	28	82.4	20	8	ADR84161	Adr84161	S. pyogen
430	29	85.3	503	5	AAU72874	Aau72874	3B10xP5-2	503	28	82.4	34	6	ADA95148	Ada95148	Protein d
431	29	85.3	507	5	ABG71552	Abg71552	Murine sc	504	28	82.4	34	6	ADA95278	Ada95278	Protein d
432	29	85.3	509	4	AAU76515	Abu76515	Corynebacter	505	28	82.4	34	6	ADA95304	Ada95304	Protein d
433	29	85.3	517	8	ADS21020	AdS21020	Bacterial	506	28	82.4	34	6	ADA95166	Ada95166	Protein d
434	29	85.3	527	8	ADU13583	Ady13583	Plant full	507	28	82.4	34	6	ADA95288	Ada95288	Protein d
435	29	85.3	528	7	ADC95011	Adc95011	E. faecium	508	28	82.4	34	6	ADA95269	Ada95269	Protein d
436	29	85.3	551	8	ADU12781	Ady12781	Plant full	509	28	82.4	34	6	ADA95203	Ada95203	Protein d
437	29	85.3	559	8	ADU19330	Adi19330	Chimeric	510	28	82.4	34	6	ADA95313	Ada95313	Protein d
438	29	85.3	570	2	AAU39451	Aay39451	Antibody	511	28	82.4	34	6	ADA95154	Ada95154	Protein d
439	29	85.3	577	6	ABU44557	Abu44557	Protein e	512	28	82.4	34	6	ADA95162	Ada95162	Protein d
440	29	85.3	579	2	AAU18301	Aaw18301	Photorehab	513	28	82.4	34	6	ADA95282	Ada95282	Protein d
441	29	85.3	579	2	AAU56574	Aaw56574	Toxin Tcd	514	28	82.4	34	6	ADA95225	Ada95225	Protein d
442	29	85.3	580	9	ABM97478	Abm97478	M. xanthus	515	28	82.4	34	6	ADA95259	Ada95259	Protein d
443	29	85.3	586	4	AAU92913	Aag92913	C. glutami	516	28	82.4	34	6	ADA95174	Ada95174	Protein d
444	29	85.3	596	4	AAU92913	Aag92913	C. glutami	517	28	82.4	34	6	ADA95274	Ada95274	Protein d
445	29	85.3	604	8	ADS28618	AdS28618	Bacterial	518	28	82.4	34	6	ADA95317	Ada95317	Protein d
446	29	85.3	608	6	ABU43152	Abu43152	Protein e	519	28	82.4	34	6	ADA95208	Ada95208	Protein d
447	29	85.3	608	6	ABU16289	Abu16289	Protein e	520	28	82.4	34	6	ADA95284	Ada95284	Protein d
448	29	85.3	611	6	ADU94628	Adw94628	Prolifera	521	28	82.4	34	6	ADA95300	Ada95300	Protein d
449	29	85.3	616	7	ADU05482	Adf05482	Protein e	522	28	82.4	34	6	ADA95215	Ada95215	Protein d
450	29	85.3	617	2	AAU15421	Aar15421	B. lautus	523	28	82.4	34	6	ADA95215	Ada95215	Protein d
451	29	85.3	620	4	AAU76514	Aab76514	Corynebacter	524	28	82.4	54	4	AAU33394	Aae11093	phAB fus
452	29	85.3	621	8	ADS24874	AdS24874	Bacterial	525	28	82.4	56	4	AAU33330	Abu33330	Eucalyptus
453	29	85.3	622	8	ADN25805	Adn25805	Bacterial	526	28	82.4	57	3	ABP33330	Abp33330	Eucalyptus
454	29	85.3	626	8	ADN17710	Adn17710	Bacterial	527	28	82.4	59	5	ABP09014	Abp09014	Human ORF
455	29	85.3	627	8	ADN22120	Adn22120	Bacterial	528	28	82.4	63	4	ABP01152	Abp01152	Human ORF
456	29	85.3	627	8	ADN24880	Adn24880	Bacterial	529	28	82.4	63	4	AAU21238	Aau21238	Human nov
457	29	85.3	628	6	ABU47429	Abu47429	Protein e	530	28	82.4	73	5	ABP39506	Abp39506	Staphylococcus
458	29	85.3	628	6	ADN18070	Adn18070	Bacterial	531	28	82.4	73	8	ADU05418	Adu05418	Staphylococcus
459	29	85.3	629	6	ABM68312	Abm68312	Photorehab	532	28	82.4	79	4	AAU5943	Aam5943	Human rep
460	29	85.3	669	3	AAU18267	Aab18267	Plasmodium	533	28	82.4	79	4	ABG596474	Abg596474	Human tes
461	29	85.3	673	8	ADY09638	Ady09638	Plant full	534	28	82.4	90	3	AAU57439	Aau57439	Arabidopsis
462	29	85.3	700	2	AAU13227	Aar13227	Novel end	535	28	82.4	92	4	AAU64955	Aau64955	Propionibacterium

536	28	82.4	92	6	ABM61474	Abm61474 Propionib	609	28	82.4	227	8	ADY10427	Ady10427 Plant ful
537	28	82.4	105	5	ABP07793	Abp07793 Human ORF	610	28	82.4	228	8	ADI43078	Adi43078 Plant tra
538	28	82.4	106	8	ADP22146	Adp22146 Human ant	611	28	82.4	228	8	ADO03222	Ado03222 Thalecres
539	28	82.4	106	8	ADP22150	Adp22150 Human ant	612	28	82.4	229	8	ABO01762	Ab001762 Soybean M
540	28	82.4	106	8	ADP22142	Adp22142 Human ant	613	28	82.4	229	8	ADJ77743	Adj77743 Soybean M
541	28	82.4	110	4	ABB71586	Abb71586 Drosophil	614	28	82.4	229	8	ADX74741	Adx74741 Plant ful
542	28	82.4	114	4	ABE013948	Abe013948 Human gen	615	28	82.4	232	8	ADX87958	Adx87958 Plant ful
543	28	82.4	114	6	ABR54977	AbR54977 Mouse Igg	616	28	82.4	232	8	ADX78815	Adx78815 Plant ful
544	28	82.4	114	9	ABP38680	Abp38680 L. pnoneor	617	28	82.4	232	8	ADO01763	Ado01763 Thalecres
545	28	82.4	117	6	ABP79598	Abp79598 N. gonor	618	28	82.4	234	8	ADJ77741	Adj77741 Soybean M
546	28	82.4	120	6	ABO01744	Ab001744 Maize Myb	619	28	82.4	235	6	ABO01761	Ab001761 Soybean M
547	28	82.4	120	8	ADJ77707	Adj77707 Corn Myb-	620	28	82.4	235	8	ADJ77741	Adj77741 Soybean M
548	28	82.4	123	4	AB63523	Ab63523 Human gas	621	28	82.4	236	8	ADX93414	Adx93414 Plant ful
549	28	82.4	130	3	AB33154	Ab33154 Eucalyptu	622	28	82.4	237	8	ADJ77779	Adj77779 Plant ful
550	28	82.4	133	7	ADC00550	Adc00550 Enterohae	623	28	82.4	237	8	AAU93061	Aau93061 Arabidops
551	28	82.4	135	2	RAY44004	Ray44004 Arabidops	624	28	82.4	238	5	ADD30031	Add30031 Plant yie
552	28	82.4	136	3	AG17993	Ag17993 Arabidops	625	28	82.4	238	8	ADI44105	Adi44105 Plant tra
553	28	82.4	136	4	ABG04672	Abg04672 Novel hum	626	28	82.4	238	8	ADI61441	Adi61441 A. thalia
554	28	82.4	136	6	ADA15579	Ada15579 A. thalia	627	28	82.4	238	8	ADO02415	Ado02415 Thalecres
555	28	82.4	136	8	ADO01713	Ado01713 Thalecres	628	28	82.4	247	7	ABM85657	Abm85657 Rice abio
556	28	82.4	139	8	ADX71535	Adx71535 Plant ful	629	28	82.4	248	8	ADX68932	Adx68932 Plant ful
557	28	82.4	140	8	ADX68934	Adx68934 Plant ful	630	28	82.4	252	8	ADX70764	Adx70764 Plant ful
558	28	82.4	145	6	ABO01750	Ab001750 Rice Myb-	631	28	82.4	252	8	ADX66591	Adx66591 Plant ful
559	28	82.4	145	8	ADJ77719	Adj77719 Rice Myb-	632	28	82.4	253	8	ADY23469	Ady23469 Plant ful
560	28	82.4	146	6	ABO01751	Ab001751 Rice Myb-	633	28	82.4	256	8	ADN73599	Adn73599 Thale cre
561	28	82.4	146	8	ADJ77721	Adj77721 Rice Myb-	634	28	82.4	257	3	AAG36350	Aag36350 Arabidops
562	28	82.4	148	8	ADS22993	Ads22993 Bacterial	635	28	82.4	258	7	ADD30312	Add30312 Plant yie
563	28	82.4	157	6	ABO01742	Ab001742 Maize Myb	636	28	82.4	258	8	ADI44233	Adi44233 Plant tra
564	28	82.4	157	8	ADJ77703	Adj77703 Corn Myb-	637	28	82.4	261	7	ADD30200	Add30200 Plant yie
565	28	82.4	166	8	ADX95421	Adx95421 Plant ful	638	28	82.4	261	8	ADI41801	Adi41801 Plant tra
566	28	82.4	167	8	ADX70781	Adx70781 Plant ful	639	28	82.4	262	9	AEA26693	Aea26693 Stress to
567	28	82.4	170	8	ADY24212	Ady24212 Plant ful	640	28	82.4	262	7	ADA47706	Ada47706 Rat Prote
568	28	82.4	170	8	ADX72870	Adx72870 Plant ful	641	28	82.4	262	8	ADA48839	Ada48839 Rat Prote
569	28	82.4	176	3	AAV77966	Aav77966 A. thalia	642	28	82.4	262	8	ADY10417	Ady10417 Plant ful
570	28	82.4	176	8	ADU92246	Adu92246 Thale cre	643	28	82.4	262	8	ADX92011	Adx92011 Plant ful
571	28	82.4	179	3	AAG22287	Aag22287 Arabidops	644	28	82.4	263	3	AAG36349	Aag36349 Arabidops
572	28	82.4	179	3	AG46272	Ag46272 Arabidops	645	28	82.4	264	8	ADX72304	Adx72304 Plant ful
573	28	82.4	179	3	AG46253	Ag46253 Arabidops	646	28	82.4	264	8	ADY74712	Ady74712 Plant ful
574	28	82.4	179	3	AG462052	Ag462052 Arabidops	647	28	82.4	269	2	AAW28052	Aaw28052 Amino aci
575	28	82.4	179	3	AG46271	Ag46271 Arabidops	648	28	82.4	269	3	AAG36348	Aag36348 Arabidops
576	28	82.4	179	6	ABO01743	Ab001743 Maize Myb	649	28	82.4	273	2	AAV05831	Aav05831 Arabidops
577	28	82.4	179	8	ADJ77705	Adj77705 Corn Myb-	650	28	82.4	273	7	ABO43112	Ab043112 A. thalia
578	28	82.4	180	8	ADI43101	Adi43101 Plant tra	651	28	82.4	273	8	ADO01749	Ado01749 Thalecres
579	28	82.4	188	3	AG17992	Ag17992 Arabidops	652	28	82.4	274	8	ADV86035	Adv86035 Lolium pe
580	28	82.4	189	8	ADX70880	Adx70880 Plant ful	653	28	82.4	276	8	ADI61465	Adi61465 A. thalia
581	28	82.4	190	9	ADW18316	Adw18316 Eucalyptu	654	28	82.4	276	8	ADO02251	Ado02251 Thalecres
582	28	82.4	192	6	ABO01766	Ab001766 Soybean M	655	28	82.4	281	9	ADW17381	Adw17381 Eucalyptu
583	28	82.4	192	8	ADJ77751	Adj77751 Soybean M	656	28	82.4	283	7	ADD30068	Add30068 Plant yie
584	28	82.4	192	8	ADX68821	Adx68821 Plant ful	657	28	82.4	283	8	ADI44443	Adi44443 Plant tra
585	28	82.4	196	6	ABO01763	Ab001763 Soybean M	658	28	82.4	285	7	ABM90050	Abm90050 Rice abio
586	28	82.4	196	8	ADJ77745	Adj77745 Soybean M	659	28	82.4	286	4	AAE01900	Aae01900 Arabidops
587	28	82.4	198	6	ABO01770	Ab001770 Bread whe	660	28	82.4	286	7	ABM86322	Abm86322 Rice abio
588	28	82.4	198	8	ADJ77759	Adj77759 Wheat Myb	661	28	82.4	286	8	ADI61453	Adi61453 A. thalia
589	28	82.4	204	6	ABO01757	Ab001757 Soybean M	662	28	82.4	286	8	ADO02433	Ado02433 Thalecres
590	28	82.4	204	6	ABU50486	Abu50486 Protein e	663	28	82.4	288	5	ABP38461	Abp38461 Staphyloc
591	28	82.4	204	8	ADJ77733	Adj77733 Soybean M	664	28	82.4	289	8	ADI43109	Adi43109 Plant tra
592	28	82.4	206	6	ABO01759	Ab001759 Soybean M	665	28	82.4	293	8	ADI43102	Adi43102 Plant tra
593	28	82.4	206	8	ADJ77737	Adj77737 Soybean M	666	28	82.4	298	4	AU33889	Au33889 Staphyloc
594	28	82.4	208	3	AB33295	Ab33295 Eucalyptu	667	28	82.4	298	6	ABU16021	Abu16021 Protein e
595	28	82.4	208	6	ABO01756	Ab001756 Soybean M	668	28	82.4	298	6	ABM73149	Abm73149 Staphyloc
596	28	82.4	208	8	ADJ77731	Adj77731 Soybean M	669	28	82.4	298	8	ADI43100	Adi43100 Plant tra
597	28	82.4	210	8	ADOS7658	Ados7658 Actinobac	670	28	82.4	298	9	ADW94694	Adw94694 Prolifera
598	28	82.4	211	8	ADX66022	Adx66022 Plant ful	671	28	82.4	303	8	ADT57578	Adt57578 Plant pol
599	28	82.4	214	9	ADY64944	Ady64944 S. mansoni	672	28	82.4	303	9	AEA49224	Aea49224 L. rhanno
600	28	82.4	216	7	ADD30164	Add30164 Plant yie	673	28	82.4	305	9	ADW17416	Adw17416 Eucalyptu
601	28	82.4	216	8	ADI44437	Adi44437 Plant tra	674	28	82.4	307	5	AAU93066	Aau93066 Arabidops
602	28	82.4	217	5	ABJ10413	Abj10413 Myb-relat	675	28	82.4	307	7	ADD30250	Add30250 Plant yie
603	28	82.4	217	8	ADH50110	Adh50110 Soybean M	676	28	82.4	307	7	ADJ77217	Adj77217 Plant yie
604	28	82.4	221	6	ABO01748	Ab001748 Rice Myb-	677	28	82.4	307	8	ADI41799	Adi41799 Plant tra
605	28	82.4	221	8	ADJ77715	Adj77715 Rice Myb-	678	28	82.4	308	7	ABO80638	Ab080638 Pseudomon
606	28	82.4	221	8	ADX70653	Adx70653 Plant ful	679	28	82.4	311	8	ADX72549	Adx72549 Plant ful
607	28	82.4	224	3	AB32870	Ab32870 Eucalyptu	680	28	82.4	312	6	ABO01765	Ab001765 Soybean M
608	28	82.4	226	5	ABP27694	Abp27694 Streptoco	681	28	82.4	312	8	ADJ77749	Adj77749 Soybean M

682	28	82.4	322	6	ABO011764	Abol1764 Soybean M	755	28	82.4	463	6	ABU43840	Protein e
683	28	82.4	322	8	ADJ77747	Adj77747 Soybean M	756	28	82.4	463	6	ABM70999	Staphyloc
684	28	82.4	323	8	AU931178	Auc931178 Arabidops	757	28	82.4	463	5	ADW94865	Prolifera
685	28	82.4	323	7	ADC35158	Adc35158 Arabidops	758	28	82.4	464	5	AAE23628	Staphyloc
686	28	82.4	323	8	AD143715	Adi43715 Plant tra	759	28	82.4	467	5	ABP23627	Lactococc
687	28	82.4	329	7	ABM90115	Abm90115 Rice abio	760	28	82.4	467	5	ABP38734	Staphyloc
688	28	82.4	329	7	ABM86418	Abm86418 Rice abio	761	28	82.4	467	8	ADS04719	Staphyloc
689	28	82.4	329	8	AD143103	Adi43103 Plant tra	762	28	82.4	468	6	ABU46827	Protein e
690	28	82.4	329	8	ADX68624	Adx68624 Plant ful	763	28	82.4	468	6	ABU46068	Protein e
691	28	82.4	335	8	ADP760285	Adt60285 Plant pol	764	28	82.4	468	8	ADR83959	S. pyogen
692	28	82.4	336	8	ADX70647	Adx70647 Plant ful	765	28	82.4	468	8	ADR83959	S. pyogen
693	28	82.4	336	8	ADX91472	Adx91472 Plant ful	766	28	82.4	468	8	ADR83959	S. pyogen
694	28	82.4	339	3	AGG22286	Aag22286 Arabidops	767	28	82.4	468	8	ADW87930	Streptoco
695	28	82.4	339	3	AGG22286	Aag22286 Arabidops	768	28	82.4	468	8	ADW87930	Streptoco
696	28	82.4	339	3	AGG22286	Aag22286 Arabidops	769	28	82.4	468	8	ADW87930	Streptoco
697	28	82.4	339	3	AGG22286	Aag22286 Arabidops	770	28	82.4	468	8	ADW87930	Streptoco
698	28	82.4	340	3	AGG22286	Aag22286 Arabidops	771	28	82.4	468	8	ADW87930	Streptoco
699	28	82.4	340	3	AGG22286	Aag22286 Arabidops	772	28	82.4	468	8	ADW87930	Streptoco
700	28	82.4	340	3	AGG22286	Aag22286 Arabidops	773	28	82.4	468	8	ADW87930	Streptoco
701	28	82.4	340	3	AGG22286	Aag22286 Arabidops	774	28	82.4	468	8	ADW87930	Streptoco
702	28	82.4	340	3	AGG22286	Aag22286 Arabidops	775	28	82.4	468	8	ADW87930	Streptoco
703	28	82.4	341	8	ADN74455	Adn74455 Thale cre	776	28	82.4	468	8	ADW87930	Streptoco
704	28	82.4	341	8	ADN74455	Adn74455 Thale cre	777	28	82.4	468	8	ADW87930	Streptoco
705	28	82.4	343	9	ADM17423	Adm17423 Eucalyptu	778	28	82.4	468	8	ADW87930	Streptoco
706	28	82.4	348	8	ADN18477	Adn18477 Bacterial	779	28	82.4	468	8	ADW87930	Streptoco
707	28	82.4	351	6	ABO011764	Abol1764 Soybean M	780	28	82.4	468	8	ADW87930	Streptoco
708	28	82.4	351	8	ADJ77711	Adj77711 Corn Myb-	781	28	82.4	468	8	ADW87930	Streptoco
709	28	82.4	354	8	ADS25975	Ads25975 Bacterial	782	28	82.4	468	8	ADW87930	Streptoco
710	28	82.4	354	8	ADS25975	Ads25975 Bacterial	783	28	82.4	468	8	ADW87930	Streptoco
711	28	82.4	357	6	ABU28999	Abu28999 Protein e	784	28	82.4	468	8	ADW87930	Streptoco
712	28	82.4	358	2	AAR71499	Aar71499 Human GLM	785	28	82.4	468	8	ADW87930	Streptoco
713	28	82.4	369	7	ADG60107	Adg60107 Rat Prote	786	28	82.4	468	8	ADW87930	Streptoco
714	28	82.4	369	7	ADG60107	Adg60107 Rat Prote	787	28	82.4	468	8	ADW87930	Streptoco
715	28	82.4	371	8	ADR67954	Adr67954 Human NF-	788	28	82.4	468	8	ADW87930	Streptoco
716	28	82.4	373	8	ADR67954	Adr67954 Human NF-	789	28	82.4	468	8	ADW87930	Streptoco
717	28	82.4	373	8	ADP54835	Adp54835 Human PRO	790	28	82.4	468	8	ADW87930	Streptoco
718	28	82.4	373	8	ADP54835	Adp54835 Human PRO	791	28	82.4	468	8	ADW87930	Streptoco
719	28	82.4	373	8	ADP54835	Adp54835 Human PRO	792	28	82.4	468	8	ADW87930	Streptoco
720	28	82.4	374	7	ADG60109	Adg60109 Human PRO	793	28	82.4	468	8	ADW87930	Streptoco
721	28	82.4	379	8	ABE67677	Abbe67677 Drosophil	794	28	82.4	468	8	ADW87930	Streptoco
722	28	82.4	383	8	ADY04631	Ady04631 Plant ful	795	28	82.4	468	8	ADW87930	Streptoco
723	28	82.4	395	4	AAU36131	Aau36131 Klebsiell	796	28	82.4	468	8	ADW87930	Streptoco
724	28	82.4	400	2	AAU36131	Aau36131 Klebsiell	797	28	82.4	468	8	ADW87930	Streptoco
725	28	82.4	402	4	ABG04674	Abg04674 Novel hum	798	28	82.4	468	8	ADW87930	Streptoco
726	28	82.4	403	7	ADG48730	Adg48730 Human PRO	799	28	82.4	468	8	ADW87930	Streptoco
727	28	82.4	403	7	ADN95149	Adn95149 Human BEC	800	28	82.4	468	8	ADW87930	Streptoco
728	28	82.4	403	7	ADN95149	Adn95149 Human BEC	801	28	82.4	468	8	ADW87930	Streptoco
729	28	82.4	403	9	ADP54615	Adp54615 Human PRO	802	28	82.4	468	8	ADW87930	Streptoco
730	28	82.4	403	9	ADP54615	Adp54615 Human PRO	803	28	82.4	468	8	ADW87930	Streptoco
731	28	82.4	403	9	ADY15694	Ady15694 PRO polyp	804	28	82.4	468	8	ADW87930	Streptoco
732	28	82.4	403	9	ADY16191	Ady16191 PRO polyp	805	28	82.4	468	8	ADW87930	Streptoco
733	28	82.4	403	9	ADY19858	Ady19858 PRO polyp	806	28	82.4	468	8	ADW87930	Streptoco
734	28	82.4	407	4	ABE65495	Abbe65495 Drosophil	807	28	82.4	468	8	ADW87930	Streptoco
735	28	82.4	408	7	ADC97365	Adc97365 E. faeciu	808	28	82.4	468	8	ADW87930	Streptoco
736	28	82.4	411	6	ABU33457	Abu33457 Protein e	809	28	82.4	468	8	ADW87930	Streptoco
737	28	82.4	415	4	AAE11161	Aae11161 phnAB fus	810	28	82.4	468	8	ADW87930	Streptoco
738	28	82.4	416	9	AAE11161	Aae11161 phnAB fus	811	28	82.4	468	8	ADW87930	Streptoco
739	28	82.4	429	4	AAE11086	Aae11086 Protein e	812	28	82.4	468	8	ADW87930	Streptoco
740	28	82.4	448	6	ADA33354	Ada33354 Acinetoba	813	28	82.4	468	8	ADW87930	Streptoco
741	28	82.4	449	6	ABU00144	Abu00144 Human nov	814	28	82.4	468	8	ADW87930	Streptoco
742	28	82.4	456	7	ADH87518	Adh87518 Enterococ	815	28	82.4	468	8	ADW87930	Streptoco
743	28	82.4	460	4	ABU60884	Abu60884 Drosophil	816	28	82.4	468	8	ADW87930	Streptoco
744	28	82.4	462	5	AAU34066	Aau34066 Staphyloc	817	28	82.4	468	8	ADW87930	Streptoco
745	28	82.4	462	5	AAU34066	Aau34066 Staphyloc	818	28	82.4	468	8	ADW87930	Streptoco
746	28	82.4	462	5	AAU34066	Aau34066 Staphyloc	819	28	82.4	468	8	ADW87930	Streptoco
747	28	82.4	462	5	AAU34066	Aau34066 Staphyloc	820	28	82.4	468	8	ADW87930	Streptoco
748	28	82.4	462	5	AAU34066	Aau34066 Staphyloc	821	28	82.4	468	8	ADW87930	Streptoco
749	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	822	28	82.4	468	8	ADW87930	Streptoco
750	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	823	28	82.4	468	8	ADW87930	Streptoco
751	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	824	28	82.4	468	8	ADW87930	Streptoco
752	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	825	28	82.4	468	8	ADW87930	Streptoco
753	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	826	28	82.4	468	8	ADW87930	Streptoco
754	28	82.4	463	3	AAU34066	Aau34066 Staphyloc	827	28	82.4	468	8	ADW87930	Streptoco

Abu43840	Protein e
Abm70999	Staphyloc
Adc94865	Prolifera
Aae23628	Staphyloc
Abp23627	Lactococc
Abp38734	Staphyloc
Adc04719	Staphyloc
Abu46827	Protein e
Abu46068	Protein e
Adr83959	S. pyogen
Adw87930	Streptoco
Adv79183	Streptoco
Adv81379	Streptoco
Abu43937	Protein e
Aau34131	Staphyloc
Aau36655	Staphyloc
Aag81994	S. epide
Abu43224	Protein e
Abu15963	Protein e
Abm73443	Staphyloc
Aau37684	Streptoco
Abu1608	S. pneumo
Adk47346	Streptoco
Aea60026	Streptoco
Aay38736	Neisseria
Aay38736	Neisseria
Aay38736	Neisseria
Aeb49296	N. mening
Aeb49299	N. mening
Aeb49299	N. mening
Abu44219	Protein e
Abu45166	Protein e
Adc07155	Staphyloc
Aau34926	Enterococ
Aau29306	Protein e
Aau38288	Salmonell
Abb49823	Listeria
Abb77748	Amino aci
Abu46974	Protein e
Abu31771	Protein e
Abu32733	Protein e
Abu28027	Protein e
Abu44476	Protein e
Abu48304	Protein e
Ads28100	Bacterial
Aau37777	Streptoco
Aau36887	Staphyloc
Aau34223	Staphyloc
Abb53724	Lactococc
Abb54802	Lactococc
Abu0652	S. pneumo
Abu45851	Protein e
Abu16061	Protein e
Abu49857	Protein e
Abm71983	Staphyloc
Ads29303	Bacterial
Aea49144	L. rhanno
Aay81555	Streptoco
Aau34695	E. coli c
Abu28750	Protein e
Ads44949	Bacterial
Ads45111	Bacterial
Abc62640	Klebsiell
Abc65454	Klebsiell
Adi67129	Lactobacil
Abu29629	Protein e
Abu25662	Protein e
Adk47531	Streptoco
Adc96088	E. faeciu
Adc95652	E. faeciu
Adc97269	E. faeciu
Adc95386	E. faeciu

828	28	82.4	510	8	ADR94513	Novel S.	901	28	82.4	2333	8	ADH71274	Human pro
829	28	82.4	510	9	Aea58317	Drosophila	902	28	82.4	2551	6	ABR58317	BCU0205A
830	28	82.4	523	4	ABR61274	Drosophila	903	28	82.4	2633	6	ABR58318	BCU0205B
831	28	82.4	523	8	ADO08099	Fly polyp	904	28	82.4	2662	4	ADH71218	Human pro
832	28	82.4	526	8	ADN46818	Thermococ	905	28	82.4	2724	4	AU080681	Human pro
833	28	82.4	533	5	ABR54368	Lactococ	906	28	82.4	2724	7	ADH32029	Human FCT
834	28	82.4	533	8	ADY12318	Plant ful	907	28	82.4	2724	8	ADH71252	Human pro
835	28	82.4	539	7	ADH47652	Human NOV	908	28	82.4	2725	5	ABG61913	Prostate
836	28	82.4	599	8	ADJ78922	Human NOV	909	28	82.4	2725	7	ADJ69881	Human hea
837	28	82.4	608	7	ADM05700	Human pro	910	28	82.4	2725	7	ADN39610	Cancer/an
838	28	82.4	616	4	AAU40216	Propionib	911	28	82.4	2725	8	ADQ21282	Human sof
839	28	82.4	616	6	ABM36735	Propionib	912	28	82.4	2725	8	ADU06625	Novel bro
840	28	82.4	627	6	ABO07272	Human p53	913	28	82.4	2733	4	AAU08680	Human FCT
841	28	82.4	627	6	ADO07984	Mouse pol	914	28	82.4	2733	7	ADH32024	Human FCT
842	28	82.4	638	5	ABR98349	Human ABC	915	28	82.4	2733	8	ADH71250	Human pro
843	28	82.4	646	5	AAE28964	Human ABC	916	28	82.4	2733	8	ADH71254	Human pro
844	28	82.4	646	5	AAE28968	Human ABC	917	28	82.4	2733	8	ADH71254	Human pro
845	28	82.4	646	5	ABR98348	Human ABC	918	28	82.4	2733	8	ADH71246	Human pro
846	28	82.4	646	5	AAO14186	Human tra	919	28	82.4	2733	8	ADH71246	Human pro
847	28	82.4	646	6	ABR99694	Amino aci	920	28	82.4	2733	8	ADH71258	Human pro
848	28	82.4	646	6	ABR99696	Amino aci	921	28	82.4	2758	5	ABG97359	Human NOV
849	28	82.4	646	8	ADO07982	Human pol	922	28	82.4	2759	5	ADH16608	Human NOV
850	28	82.4	649	8	ADS43648	Bacterial	923	28	82.4	2759	8	ADH71272	Human pro
851	28	82.4	661	8	ADH22557	Human tra	924	28	82.4	2764	5	ADJ16951	Murine NO
852	28	82.4	662	6	ABO07271	Human p53	925	28	82.4	2765	8	ADJ76262	Marker ge
853	28	82.4	666	5	ABR82647	Human Dev	926	28	82.4	2765	5	ADH16952	Rat NOVX
854	28	82.4	666	8	ADH71112	Mouse isc	927	28	82.4	2765	8	ADH71220	Human pro
855	28	82.4	666	8	ADO07983	Mouse pol	928	28	82.4	2769	7	ADH70388	Human TEN
856	28	82.4	671	7	ADH70231	C. neofo	929	28	82.4	2769	8	ADH74830	Murine NO
857	28	82.4	674	5	ABP52126	Homo sapi	930	28	82.4	2769	7	ADN42622	Human nov
858	28	82.4	674	7	ADP65268	Homo sapi	931	28	82.4	2775	7	ADH74842	Murine NO
859	28	82.4	674	8	ADU45479	Human ATP	932	28	82.4	2794	5	ABR98401	Human NOV
860	28	82.4	674	8	ADL61290	Human ATP	933	28	82.4	2802	5	ADH16953	Chicken N
861	28	82.4	674	8	ADN04060	Antipsori	934	27	79.4	22	2	AAE49635	Camel imm
862	28	82.4	674	8	ADO07981	Human pol	935	27	79.4	46	4	AAE84122	Human imm
863	28	82.4	674	8	ADP23732	PRO polyp	936	27	79.4	46	4	ABR17970	Human ner
864	28	82.4	674	9	ADY15356	PRO polyp	937	27	79.4	66	3	ABR33405	Pinus rad
865	28	82.4	685	7	ABO66464	Klebsiell	938	27	79.4	67	3	ABR33377	Pinus rad
866	28	82.4	730	7	ADJ70659	Human hea	939	27	79.4	67	3	ABR33407	Pinus rad
867	28	82.4	754	7	ABR66529	Ixodes sc	940	27	79.4	67	3	ABR33411	Pinus rad
868	28	82.4	777	4	ABR66529	Drosophila	941	27	79.4	67	3	ABR33345	Eucalyptu
869	28	82.4	805	5	ABR29962	Streptoco	942	27	79.4	67	3	ABR33413	Pinus rad
870	28	82.4	805	8	ADH39329	S. pyogen	943	27	79.4	67	3	ABR33390	Eucalyptu
871	28	82.4	812	8	ADH10735	Human the	944	27	79.4	72	5	ABG90981	Breast sp
872	28	82.4	828	5	ABP26754	Streptoco	945	27	79.4	84	9	AEA27425	Stress to
873	28	82.4	867	6	ABU41082	Protein e	946	27	79.4	84	9	AEA27426	Stress to
874	28	82.4	870	7	ADJ04483	Bacterial	947	27	79.4	84	9	AEA27429	Stress to
875	28	82.4	907	7	ADJ95405	Worm angi	948	27	79.4	84	9	AEA27427	Stress to
876	28	82.4	907	8	ADN24124	Bacterial	949	27	79.4	85	6	ABU41760	Protein e
877	28	82.4	910	7	ABR89812	Rice abio	950	27	79.4	99	3	ABR33156	Eucalyptu
878	28	82.4	913	8	ADH09465	Human pro	951	27	79.4	99	3	ABR33409	Pinus rad
879	28	82.4	921	6	AAE29914	Human tra	952	27	79.4	101	6	ABP73028	Human dig
880	28	82.4	927	7	ADJ71132	Human hea	953	27	79.4	101	6	ABP73021	Amino aci
881	28	82.4	935	4	AAW78589	Human pro	954	27	79.4	101	6	ABP71661	Amino aci
882	28	82.4	935	4	AAW00994	Human bon	955	27	79.4	101	7	ADJ75901	Carbohydr
883	28	82.4	994	8	ADH08940	Human pro	956	27	79.4	101	7	ADJ38295	A. cellul
884	28	82.4	1006	4	ABR60856	Drosophila	957	27	79.4	101	8	ADH36643	A. cellul
885	28	82.4	1015	4	AAW79679	Human pro	958	27	79.4	104	3	ABR32822	Eucalyptu
886	28	82.4	1081	8	ADN21336	Bacterial	959	27	79.4	113	3	ABR32818	Eucalyptu
887	28	82.4	1086	8	ADQ20350	Human sof	960	27	79.4	113	3	ABR33050	Pinus rad
888	28	82.4	1150	8	ADN23187	Bacterial	961	27	79.4	115	3	AAE12915	Arabidops
889	28	82.4	1162	4	ABG05052	Novel hum	962	27	79.4	119	3	ABR33033	Pinus rad
890	28	82.4	1169	8	ADH43878	Bacterial	963	27	79.4	120	5	ABJ10431	Myb-relat
891	28	82.4	1380	4	ABG02714	Novel hum	964	27	79.4	120	8	ADH50146	Wheat Myb
892	28	82.4	1462	7	ABR88208	Rice abio	965	27	79.4	122	3	ABG21226	Zea mays
893	28	82.4	1557	8	ADQ93323	Dictyocau	966	27	79.4	122	6	ABO01772	Bread whe
894	28	82.4	1557	8	ADQ93309	Dictyocau	967	27	79.4	122	8	ADJ77763	Wheat Myb
895	28	82.4	1592	7	ABR88402	Rice abio	968	27	79.4	123	3	ABR33264	Pinus rad
896	28	82.4	1688	6	ABR58344	XM 047995	969	27	79.4	124	3	ABR33267	Pinus rad
897	28	82.4	1737	7	ABR88597	RiCe abio	970	27	79.4	125	3	ABG32927	Zea mays
898	28	82.4	1737	8	ADK52107	Human ato	971	27	79.4	125	3	AAE44889	Zea mays
899	28	82.4	2136	4	AAW78695	Human pro	972	27	79.4	128	3	ABR33034	Pinus rad
900	28	82.4	2144	8	ADQ19484	Human sof	973	27	79.4	138	8	ADX72780	Plant ful

Fri May 12 11:16:48 2006

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974 27 79.4 139 3 AAB33036
975 27 79.4 144 3 AAB33305
976 27 79.4 145 3 AAG32926
977 27 79.4 146 3 AAB33155
978 27 79.4 146 3 AAB33260
979 27 79.4 148 3 AAB33044
980 27 79.4 149 5 ABJ10421
981 27 79.4 149 7 ABO62762
982 27 79.4 149 8 ADH50126
983 27 79.4 149 8 ADX68881
984 27 79.4 153 3 AAB32861
985 27 79.4 155 3 AAG12914
986 27 79.4 156 3 AAG44280
987 27 79.4 156 6 ABU39934
988 27 79.4 158 3 AAG44888
989 27 79.4 167 8 ADJ48762
990 27 79.4 168 3 AAB33290
991 27 79.4 171 3 AAB33246
992 27 79.4 173 8 ADX80220
993 27 79.4 176 3 AAB33283
994 27 79.4 176 3 AAG36520
995 27 79.4 178 3 AAG27843
996 27 79.4 180 7 ABM86159
997 27 79.4 180 8 ADJ84480
998 27 79.4 185 3 AAG27842
999 27 79.4 185 7 ADF07621
1000 27 79.4 187 3 AAB32794

Aab33036 Pinus rad
Aab33305 Pinus rad
Aag32926 Zea mays
Aab33155 Eucalyptu
Aab33260 Pinus rad
Aab33044 Pinus rad
Abj10421 Myb-relat
Aoc62762 Klebsiell
Adh50126 Soybean M
Adx68881 Plant ful
Aab32861 Eucalyptu
Aag12914 Arabidops
Aag44280 Arabidops
Abu39934 Protein e
Aag44888 Zea mays
Adj48762 Oil-assoc
Aab33290 Pinus rad
Aab33246 Eucalyptu
Adx80220 Plant ful
Aab33283 Pinus rad
Aag36520 Arabidops
Aag27843 Arabidops
Abm86159 Rice abio
Adj84480 Mouse T2R
Aag27842 Arabidops
Adf07621 Bacterial
Aab32794 Eucalyptu

ALIGNMENTS

RESULT 1
ID AAW23429 standard; peptide; 5 AA.
XX
AC AAW23429;
DT
DT 23-APR-1998 (first entry)
XX
DE CDR-1 of rW12 heavy chain.
XX
XX Antibody; complementarity determining region; CDR; heavy chain; rat; CEA;
KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
KW therapy; idiotype region.
XX
OS Rattus sp.
XX
XX WO9734636-A1.
XX
XX
XX
XX
XX 19-MAR-1997; 97WO-US004696.
XX
XX 20-MAR-1996; 96US-0013708P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX Leung S, Loeman MJ, Hansen H;
XX
XX WPI; 1997-479997/44.
XX
XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
XX antibodies- useful in detection of anti-CEA antibodies and as vaccine to
XX stimulate immune response against cancer.
XX
XX Claim 3; Page 30; 46pp; English.
XX
XX This sequence represents the complementarity determining region-1 (CDR-1)
XX of the rW12 heavy chain. This sequence is used in an antibody of the
XX invention. The antibody of the invention is a chimeric or humanised anti-
XX idiotype antibodies (cAb and hAb, respectively) or a fragment which
XX specifically binds to the idiotype region of an anti-carcinoembryonic

CC antigen (CEA), where: (i) cAb comprises the rW12 light (L) and heavy (H)
CC chain variable regions, or silent mutations; and (ii) hAb comprises rW12
CC complementarity determining regions (CDR) and humanised framework (FR)
CC regions. The hAb is used as a vaccine to stimulate an immune response in
CC a patient against cancers expressing CEA. The hAb, can be used to clear
CC non-targeted antibody in a method of diagnosis or treatment of a patient
CC where a CEA antibody is used as a (pre-)targeting or therapy agent. The
CC cAb is used to detect the presence of an antibody that specifically binds
CC to CEA in a sample
XX
XX Sequence 5 AA;
SQ
Query Match 100.0%; Score 34; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. NO. 2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
Qy 1 NYWNT 5
Db 1 NYWNT 5
RESULT 2
ADU81132
ID ADU81132 standard; peptide; 5 AA.
XX
AC ADU81132;
XX
DT 10-FEB-2005 (first entry)
XX
XX MAb 2E9-VH3 heavy chain CDR1.
XX
XX antibody; G14F7E5; G15B4G5; G19B9G7; variable; constant; region;
KW complementarity determining region; CDR; MAb; monoclonal;
KW capsular polysaccharide; glucuronoxylomannan; GXM;
KW Cryptococcus neoformans; VH 3-64; VH-6-1; Vh A27; infection.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004099251-A2.
XX
XX 18-NOV-2004.
XX
XX 06-MAY-2004; 2004WO-US014276.
XX
XX 06-MAY-2003; 2003US-0468475P.
XX
XX 30-MAY-2003; 2003US-0474530P.
XX
XX 23-MAR-2004; 2004US-0555540P.
XX
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE MEDICINE.
XX
XX Pirofski L, Maitta RW;
XX
XX WPI; 2004-814048/80.
XX
XX New human monoclonal antibody specifically binding the capsular
XX polysaccharide glucuronoxylomannan (GXM) of Cryptococcus neoformans,
XX useful for treating or diagnosing cryptococcal infections.
XX
XX Example 4; Fig 3; 56pp; English.
XX
XX This sequence represents a complementarity determining region (CDR) which
XX was used in the generation of the monoclonal antibody (MAb) of the
XX invention. The MAb of the invention or its antigen-binding portion
XX specifically binds the capsular polysaccharide glucuronoxylomannan (GXM)
XX of Cryptococcus neoformans and comprises a heavy and/or light chain amino
XX acid sequence having CDR1, CDR2 and CDR3 amino sequences of a human VH 3-
XX 64 or VH-6-1 gene, or human Vh A27 gene, respectively, with or without a
XX signal sequence, where the sequence have up to 6 mutations from the
XX germline gene sequence. The MAb of the invention may be used for
XX detection, prevention and/or treatment of C. neoformans infection.
XX
XX Sequence 5 AA;
SQ
```


XX
DT 23-APR-1998 (first entry)XX
DT 23-APR-1998 (first entry)

DT 23-

DE Modified heavy chain variable region KOLWI2VH-1.
 XX Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.
 XX
 OS Synthetic.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "D to G mutation"
 FT Misc-difference 11 /note= "L to V mutation"
 FT Misc-difference 19 /note= "K to R mutation"
 FT Misc-difference 23 /note= "V to S mutation"
 FT Misc-difference 24 /note= "A to S mutation"
 FT Region 31..35
 FT /note= "complementarity determining region-1"
 FT Misc-difference 43 /note= "E to K mutation"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Misc-difference 77 /note= "S to N mutation"
 FT Misc-difference 80 /note= "Y to F mutation"
 FT Misc-difference 84 /note= "N to D mutation"
 FT Misc-difference 92 /note= "A to G mutation"
 FT Misc-difference 93 /note= "T to V mutation"
 FT Region 99..111
 FT /note= "complementarity determining region-3"
 FT Misc-difference 116 /note= "S to T mutation"
 FT Misc-difference 117 /note= "S to P mutation"
 FT
 FT WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX Claim 7; Fig 1; 46pp; English.
 XX
 XX This sequence represents a modified version of the rat rW12 heavy chain
 CC variable region, designated KOLWI2VH-1. This sequence is used in an
 CC antibody of the invention. The antibody of the invention is a chimeric or
 CC humanised anti-idiotype antibodies (cAb and hAb, respectively) or a
 CC fragment which specifically binds to the idiotype region of an anti-
 CC carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light
 CC (L) and heavy (H) chain variable regions, or silent mutations; and (ii)
 CC hAb comprises rW12 complementarity determining regions (CDR) and
 CC humanised framework (FR) regions. The hAb is used as a vaccine to
 CC stimulate an immune response in a patient against cancers expressing CEA.

CC The hAb, can be used to clear non-targeted antibody in a method of
 CC diagnosis or treatment of a patient where a CEA antibody is used as a
 CC (pre-)targeting or therapy agent. The cAb is used to detect the presence
 CC of an antibody that specifically binds to CEA in a sample
 XX
 SQ Sequence 122 AA;
 Query Match 100.0%; Score 34; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 1 NYWMT 5
 Db 31 NYWMT 35
 ID AAW23441 standard; protein; 122 AA.
 XX AC AAW23441;
 XX 23-APR-1998 (first entry)
 XX hW12 heavy chain.
 XX Antibody; complementarity determining region; heavy chain; human; CEA;
 KW hW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Region 31..35
 FT /note= "complementarity determining region-1"
 FT Region 50..66
 FT /note= "complementarity determining region-2"
 FT Region 99..111
 FT /note= "complementarity determining region-3"
 FT
 FT WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86299.
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX Disclosure; Fig 3; 46pp; English.
 XX
 XX This sequence represents the human hW12 heavy chain. This sequence is
 CC used in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotype antibodies (cAb and hAb, idiotype
 CC respectively) or a fragment which specifically binds to the CEA
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb
 CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cAb is used to detect the

CC presence of an antibody that specifically binds to CEA in a sample

XX Sequence 122 AA;

SO Query Match 100.0%; Score 34; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||||

Db 31 NYWMT 35

RESULT 7

AAW23438

ID AAW23438 standard; protein; 122 AA.

XX AC AAW23438;

XX DT 23-APR-1998 (first entry)

XX DE Modified heavy chain variable region KOLW12VH-2.

XX KW Antibody; complementarity determining region; heavy chain; rat; CEA;
 rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.

XX OS Synthetic.

OS Rattus sp.

XX PH Key Location/Qualifiers

FT Misc-difference 5 /note= "Q to V mutation"

FT Misc-difference 10 /note= "D to G mutation"

FT Misc-difference 11 /note= "L to V mutation"

FT Misc-difference 19 /note= "K to R mutation"

FT Misc-difference 23 /note= "V to S mutation"

FT Misc-difference 24 /note= "A to S mutation"

FT Region 31..35

FT Misc-difference 43 /note= "complementarity determining region-1"

FT Region 50..66 /note= "B to K mutation"

FT Misc-difference 77 /note= "complementarity determining region-2"

FT Misc-difference 80 /note= "S to N mutation"

FT Misc-difference 84 /note= "Y to F mutation"

FT Misc-difference 92 /note= "N to D mutation"

FT Misc-difference 93 /note= "A to G mutation"

FT Region 99..111 /note= "T to V mutation"

FT Misc-difference 116 /note= "complementarity determining region-3"

FT Misc-difference 117 /note= "S to T mutation"

FT /note= "S to P mutation"

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Loeman MJ, Hansen H;

XX WPI; 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 stimulate immune response against cancer.

XX Claim 7; Fig 1; 46pp; English.

XX This sequence represents a modified version of the rat rW12 heavy chain
 variable region, designated KOLW12VH-2. This sequence is used in an
 antibody of the invention. The antibody of the invention is a chimeric or
 humanised anti-idiotype antibodies (cAb and hAb, respectively) or a
 fragment which specifically binds to the idiotype region of an anti-
 carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light
 (L) and heavy (H) chain variable regions, or silent mutations; and (ii)
 hAb comprises rW12 complementarity determining regions (CDR) and
 humanised framework (FR) regions. The hAb is used as a vaccine to
 stimulate an immune response in a patient against cancers expressing CEA.
 The hAb, can be used to clear non-targeted antibody in a method of
 diagnosis or treatment of a patient where a CEA antibody is used as a
 (pre-)targeting or therapy agent. The cAb is used to detect the presence
 of an antibody that specifically binds to CEA in a sample

XX Sequence 122 AA;

Qy 1 NYWMT 5
 |||||

Db 31 NYWMT 35

RESULT 8

ID AAU76696 standard; protein; 151 AA.

XX AAU76696;

XX 21-MAY-2002 (first entry)

XX Mouse heavy chain variable domain region of PSCA antibody 2H9 protein.

XX Mouse; prostate stem cell antigen; PSCA; antibody; immunogen;
 KW prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;
 KW PSCA-associated cancer; heavy chain variable domain region; PSCA antigen;
 XX PSCA antibody 2H9.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 45..54 /note= "Complementarity determining region 1 (CDR1)"

FT Region 69..87 /note= "Complementarity determining region 2 (CDR2)"

FT Region 120..125 /note= "Complementarity determining region 3 (CDR3)"

XX US2001055751-A1.

XX 27-DEC-2001.

XX 03-MAY-2000; 2000US-00564329.

XX 10-MAR-1997; 97US-0228816P.

XX 12-JAN-1998; 98US-0071141P.

XX 13-FEB-1998; 98US-0074675P.

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PR 10-MAR-1998; 98US-00038261.
PR 02-DEC-1998; 98US-00203939.
PR 21-DEC-1998; 98US-01132308.
PR 17-FEB-1999; 98US-00251835.
PR 17-FEB-1999; 98US-0120536P.
PR 16-MAR-1999; 98US-0124658P.
PR 25-MAY-1999; 98US-00318503.
PR 20-JUL-1999; 98US-00359326.
XX (REIT/) REITER R E.
PA (WITT/) WITTE O N.
PA (SAFF/) SAFFRAN D C.
PA (JAKO/) JAKOBOVITS A.
XX
PI Reiter RE, Witte ON, Saffran DC, Jakobovits A;
XX
XX WPI; 2001-159478/16.
DR N-PSDB; ABK09984.
XX
XX Antibodies binding to prostate stem cell antigen inhibit the growth of
PT cancer cells and are used to detect and treat prostate, pancreatic or
PT bladder cancers.
XX
XX Example 21; Fig 60; 127pp; English.
XX
XX The present invention relates to new antibodies that specifically bind a
CC novel prostate stem cell antigen (PSCA), which is widely over-expressed
CC across all stages of prostate cancer. The antibodies of the invention are
CC useful to kill tumour cells expressing PSCA and as PSCA expression is
CC observed in prostate tumour cells and in other human cancers,
CC particularly bladder and pancreatic carcinomas, the antibodies are useful
CC therapeutically to treat these diseases. In particular, monoclonal
CC antibodies can be administered to subjects suffering from PSCA-associated
CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic
CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong
CC the subject's life. The antibodies can be combined with a therapeutic
CC agent in immunoconjugates useful to treat subjects suffering from
CC malignant diseases, characterised by cells having PSCA antigen on the
CC cell surface e.g. cancers, by killing the cells. The antibodies and
CC immunoconjugates may also be included with a carrier in pharmaceutical
CC compositions useful to kill human cells expressing PSCA antigen on the
CC cell surface. The antibodies are also useful diagnostically to detect
CC cancers, especially prostate cancer, to isolate prostate cancer cells
CC e.g. to enable culture growth to evaluate candidate therapeutic
CC compounds, assist in identification of rare genes associated with
CC prostate cancer, and to isolate and purify PSCA and PSCA homologues. The
CC present amino acid sequence represents the mouse heavy chain variable
CC domain region of the PSCA monoclonal antibody 2H9 of the invention
XX
XX Sequence 151 AA;
XX
XX Query Match 100.0%; Score 34; DB 4; Length 151;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NYWMT 5
XX |||||
XX Db 50 NYWMT 54
XX
XX RESULT 9
XX AAB35292
XX ID AAB35292 standard; protein; 151 AA.
XX
XX AC AAB35292;
XX
XX DT 08-MAY-2001 (first entry)
XX
XX DE Murine PSCA antibody 2H9 H chain V region.
XX
XX KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
XX diagnosis; treatment; chromosome 8q24.2.
XX
XX
XX Mus sp.
XX WO200105427-A1.
XX
XX PD 25-JAN-2001.
XX
XX PF 20-JUL-2000; 2000WO-US019967.
XX
XX PR 20-JUL-1999; 99US-00359326.
XX PR 03-MAY-2000; 2000US-00564329.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (UROC-) UROGENESYS.
XX
XX PI Reiter R, Witte O, Saffran DC, Jakobovits A;
XX
XX WPI; 2001-159478/16.
DR N-PSDB; AAP27975.
XX
XX Antibodies binding to prostate stem cell antigen inhibit the growth of
PT cancer cells and are used to detect and treat prostate, pancreatic or
PT bladder cancers.
XX
XX Example 21; Fig 60; 229pp; English.
XX
XX The present invention describes a method of treating cancer associated
CC with prostate stem cell antigen (PSCA) by administering an antibody which
CC selectively binds to PSCA and inhibits the growth of the cancer cells.
CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
CC the human and murine PSCA protein and coding sequences, which can be used
CC not only in the treatment of, but also in detection and prognosis of
CC prostate cancer
XX
XX Sequence 151 AA;
XX
XX Query Match 100.0%; Score 34; DB 4; Length 151;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NYWMT 5
XX |||||
XX Db 50 NYWMT 54
XX
XX RESULT 10
XX ABP44963
XX ID ABP44963 standard; protein; 249 AA.
XX
XX AC ABP44963;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human BlyS binding scFv SEQ ID 974.
XX
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX PD 10-JAN-2002.
XX
XX PF 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.

```

PR 25-MAY-2001; 2001US-0293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI; 2002-114799/15.
 XX
 DR
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 1564-1565; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 249 AA;
 Query Match 100.0%; Score 34; DB 5; Length 249;
 Best Local Similarity 100.0%; Pred. NO. 4.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NYWMT 5
 Db 31 NYWMT 35
 |||||
 RESULT 11
 ADG95790
 ID ADG95790 standard; protein; 249 AA.
 XX
 AC ADG95790;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds Blys SeqID 974.
 XX
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 XX WO2003055979-A2.
 PN
 XX
 XX 10-JUL-2003.
 PD
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 XX 16-NOV-2001; 2001US-0331469P.
 XX
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 PI

XX WPI; 2003-505530/47.
 DR
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 XX Example 1; SEQ ID NO 974; 394pp; English.
 PS
 XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiasthmatic, antiallergic and cytostatic.
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 249 AA;
 Query Match 100.0%; Score 34; DB 7; Length 249;
 Best Local Similarity 100.0%; Pred. NO. 4.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NYWMT 5
 Db 31 NYWMT 35
 |||||
 RESULT 12
 ADH87596
 ID ADH87596 standard; protein; 489 AA.
 XX
 AC ADH87596;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Enterococcus faecalis polypeptide #2076.
 XX
 KW Enterococcus faecalis infection; transcription regulatory element;
 KW antibacterial.
 XX
 OS Enterococcus faecalis.
 XX
 XX US6617156-B1.
 PN
 XX
 XX 09-SEP-2003.
 PD
 XX
 XX 13-AUG-1998; 98US-00134000.
 PF
 XX
 PR 15-AUG-1997; 97US-0055778P.
 XX
 XX (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 XX
 XX Doucette-Stamm LA, Bush D;
 PI
 XX WPI; 2003-895394/82.
 DR N-PSDB; ADH84191.
 DR

XX New nucleic acid comprising a sequence encoding an *Enterococcus faecalis*
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating *E. faecalis* infection.
XX
PS Disclosure; SEQ ID NO 5481; 193pp; English.
XX
CC The invention relates to *Enterococcus faecalis* polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an *E. faecalis* polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of *E. faecalis* in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating *Enterococcus faecalis* infection. This sequence
CC represents an *E. faecalis* polypeptide of the invention.
XX
SQ Sequence 489 AA;

Query Match 100.0%; Score 34; DB 7; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||||
Db 185 NYWMT 189

RESULT 13
ABB92290
ID ABB92290 standard; protein; 1314 AA.
XX AC ABB92290;
XX
XX 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 1501.
XX
XX Herbicidal; plant; agriculture; herbicide.
XX
XX Arabidopsis thaliana.
XX
XX WO200210210-A2.
XX
XX 07-FEB-2002.
XX
XX 28-AUG-2001; 2001WO-EP009892.
XX
XX 28-AUG-2001; 2001WO-EP009892.
XX
XX (PARB) BAYER AG.
XX
XX Tietjen K, Weidler M;
XX
XX WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
XX Claim 5; SEQ ID NO 1501; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as

CC herbicides
XX
SQ Sequence 1314 AA;

Query Match 100.0%; Score 34; DB 5; Length 1314;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||||
Db 766 NYWMT 770

RESULT 14
AAU62804
ID AAU62804 standard; protein; 226 AA.
XX AC AAU62804;
XX
XX 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #23700.
DE
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

XX 02-JUN-2000; 2000US-0208841P.

XX 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX N-PSDB; AASS9629.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX

XX Example 1; SEQ ID NO 23999; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent *Propionibacterium acnes* immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC *P. acnes*. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC *P. acnes* is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of *P. acnes* in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for *P. acnes* proteins. These antibodies can be used to
CC downregulate expression and activity of *P. acnes* polypeptides and
CC therefore treat *P. acnes* infections. The antibodies may also be used as
CC diagnostic agents for determining *P. acnes* presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 226 AA;

Query Match 91.2%; Score 31; DB 4; Length 226;

Best Local Similarity 80.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

DB 179 NYWLT 183

RESULT 15

ABMS9323
ID ABMS9323 standard; protein; 226 AA.

XX AC ABMS9323;

XX DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #23999.

XX KW Acne vulgaris; antiacne; dermatological; antibacterial;

XX KW immunostimulant; immune response; vaccine.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

XX PI Barth B, Vallie-Douglass J;

XX DR WPI; 2003-381789/36.

XX DR N-PSDB; ACF64558.

XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.

PS Example 1; SEQ ID NO 23999; 1481pp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABMS5624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present

CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 226 AA;

Query Match 91.2%; Score 31; DB 6; Length 226;

Best Local Similarity 80.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

DB 179 NYWLT 183

RESULT 16

ABU35375
ID ABU35375 standard; protein; 233 AA.

XX AC ABU35375;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #20902.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Moraxella catarrhalis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH,

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA39245.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 63299; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 233 AA;

Query Match 91.2%; Score 31; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 122 NYWLT 126

RESULT 17

ADL05135
ID ADL05135 standard; protein; 241 AA.

AC ADL05135;

DT 06-MAY-2004 (first entry)

DE M. catarrhalis protein #901.

XX Moraxella catarrhalis; infection.

XX Moraxella catarrhalis.

XX US6673910-B1.

XX 06-JAN-2004.

XX 04-APR-2000; 2000US-00540236.

XX 08-APR-1999; 99US-0128416P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL;

XX WPI; 2004-178127/17.

XX N-PSDB; ADL03215.

XX New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for
XX preparing a composition for diagnosing, preventing or treating infection
XX caused by Moraxella catarrhalis.

XX Disclosure; SEQ ID NO 2821; 429pp; English.

XX The invention relates to an isolated nucleic acid encoding an Moraxella
XX catarrhalis polypeptide. The nucleic acid is useful for preparing a
XX composition for diagnosing, preventing or treating infection caused by
XX Moraxella catarrhalis. The present sequence represents the amino acid
XX sequence of a M. catarrhalis protein.

XX Sequence 241 AA;

Query Match 91.2%; Score 31; DB 8; Length 241;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 130 NYWLT 134

RESULT 18

ID ABP73979 standard; protein; 454 AA.

XX AC ABP73979;

XX 30-JAN-2003 (first entry)

XX Candida albicans essential protein SEQ ID NO 7816.

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX signal transduction; DNA replication; cell division; growth;
XX proliferation; Candida albicans; fungicide; antifungal.

XX Candida albicans.

XX WO200253728-A2.

XX 11-JUL-2002.

XX 26-DEC-2001; 2001WO-US049486.

XX 29-DEC-2000; 2000US-0259128P.

XX 20-FEB-2001; 2001US-00792024.

XX 22-AUG-2001; 2001US-0314050P.

XX (ELIT-) ELITRA PHARM INC.

XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX WPI; 2002-566694/60.

XX N-PSDB; AB232529.

XX Constructing strains for identifying gene products as effective targets
XX for therapeutic intervention, by inactivating in the strain one allele of
XX a gene and placing other allele of the gene under conditional expression.

XX Claim 44; SEQ ID NO 7816; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of *C. albicans* cells and for
XX treating infection by *C. albicans*. The present sequence is that of an
XX essential Candida albicans protein used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office

XX Sequence 454 AA;

Query Match 91.2%; Score 31; DB 5; Length 454;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYWMT 5
 |||:|
 Db 136 NYWLT 140

RESULT 19
 ABU39334
 ID ABU39334 standard; protein; 489 AA.
 XX
 AC ABU39334;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #24861.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pasteurella multocida.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA43204.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 67258; 1766pp; English.
 XX

The invention relates to an isolated nucleic acid comprising any one of
 the 6213 antisense sequences given in the specification where expression
 of the nucleic acid inhibits proliferation of a cell. Also included are:
 (1) a vector comprising a promoter operably linked to the nucleic acid
 encoding a polypeptide whose expression is inhibited by the antisense
 nucleic acid; (2) a host cell containing the vector; (3) an isolated
 polypeptide or its fragment whose expression is inhibited by the
 antisense nucleic acid; (4) an antibody capable of specifically binding
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 proliferation or the activity of a gene in an operon required for
 proliferation; (7) identifying a compound that influences the activity of
 the gene product or that has an activity against a biological pathway
 required for proliferation, or that inhibits cellular proliferation; (8)
 identifying a gene required for cellular proliferation or the biological
 pathway in which a proliferation-required gene or its gene product lies
 or a gene on which the test compound that inhibits proliferation of an
 organism acts; (9) manufacturing an antibiotic; (10) profiling a
 compound's activity; (11) a culture comprising strains in which the gene
 product is overexpressed or underexpressed; (12) determining the extent
 to which each of the strains is present in a culture or collection of
 strains; or (13) identifying the target of a compound that inhibits the
 proliferation of an organism. The antisense nucleic acids are useful for
 identifying proteins or screening for homologous nucleic acids required
 for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 489 AA;
 Query Match 91.2%; Score 31; DB 6; Length 489;
 Best Local Similarity 80.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYWMT 5
 |||:|
 Db 163 NYWLT 167

RESULT 20
 ABM68236
 ID ABM68236 standard; protein; 504 AA.
 XX
 AC ABM68236;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Photorhabdus luminescens protein sequence #1333.
 XX
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough.
 XX
 OS Photorhabdus luminescens.
 XX
 PN WO200294867-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 07-FEB-2002; 2002WO-IB003040.
 XX
 PR 07-FEB-2001; 2001FR-00001659.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;
 XX
 DR WPI; 2003-148459/14.
 XX
 PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 1333; 1205pp; French.
 XX

The invention relates to the isolation of genes and their encoded
 proteins from Photorhabdus luminescens. The isolated sequences are
 sources of probes and primers for detecting the genome of *P. luminescens*
 and related species; to study polymorphisms; for gene analysis and for
 detection/amplification of the genes. Antibodies (Ab) raised against the
 polypeptides encoded by the genes are used for detection/identification
 of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that
 carry a gene-containing vector are used to select compounds that
 modulate, regulate, induce or inhibit expression of the genes in plants,
 animals or microorganisms other than *P. luminescens* and are able to alter
 response or sensitivity to toxins and antibiotics produced by *P.*
luminescens. Cells transformed to express the genes are useful for
 recombinant production of the proteins, particularly toxins and
 antibacterials useful as insecticides, bactericides and fungicides. The
 genes, proteins, vectors containing the genes and Ab are also useful
 therapeutically (to treat microbial infection by bacteria or fungi that

are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins

Sequence 504 AA;

Query Match 91.2%; Score 31; DB 6; Length 504;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||:|
 Db 165 NYWLT 169

RESULT 21
 ABU30485
 ID ABU30485 standard; protein; 511 AA.
 XX
 AC ABU30485;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #16012.
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Haemophilus influenzae.
 OS WO200277183-A2.
 PN 03-OCT-2002.
 PD
 XX 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 08-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-0299926/02.
 DR N-PSDB; ACA34355.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 PT
 PS Claim 25; SEQ ID NO 58409; 1766pp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 511 AA;

Query Match 91.2%; Score 31; DB 6; Length 511;
 Best Local Similarity 80.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||:|
 Db 185 NYWLT 189

RESULT 22
 AEB41540
 ID AEB41540 standard; protein; 520 AA.
 XX
 AC AEB41540;
 DT 08-SEP-2005 (first entry)
 DE L. pneumophila protein SEQ ID NO 5872.
 XX
 XX detection; infection; Antibacterial; Vaccine.
 KW Legionella pneumophila.
 OS WO2005049642-A2.
 PN 02-JUN-2005.
 PD
 XX 23-SEP-2004; 2004WO-IB003578.
 XX 21-NOV-2003; 2003FR-00013687.
 XX (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (JULY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Rueniock C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;
 XX WPI; 2005-388305/40.
 DR
 XX New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the strain and for treatment and prevention of infections.
 PT
 PT Claim 3; SEQ ID NO 5872; 660pp; English.
 PS
 XX The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of

CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 CC
 SQ Sequence 520 AA;

Query Match 91.2%; Score 31; DB 9; Length 520;
 Best Local Similarity 80.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 34 NYWLT 38

RESULT 23

ABE38256
 ID AEB38256 standard; protein; 525 AA.

XX AEB38256;

DT 08-SEP-2005 (first entry)

DE L. pneumophila protein SEQ ID NO 2588.

XX detection; infection; Antibacterial; Vaccine.

OS Legionella pneumophila.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UYLY-) UNIV LYON I BERNARD CLAUDE.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandeneesch F;
 PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 2588; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)
 CC from Legionella pneumophila Paris strain (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 CC
 SQ Sequence 525 AA;

Query Match 91.2%; Score 31; DB 9; Length 525;
 Best Local Similarity 80.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 39 NYWLT 43

RESULT 24

ABB72015
 ID ABB72015 standard; protein; 539 AA.

XX ABB72015;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 42837.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL16118.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 42837; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABE57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 539 AA;

Query Match 91.2%; Score 31; DB 4; Length 539;
 Best Local Similarity 80.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 531 NYWLT 535

RESULT 25

AAW90977
 ID AAW90977 standard; protein; 762 AA.

XX AAW90977;

XX DT 21-JUL-2000 (first entry)

XX DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan protein.

XX DE Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;

KW transgenic plant; flavor; perfume; packaging material; papermaking;

KW ultra-violet light adsorber; starch; textile; wetting agent.

XX OS Neisseria denitrificans.

XX WO200022140-A1.

XX PD 20-APR-2000.

XX PF 08-OCT-1999; 99WO-EP007562.

XX PR 09-OCT-1998; 98DE-01046635.

XX PR 27-MAY-1999; 99DE-01024342.

XX (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Buettcher V, Quanz M;

XX WPI; 2000-317992/27.

DR N-PSDB; AAL1731.

XX New nucleic acid encoding a branching enzyme, useful for in vitro

PT synthesis of branched glucans and to prepare transgenic plants producing

PT modified starch.

XX Claim 1a; Page 96-99; 115pp; German.

XX This invention describes a novel nucleic acid (I) isolated from Neisseria

CC which encodes a branching enzyme (II). (I) is used for recombinant

CC production of (II) subsequently used in the in vitro production of alpha-

CC 1,6-branched alpha-1,4-glucans. It is also used to prepare transgenic

CC plants that produce starches with modified properties. (III) are used as

CC binders for tablets, carriers for pharmaceuticals, flavors and perfumes

CC and powdered additives, packaging materials, ultra-violet light adsorbers

CC in sunscreens and also for any of the usual applications of starch in

CC foods, papermaking, as textile size, in soil stabilization, as wetting

CC agent for agricultural chemicals, as polymer additives etc. Fragments of

CC (I) are useful as PCR primers and antisense molecules or ribozymes for

CC inhibiting expression of (II), and the regulatory region of (II) can be

CC used to control expression of heterologous sequences in host cells. (I)

CC provides an inexpensive method for producing alpha-1,6-branched alpha-1,4

CC -glucans (III), producing products that can be tailored for particular

CC applications, particularly by controlling the degree of branching. Starch

CC from transgenic plants has increased gel strength, reduced phosphate

CC content; reduced peak viscosity; lower pasting temperature and granule

CC size and/or altered sidechain distribution. This sequence represents an

CC alpha-1,6-branched alpha-1,4-glucan isolated from Neisseria denitrificans

CC which is described in the method of the invention

XX Sequence 762 AA;

Query Match 91.2%; Score 31; DB 3; Length 762;

Best Local Similarity 80.0%; Pred. No. 4.5e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5

Db 272 NYWLT 276

RESULT 26

ADA55068

ID ADA55068 standard; protein; 781 AA.

XX AC ADA55068;

XX

DT 20-NOV-2003 (first entry)

XX DE Human protein, SEQ ID 2636.

XX KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

KW Gene Therapy; human; secretory protein; membrane proteins; cancer;

KW inflammatory disease; osteoporosis; neurological disease.

XX OS Homo sapiens.

XX EP1293569-A2.

XX PD 19-MAR-2003.

XX PF 21-MAR-2002; 2002EP-00006586.

XX PR 14-SEP-2001; 2001JP-00328381.

XX PR 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-395539/38.

DR N-PSDB; ADA53429.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory

PT and/or membrane proteins, useful for developing medicines for diseases in

PT which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 2636; 205pp; English.

XX The present invention relates to novel human secretory or membrane

CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

CC ADA54071). The coding sequences are useful in the gene therapy of

CC diseases caused by abnormalities of the proteins, e.g. cancer,

CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 781 AA;

Query Match 91.2%; Score 31; DB 6; Length 781;

Best Local Similarity 80.0%; Pred. No. 4.8e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5

Db 372 NYWLT 376

RESULT 27

AAO19309

ID AAO19309 standard; protein; 789 AA.

XX AC AAO19309;

XX 02-DEC-2002 (first entry)

XX DE Human chloride channel protein related protein SEQ ID NO: 14.

XX KW Human; endocytosis; ectocytosis; neurology; neurological disease; osteopathic;

KW cytosolic; neuroleptic; neuromuscular disease; chloride channel protein;

KW CIC-3; CIC-4; CIC-6; CIC-7; osteoporosis; Paget's disease; inhibitor;

KW psychopharmaceutical.

XX OS Homo sapiens.

XX DE10102977-A1.

XX PD 01-AUG-2002.

XX

CC including use in gene therapy. The same materials can also be used for
 CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
 CC present sequence is that of a polypeptide of the invention

XX SQ Sequence 803 AA;

Query Match 91.2%; Score 31; DB 5; Length 803;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 394 NYWLT 398

RESULT 30
 AAO19308
 ID AAO19308 standard; protein; 803 AA.

XX AC AAO19308;
 DT 02-DEC-2002 (first entry)

XX DE Rat chloride channel protein related protein SEQ ID NO: 12.

XX KW Rat; endocytosis; ectocytosis; neurological disease; osteopathic;
 KW cytosatic; neuroleptic; neuromuscular disease; chloride channel protein;
 KW CIC-3; CIC-4; CIC-6; CIC-7; osteoporosis; Paget's disease; inhibitor;
 KW psychopharmaceutical.

XX OS Rattus norvegicus.
 XX DE D010102977-A1.

XX PD 01-AUG-2002.

XX PF 23-JAN-2001; 2001DE-01002977.

XX PR 23-JAN-2001; 2001DE-01002977.

XX PA (JENTV/) JENTSCH T.

XX PI Jentsch T;

XX DR WPI; 2002-658892/71.

XX DR N-PSDB; AAL49805.

XX PT New nucleic acid encoding mutated chloride channel proteins, useful for
 PT identifying specific channel inhibitors, as potential agents for treating
 PT e.g. osteoporosis.

XX PS Disclosure; Page 39-40; 52pp; German.

XX CC The present invention relates to coding sequences of chloride channel
 CC proteins CIC-3, CIC-4, CIC-6 and CIC-7 which have been altered by
 CC mutation, truncation or (partial) deletion. Cell lines containing such
 CC coding sequences are used to identify and test substances that inhibit
 CC chloride channel proteins, especially specific inhibitors. Inhibitors of
 CC CIC-7 are used for treating osteoporosis and Paget's disease; inhibitors
 CC of other chloride channel proteins are useful for treating neurological
 CC or neuromuscular diseases or other nerve disorders, also generally used
 CC as psychopharmaceuticals. The present sequence is a rat protein shown in
 CC the exemplification of the invention

XX SQ Sequence 803 AA;

Query Match 91.2%; Score 31; DB 5; Length 803;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 394 NYWLT 398

RESULT 31
 AAG79649
 ID AAG79649 standard; protein; 803 AA.

XX AC AAG79649;

XX DT 19-FEB-2003 (first entry)

XX DE Murine CLCN7 protein.

XX KW Murine; CLCN7; chloride ion channel; transgenic; musculoskeletal;
 KW immune system; abnormality.

XX OS Mus musculus.

XX PN WO200279414-A2.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-US009646.

XX PR 29-MAR-2001; 2001US-0280324P.

XX PR 24-SEP-2001; 2001US-0324664P.

XX PR 28-MAR-2002; 2002US-00109536.

XX PA (DELT-) DELTAGEN INC.

XX PI Allen KD;

XX WPI; 2003-067438/06.

XX DR N-PSDB; ABA00548.

XX PT New transgenic mouse comprising a disruption in a CLCN7 (chloride ion
 PT channel) gene useful as models for diseases, disorders or conditions
 PT associated with phenotypes relating to a disruption in a CLCN7 gene.

XX PS Disclosure; Fig 2; 65pp; English.

XX CC This sequence shows the murine CLCN7 (chloride ion channel) protein. The
 CC CLCN7 cDNA sequence was disrupted in the transgenic mouse of the
 CC invention in which there is no native expression of endogenous CLCN7
 CC gene. Mice having disruptions in the CLCN7 gene exhibit musculoskeletal
 CC abnormalities, and may alternatively or additionally exhibit an immune
 CC system abnormality. The transgenic mice are useful as models for
 CC diseases, disorders or conditions associated with phenotypes relating to
 CC a disruption in a CLCN7 gene; in the identification of drugs,
 CC pharmaceuticals, therapies and interventions that may be effective in
 CC treating a disease or other phenotypic characteristic of the animal; in
 CC the identification of compounds capable of ameliorating disease symptoms;
 CC and in testing and developing new treatments relating to behavioural
 CC phenotypes

XX SQ Sequence 803 AA;

Query Match 91.2%; Score 31; DB 6; Length 803;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||:|
 Db 394 NYWLT 398

RESULT 32
 ADF60665
 ID ADF60665 standard; protein; 803 AA.

XX AC ADF60665;

XX DT 12-FEB-2004 (first entry)

DE Rat CLC-7 #SEQ ID 4.
 XX Osteopathic; chloride channel; CLC-7; osteoclast; bone resorption;
 KW osteoporosis; human.
 XX Rattus sp.
 OS WO2003062821-A1.
 PN 31-JUL-2003.
 XX 23-JAN-2003; 2003WO-US002074.
 PF 23-JAN-2002; 2002US-0351187P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Yang W, Knapp-Ryseck A, Wu Y, Huang J, Wardwell-Swanson J;
 PI Walker SG, Chen J, Kalinowski SS, Sheng Z, Hellings SE;
 XX WPI; 2003-902662/82.
 DR N-PSDB; ADF60664.
 XX Assay for identifying modulators of chloride channel CLC-7, useful for
 PT treatment and prevention of osteoporosis.
 XX Disclosure; Page 11; 47pp; English.
 XX The invention relates to an assay for identifying a compound that
 CC modulates the activity of the chloride channel CLC-7, comprising treating
 CC a cell that expresses CLC-7 with a test compound and detecting any
 CC alteration in channel activity. Compounds of the invention decrease the
 CC differentiation of osteoclast precursor cells and the activity of mature
 CC osteoclasts, so reducing bone resorption. Compounds identified by the
 CC method are useful for treatment and prevention of osteoporosis, and also
 CC for the diagnosis of osteoporosis and other conditions associated with
 CC CLC-7, in humans or other animals. The current sequence represents the
 CC rat CLC-7 amino acid sequence.
 XX Sequence 803 AA;
 SQ

Query Match 91.2%; Score 31; DB 7; Length 803;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||||
 Db 394 NYWLT 398

RESULT 33
 ADF60667
 ID ADF60667 standard; protein; 803 AA.
 XX
 AC ADF60667;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Mouse CLC-7 #SEQ ID 6.
 XX
 KW Osteopathic; chloride channel; CLC-7; osteoclast; bone resorption;
 KW osteoporosis; mouse.
 XX Mus sp.
 OS WO2003062821-A1.
 PN 31-JUL-2003.
 XX 23-JAN-2003; 2003WO-US002074.
 PF 23-JAN-2002; 2002US-0351187P.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI

PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Yang W, Knapp-Ryseck A, Wu Y, Huang J, Wardwell-Swanson J;
 PI Walker SG, Chen J, Kalinowski SS, Sheng Z, Hellings SE;
 XX WPI; 2003-902662/82.
 DR N-PSDB; ADF60666.
 XX Assay for identifying modulators of chloride channel CLC-7, useful for
 PT treatment and prevention of osteoporosis.
 XX Disclosure; Page 15; 47pp; English.
 XX The invention relates to an assay for identifying a compound that
 CC modulates the activity of the chloride channel CLC-7, comprising treating
 CC a cell that expresses CLC-7 with a test compound and detecting any
 CC alteration in channel activity. Compounds of the invention decrease the
 CC differentiation of osteoclast precursor cells and the activity of mature
 CC osteoclasts, so reducing bone resorption. Compounds identified by the
 CC method are useful for treatment and prevention of osteoporosis, and also
 CC for the diagnosis of osteoporosis and other conditions associated with
 CC CLC-7, in humans or other animals. The current sequence represents the
 CC mouse CLC-7 amino acid sequence.
 XX Sequence 803 AA;
 SQ

Query Match 91.2%; Score 31; DB 7; Length 803;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
 |||||
 Db 394 NYWLT 398

RESULT 34
 AAM38696
 ID AAM38696 standard; protein; 805 AA.
 XX
 AC AAM38696;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1841.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AAI57852.
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX Example 3; SEQ ID NO 1841; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAW42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX Sequence 805 AA;
SQ

Query Match 91.2%; Score 31; DB 4; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYWMT 5
Db 396 NYWLT 400

RESULT 35
ABB85023
ID ABB85023 standard; protein; 805 AA.
AC
XX ABB85023;
XX 16-MAY-2002 (first entry)
DT
DE Pain regulated protein sequence 18.
XX
XX Pain; analgesic; gene therapy; neurological disorder;
KW neurodegenerative disease.
XX
XX Homo sapiens.
XX
XX WO200212338-A2.
XX
XX 14-FEB-2002.
PD
XX 03-AUG-2001; 2001WO-EP009011.
XX
XX 03-AUG-2000; 2000DE-01037759.
XX
XX (CHEF) GRUENTHAL GMBH.
PA
XX Gillen C, Wetzels I, Wnendt S, Weihe E, Schaefer MK;
PI WPI; 2002-257469/30.
XX N-PSDB; ABL88427.
DR
XX Identifying pain-regulating compounds, useful for treating chronic pain
PT and for diagnosis, by measuring binding of compounds to specific peptides
PT and proteins.
XX
XX Claim 1; Fig 40; 213pp; German.
PS

XX The invention relates to identifying pain-regulating substances (A)
CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-
CC ABB85037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a polypeptide of the invention
XX Sequence 805 AA;
SQ

Query Match 91.2%; Score 31; DB 5; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYWMT 5
Db 396 NYWLT 400

RESULT 36
ADF60663
ID ADF60663 standard; protein; 805 AA.
XX
XX ADF60663;
AC
XX 12-FEB-2004 (first entry)
DT
XX Human CLC-7 #SEQ ID 2.
DE
XX Osteopathic; chloride channel; CLC-7; osteoclast; bone resorption;
KW osteoporosis; human.
XX
XX Homo sapiens.
OS
XX WO2003062821-A1.
XX
XX 31-JUL-2003.
PD
XX 23-JAN-2003; 2003WO-US002074.
XX
XX 23-JAN-2002; 2002US-0351187P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX Yang W, Knapp-Rysek A, Wu Y, Huang J, Wardwell-Swanson J;
PI Walker SG, Chen J, Kalinowski SS, Sheng Z, Hellings SE;
PI WPI; 2003-902662/82.
XX N-PSDB; ADF60662.
DR
XX Assay for identifying modulators of chloride channel CLC-7, useful for
PT treatment and prevention of osteoporosis.
XX
XX Disclosure; Page 8; 47pp; English.
PS
XX The invention relates to an assay for identifying a compound that
CC modulates the activity of the chloride channel CLC-7, comprising treating
CC a cell that expresses CLC-7 with a test compound and detecting any
CC alteration in channel activity. Compounds of the invention decrease the
CC differentiation of osteoclast precursor cells and the activity of mature
CC osteoclasts, so reducing bone resorption. Compounds identified by the
CC method are useful for treatment and prevention of osteoporosis, and also
CC for the diagnosis of osteoporosis and other conditions associated with
CC CLC-7, in humans or other animals. The current sequence represents the
CC human CLC-7 amino acid sequence.
XX

SQ Sequence 805 AA;

Query Match 91.2%; Score 31; DB 7; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 396 NYWLT 400

RESULT 37
ADJ70009
ID ADJ70009 standard; protein; 805 AA.
XX
AC ADJ70009;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1815.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
FN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PE 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1815; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 805 AA;

Query Match 91.2%; Score 31; DB 7; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 396 NYWLT 400

RESULT 38
ADQ18241
ID ADQ18241 standard; protein; 805 AA.
XX
AC ADQ18241;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1059.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
FN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PE 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 1059; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 805 AA;

Query Match 91.2%; Score 31; DB 8; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 396 NYWLT 400

RESULT 39
ABM81693
ID ABM81693 standard; protein; 805 AA.

XX ABM81693;
AC
XX
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO38480, SEQ:4373.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX
XX WO2004030615-A2.
PN
XX
XX 15-APR-2004.
PD
XX
XX 29-SEP-2003; 2003WO-US028547.
PF
XX
XX 02-OCT-2002; 2002US-0414971P.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Wu TD, Zhang Z, Zhou Y;
PI
XX
XX WPI; 2004-347921/32.
PR
XX
XX N-PSDB; ACN39923.
DR
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
PT
XX
XX Claim 12; SEQ ID NO 4373; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 805 AA;

Query Match 91.2%; Score 31; DB 8; Length 805;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYNWT 5
Db 396 NYMLT 400
|||:|

RESULT 40
AAM40482

ID AAM40482 standard; protein; 816 AA.
XX
AC AAM40482;
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 5413.
DE
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemocortic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200153312-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000WO-US034263.
PF
XX
XX 23-DEC-1999; 99US-00471275.
PR
XX
XX 21-JAN-2000; 2000US-00488725.
PR
XX
XX 25-APR-2000; 2000US-00552317.
PR
XX
XX 20-JUN-2000; 2000US-00598042.
PR
XX
XX 19-JUL-2000; 2000US-00620312.
PR
XX
XX 03-AUG-2000; 2000US-00653450.
PR
XX
XX 14-SEP-2000; 2000US-00662191.
PR
XX
XX 19-OCT-2000; 2000US-00693036.
PR
XX
XX 29-NOV-2000; 2000US-00727344.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
PI
XX
XX WPI; 2001-442253/47.
DR
XX
XX N-PSDB; AAI59638.
DR
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
XX Example 2; SEQ ID NO 5413; 10078pp; English.
PS
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAI42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemocortic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 816 AA;

Query Match 91.2%; Score 31; DB 4; Length 816;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYNWT 5
Db 407 NYMLT 411
|||:|

```

RESULT 41
ABG19474
ID  ABG19474 standard; protein; 816 AA.
XX
AC  ABG19474;
XX
DT  13-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19465.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
FN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US008631.
XX
PR  31-MAR-2000; 2000US-00540217.
XX
PR  23-AUG-2000; 2000US-00649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
XX  N-PSDB; AAS83661.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity.
XX
PS  Claim 20; SEQ ID NO 49833; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX  sequences. (I) is useful as hybridisation probes, polymerase chain
XX  reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX  and in recombinant production of (II). The polynucleotides are also used
XX  in diagnostics as expressed sequence tags for identifying expressed
XX  genes. (I) is useful in gene therapy techniques to restore normal
XX  activity of (II) or to treat disease states involving (II). (II) is
XX  useful for generating antibodies against it, detecting or quantitating a
XX  polypeptide in tissue, as molecular weight markers and as a food
XX  supplement. (II) and its binding partners are useful in medical imaging
XX  of sites expressing (II). (I) and (II) are useful for treating disorders
XX  involving aberrant protein expression or biological activity. The
XX  polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits to assess biodiversity
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
XX  amino acid sequences of the invention. Note: The sequence data for this
XX  patent did not appear in the printed specification, but was obtained in
XX  electronic format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 816 AA;

Query Match          91.2%; Score 31; DB 4; Length 816;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 NYNWT 5
    |||:|
Db  407 NYWLT 411

RESULT 42
ABG19474
ID  ABG19474 standard; protein; 816 AA.
XX
AC  ABG19474;
XX
DT  13-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #19465.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
FN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US008631.
XX
PR  31-MAR-2000; 2000US-00540217.
XX
PR  23-AUG-2000; 2000US-00649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
XX  N-PSDB; AAS83661.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity.
XX
PS  Claim 20; SEQ ID NO 49833; 103pp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX  sequences. (I) is useful as hybridisation probes, polymerase chain
XX  reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX  and in recombinant production of (II). The polynucleotides are also used
XX  in diagnostics as expressed sequence tags for identifying expressed
XX  genes. (I) is useful in gene therapy techniques to restore normal
XX  activity of (II) or to treat disease states involving (II). (II) is
XX  useful for generating antibodies against it, detecting or quantitating a
XX  polypeptide in tissue, as molecular weight markers and as a food
XX  supplement. (II) and its binding partners are useful in medical imaging
XX  of sites expressing (II). (I) and (II) are useful for treating disorders
XX  involving aberrant protein expression or biological activity. The
XX  polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits to assess biodiversity
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
XX  amino acid sequences of the invention. Note: The sequence data for this
XX  patent did not appear in the printed specification, but was obtained in
XX  electronic format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 816 AA;

Query Match          91.2%; Score 31; DB 4; Length 816;
Best Local Similarity 80.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 NYNWT 5
    |||:|
Db  407 NYWLT 411

RESULT 43
ABM82606
ID  ABM82606 standard; protein; 925 AA.
XX
AC  ABM82606;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Human diagnostic and therapeutic pprotein SEQ ID NO:2855.
XX
KW  gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS  Homo sapiens.
XX
PN  WO2004023973-A2.
XX

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ADK70509
ID  ADK70509 standard; protein; 823 AA.
XX
AC  ADK70509;
XX
DT  06-MAY-2004 (first entry)
XX
DE  Respiratory disease differentially expressed protein #75.
XX
KW  cytosstatic; respiratory; antiasthmatic; gene therapy;
XX  differential gene expression; respiratory disorder; lung cancer;
XX  chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS  Homo sapiens.
XX
FN  WO2003101283-A2.
XX
PD  11-DEC-2003.
XX
PF  02-JUN-2003; 2003WO-US017409.
XX
PR  04-JUN-2002; 2002US-0386005P.
XX
PA  (INCY-) INCYTE CORP.
XX
PI  Rickert PK, Krasnow R;
XX
DR  WPI; 2004-042945/04.
XX
PT  New combination comprising cDNAs and proteins that are differentially
XX  expressed in respiratory disorders, useful for diagnosing or treating
XX  respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
XX  diseases or asthma.
XX
PS  Claim 14; SEQ ID NO 245; 343pp; English.
XX
CC  The invention relates to cDNA sequences that are differentially expressed
XX  in respiratory disorders or their complements or encoded proteins. The
XX  cDNAs and proteins are useful for diagnosing, treating or monitoring
XX  treatment of a subject with a respiratory disease including lung cancer,
XX  chronic obstructive pulmonary diseases, emphysema or asthma. The protein
XX  is also useful for screening molecules or compounds to identify at least
XX  one ligand which specifically binds the protein. It is also useful for
XX  preparing and purifying a polyclonal or monoclonal antibody. This
XX  sequence corresponds to a protein of the invention.
XX
SQ  Sequence 823 AA;

Query Match          91.2%; Score 31; DB 8; Length 823;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 NYNWT 5
    |||:|
Db  414 NYWLT 418

RESULT 43
ABM82606
ID  ABM82606 standard; protein; 925 AA.
XX
AC  ABM82606;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Human diagnostic and therapeutic pprotein SEQ ID NO:2855.
XX
KW  gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS  Homo sapiens.
XX
PN  WO2004023973-A2.
XX

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12-SEP-2003; 2003WO-US028227.
12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
(INCY-) INCYTE CORP.
Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Hathshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CU;
WPI: 2004-329368/30.
N-PSDB; ACN41259.
New diagnostic and therapeutic polynucleotides and polypeptides, useful
in diagnosing a condition, disease or disorder associated with human
molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
in gene mapping.
Claim 27; Page; 190pp; English.
The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The dithp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a dithp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly
from WIPO at www.wipo.int/pct/en/sequences/listing.htm
Sequence 926 AA;
Query Match 91.2%; Score 31; DB 8; Length 926;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYWMT 5
Db 397 NYWLT 401
RESULT 45
ABM82605
ID ABM82605 standard; protein; 926 AA.
XX AC ABM82605;
XX AC ABM82605;
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pproteins SEQ ID NO:2854.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX PN
XX PD 25-MAR-2004.

25-MAR-2004.
12-SEP-2003; 2003WO-US028227.
12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
(INCY-) INCYTE CORP.
Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Hathshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CU;
WPI: 2004-329368/30.
N-PSDB; ACN41258.
New diagnostic and therapeutic polynucleotides and polypeptides, useful
in diagnosing a condition, disease or disorder associated with human
molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
in gene mapping.
Claim 27; Page; 190pp; English.
The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The dithp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a dithp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly
from WIPO at www.wipo.int/pct/en/sequences/listing.htm
Sequence 925 AA;
Query Match 91.2%; Score 31; DB 8; Length 925;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYWMT 5
Db 396 NYWLT 400
RESULT 44
ABM82607
ID ABM82607 standard; protein; 926 AA.
XX AC ABM82607;
XX AC ABM82607;
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pproteins SEQ ID NO:2856.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX PN
XX PD 25-MAR-2004.

PP 12-SEP-2003; 2003WO-US028227.
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 XX (INCY-) INCYTE CORP.
 XX
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JA, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN41257.
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 XX Claim 27; Page; 190pp; English.
 PS
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 XX Sequence 926 AA;
 SQ
 Query Match 91.2%; Score 31; DB 8; Length 926;
 Best Local Similarity 80.0%; Pred. No. 5.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 Db 397 NYWLT 401
 RESULT 46
 ABB11833
 ID ABB11833 standard; peptide; 1097 AA.
 XX
 XX ABB11833;
 AC
 XX
 XX 11-JAN-2002 (first entry)
 DT
 XX
 XX Human C1 channel homologue, SEQ ID NO:2203.
 DE
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytotatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200157188-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US003800.
 PF
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 XX
 DR N-PSDB; ABA09077.
 DR
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 PT
 XX Claim 20; Page 263-264; 1963pp; English.
 PS
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, and hence
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis; cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 SQ
 Sequence 1097 AA;
 Query Match 91.2%; Score 31; DB 4; Length 1097;
 Best Local Similarity 80.0%; Pred. No. 6.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Fri May 12 11:16:48 2006

CC represents a Lactobacillus acidophilus fructo-oligosaccharide (FOS)
 CC utilization compound related protein of the invention.
 XX
 SQ Sequence 1217 AA;
 Query Match 91.2%; Score 31; DB 9; Length 1217;
 Best Local Similarity 80.0%; Pred. No. 7.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 499 NYWLT 503
 RESULT 48
 ABG19475
 ID ABG19475 standard; protein; 1229 AA.
 XX AC ABG19475;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #19466.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS93662.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 49834; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities in
 CC polypeptide and polynucleotide sequences have application of mutations
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

QY 1 NYWMT 5
 DB 460 NYWLT 464
 RESULT 47
 ADW26751
 ID ADW26751 standard; protein; 1217 AA.
 XX AC ADW26751;
 XX DT 24-MAR-2005 (first entry)
 XX DE Fructo-oligosaccharide related protein, SEQ ID 150.
 XX fructo-oligosaccharide; FOS; antimicrobial; antidiarrhetic; cytostatic;
 KW gastrointestinal-gen.; immunostimulant; food-additive;
 KW enterobacter infection; diarrhea; cancer; immune disorder; milk.
 XX OS Lactobacillus acidophilus.
 XX PN WO2005001057-A2.
 XX PD 06-JAN-2005.
 XX PF 22-JUN-2004; 2004WO-US019924.
 XX PR 23-JUN-2003; 2003US-0480764P.
 XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX PI Klaenhammer TR, Russell WM, Alterman E;
 XX WPI; 2005-075547/08.
 XX N-PSDB; ADW26750.
 XX New Lactobacillus acidophilus nucleic acids and encoded polypeptides
 PT useful for imparting better fructo-oligosaccharide-utilizing capacity to
 PT probiotic bacteria, or for preventing or treating enteric infections or
 PT cancer.
 XX Claim 6; SEQ ID NO 150; 462pp; English.
 PS The invention relates to novel isolated nucleic acid molecule encoding
 CC fructo-oligosaccharide (FOS) utilization compounds. The invention further
 CC comprises: a vector comprising the nucleic acid; a host cell containing
 CC the vector; an isolated polypeptide encoded by the nucleic acid; an
 CC antibody that selectively binds the polypeptide; a method for producing
 CC the polypeptide from a culture of the host cell; detecting the
 CC bacterium to metabolize fructo-oligosaccharide (FOS) and/or other complex
 CC carbohydrates; modifying the ability of a bacterium to colonize the
 CC gastrointestinal tract of a host; stimulating the growth of beneficial
 CC commensals in the gastrointestinal tract of a mammal; a Lactobacillus
 CC bacterial strain with a modified ability to colonize the gastrointestinal
 CC tract of a host compared to a wild-type Lactobacillus bacterial strain,
 CC where the modified ability is due to overexpression of one or more
 CC heterologous FOS-related polypeptides cited above; a culture comprising
 CC the Lactobacillus bacterial strain; and an isolated nucleic acid comprising
 CC regulatory element comprising a nucleotide sequence selected from: SEQ ID
 CC NOs: 173, 174, 175, 353 or 354; a biologically active sequence comprising
 CC at least 50 consecutive residues of SEQ ID NO: 173, 353 or 354; a
 CC nucleotide sequence that hybridizes to the complement of the FOS isolated
 CC nucleic acid under stringent conditions; or a sequence with at least 90%
 CC identity to the FOS isolated nucleic acid which has biological activity
 CC as a regulatory control element. The FOS isolated nucleic acid has
 CC antimicrobial, antidiarrhetic, cytostatic, gastrointestinal-gen., and
 CC immunostimulant activities. The nucleic acids are useful for imparting
 CC better FOS-utilizing capacity to probiotic bacteria, including
 CC Lactobacillus. The bacteria or purified polypeptides may be used as food
 CC supplements in preventing or treating enteric infections, diarrheal
 CC diseases or cancer, and for stimulating the immune system. The bacteria
 CC are useful in the production of fermented milk products. This sequence

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XX SQ Sequence 1229 AA;
Query Match          91.2%; Score 31; DB 4; Length 1229;
Best Local Similarity 80.0%; Pred. No. 7.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
        |||:|
Db      481 NYWLT 485

RESULT 49
ADY26847
ID ADY26847 standard; protein; 1872 AA.
XX AC
XX AC ADY26847;
XX DT 19-MAY-2005 (first entry)
XX DE S. pulveraceus fostricetin synthase gene cluster protein SEQ ID NO 24.
XX KW fostricetin synthase.
XX OS Streptomyces pulveraceus.
XX FN WO2005019426-A2.
XX PD 03-MAR-2005.
XX PF 18-AUG-2004; 2004WO-US026978.
XX PR 18-AUG-2003; 2003US-0496306P.
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX PI Reid RC, Hu Z, Tang L;
XX DR WPI; 2005-202635/21.
XX DR N-PSDB; ADY26846.
XX PT Produces polyketide involves culturing a cell under conditions under
XX PS which cell produces polyketide.
XX FS Disclosure; SEQ ID NO 24; 306pp; English.
XX CC The invention relates to a method of producing polyketide by culturing a
XX CC cell under conditions under which the cell produces the polyketide. The
XX CC cell comprises a recombinant polynucleotide synthase that comprises a
XX CC domain from the Streptomyces pulveraceus fostricetin polyketide synthase.
XX CC It does not make the polyketide in the absence of the recombinant
XX CC polynucleotide. The method is useful for producing a polyketide, e.g.
XX CC fostricetin, PD 113,270 or PD 113,271. The present sequence represents a
XX CC S. pulveraceus fostricetin synthase gene cluster protein.
XX SQ Sequence 1872 AA;

Query Match          91.2%; Score 31; DB 9; Length 1872;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
        |||:|
Db      933 NYWLT 937

RESULT 50
ADY26830
ID ADY26830 standard; protein; 1880 AA.
XX AC ADY26830;
XX DT 19-MAY-2005 (first entry)

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XX DE S. pulveraceus fostricetin synthase gene cluster protein Poss.
XX KW fostricetin synthase; enzyme.
XX OS Streptomyces pulveraceus.
XX FN WO2005019426-A2.
XX PD 03-MAR-2005.
XX PF 18-AUG-2004; 2004WO-US026978.
XX PR 18-AUG-2003; 2003US-0496306P.
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX PI Reid RC, Hu Z, Tang L;
XX DR WPI; 2005-202635/21.
XX DR N-PSDB; ADY26824.
XX PT Produces polyketide involves culturing a cell under conditions under
XX PS which cell produces polyketide.
XX FS Disclosure; SEQ ID NO 7; 306pp; English.
XX CC The invention relates to a method of producing polyketide by culturing a
XX CC cell under conditions under which the cell produces the polyketide. The
XX CC cell comprises a recombinant polynucleotide synthase that comprises a
XX CC domain from the Streptomyces pulveraceus fostricetin polyketide synthase.
XX CC It does not make the polyketide in the absence of the recombinant
XX CC polynucleotide. The method is useful for producing a polyketide, e.g.
XX CC fostricetin, PD 113,270 or PD 113,271. The present sequence represents a
XX CC enzyme encoded by the S. pulveraceus fostricetin synthase gene cluster.
XX SQ Sequence 1880 AA;

Query Match          91.2%; Score 31; DB 9; Length 1880;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
        |||:|
Db      933 NYWLT 937

Search completed: May 11, 2006, 16:27:49
Job time : 76.2295 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 7.37705 Seconds
(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-1

Perfect score: 34

Sequence: 1 NTWMT 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	255	2 S41690	cytochrome-c oxida
2	31	91.2	270	2 C86295	hypothetical prote
3	31	91.2	511	2 E64183	xylokinase homol
4	31	91.2	561	2 S73087	alpha-amylase (EC
5	31	91.2	606	2 H97012	hypothetical prote
6	31	91.2	789	2 S68427	chloride channel p
7	31	91.2	802	2 S68426	chloride channel p
8	31	91.2	1055	2 T10432	DNA-directed RNA p
9	30	88.2	90	2 PH1159	Ig heavy chain V r
10	30	88.2	101	2 E90448	hypothetical prote
11	30	88.2	234	2 H85268	hypothetical prote
12	30	88.2	234	2 T05379	hypothetical prote
13	30	88.2	301	1 WMVZP4	F4 protein - fowlp
14	30	88.2	361	2 AE1979	ABC transporter AT
15	30	88.2	362	2 T24706	hypothetical prote
16	30	88.2	394	2 JC4039	actin-like protein
17	30	88.2	401	2 F97260	uncharacterized co
18	30	88.2	410	2 H71125	hypothetical prote
19	30	88.2	449	2 G70216	hypothetical prote
20	30	88.2	533	2 T01864	hypothetical prote
21	30	88.2	554	2 C86366	protein F26F24.2 l
22	30	88.2	582	2 T05020	L-ascorbate oxidas
23	30	88.2	696	2 H90798	Iha adhesin limpor
24	30	88.2	696	2 G85607	probable receptor
25	30	88.2	875	1 URXLA2	peptidylglycine mo
26	30	88.2	919	2 S45298	retinoblastoma-as
27	30	88.2	923	2 S03583	peptidylglycine mo
28	30	88.2	935	2 S17855	peptidylglycine mo
29	30	88.2	972	1 URBOAP	peptidylglycine mo

30	88.2	974	1	URHUAP	peptidylglycine mo
31	88.2	976	1	URRTAP	peptidylglycine mo
32	88.2	1550	2	AB2276	two-component hybr
33	88.2	1684	2	S10789	amylase A-180 - al
34	88.2	4540	2	T30838	cytoplasmic dynein
35	85.3	59	2	S36381	Ig heavy chain V r
36	85.3	66	2	S36384	Ig heavy chain V r
37	85.3	89	2	G28833	Ig kappa chain V r
38	85.3	91	2	PH1004	Ig heavy chain V r
39	85.3	96	2	S17613	Ig heavy chain V r
40	85.3	97	2	PH1155	Ig heavy chain V r
41	85.3	98	2	PH1106	Ig heavy chain V r
42	85.3	98	2	PH1160	Ig heavy chain V r
43	85.3	98	2	PH1144	Ig heavy chain V r
44	85.3	98	2	PH1151	Ig heavy chain V r
45	85.3	98	2	PH1112	Ig heavy chain V r
46	85.3	101	2	I60919	HNF-3/fork-head ho
47	85.3	107	2	PH0987	Ig heavy chain V r
48	85.3	109	2	S26318	Ig heavy chain V r
49	85.3	109	2	B54743	transcription fact
50	85.3	111	1	MHMS76	Ig heavy chain V-I
51	85.3	112	2	C54743	transcription fact
52	85.3	113	1	AVMS09	Ig heavy chain V-I
53	85.3	113	1	AVMS57	Ig heavy chain V-I
54	85.3	113	1	AVMS61	Ig heavy chain V-I
55	85.3	113	1	AVMSAB	Ig heavy chain V-I
56	85.3	113	1	AVMSB7	Ig heavy chain V-I
57	85.3	113	1	HVMSAM	Ig heavy chain V r
58	85.3	114	2	PL0247	Ig heavy chain V r
59	85.3	114	2	A27563	Ig heavy chain V r
60	85.3	115	1	AVMS06	Ig heavy chain V-I
61	85.3	115	1	AVMS82	Ig heavy chain V-I
62	85.3	115	2	A25803	Ig heavy chain V r
63	85.3	119	2	PL0089	Ig heavy chain V r
64	85.3	120	2	A54256	Ig heavy chain V r
65	85.3	123	2	S72389	hypothetical prote
66	85.3	136	2	PL0208	Ig heavy chain pre
67	85.3	137	2	E34903	Ig heavy chain pre
68	85.3	214	2	AG3525	hydrolase family p
69	85.3	214	2	T44701	probable integral
70	85.3	225	2	T31614	hypothetical prote
71	85.3	236	2	E86635	hypothetical prote
72	85.3	246	2	F75453	5,10-methylenetet
73	85.3	246	2	F74408	lipopeptide antibi
74	85.3	262	2	T48954	hypothetical prote
75	85.3	270	2	T16880	hypothetical prote
76	85.3	274	2	AD1339	hypothetical prote
77	85.3	277	2	AB1710	hypothetical prote
78	85.3	285	2	B64886	ydau protein - Esc
79	85.3	289	2	A81874	probable periplasm
80	85.3	295	2	E81179	spermidine/putresc
81	85.3	295	2	A81927	probable polyamine
82	85.3	306	2	A69670	choline ABC transp
83	85.3	321	2	B72384	bacterioferritin c
84	85.3	324	2	B96738	probable ABC trans
85	85.3	327	2	G75395	ABC transporter, p
86	85.3	346	2	T33309	hypothetical prote
87	85.3	349	2	E82349	probable lipopolys
88	85.3	380	2	T16883	hypothetical prote
89	85.3	380	2	S45116	hypothetical prote
90	85.3	382	2	A83325	conserved hypotet
91	85.3	383	2	S76812	hypothetical prote
92	85.3	387	2	A47446	HNF-3/fork head fa
93	85.3	394	1	WHP5BF	4-hydroxybenzoate
94	85.3	416	2	F89779	hypothetical prote
95	85.3	425	2	S73491	MG461 homolog K05
96	85.3	439	2	I60916	HNF-3/forkhead hom
97	85.3	445	2	S23055	Slp2 protein - fru
98	85.3	445	2	S23056	Slp2 protein - fru
99	85.3	447	2	G95068	cysteine-tRNA syn
100	85.3	447	2	G97936	cysteine-tRNA liga
101	85.3	448	2	C86856	cysteine-tRNA liga
102	85.3	451	2	A55909	transforming prote

103 29 85.3 461 1 YBRC
 104 29 85.3 461 2 AC0569
 105 29 85.3 461 2 G85552
 106 29 85.3 461 2 D90702
 107 29 85.3 461 2 AH0373
 108 29 85.3 463 2 C87306
 109 29 85.3 466 2 C89820
 110 29 85.3 469 2 C89820
 111 29 85.3 471 2 I37451
 112 29 85.3 471 2 AH1104
 113 29 85.3 473 2 T15998
 114 29 85.3 476 2 A54743
 115 29 85.3 480 2 JH87346
 116 29 85.3 504 2 H87346
 117 29 85.3 512 2 T19806
 118 29 85.3 568 2 A34891
 119 29 85.3 573 2 AE1718
 120 29 85.3 597 2 AF2802
 121 29 85.3 604 2 F69802
 122 29 85.3 608 2 S76192
 123 29 85.3 618 2 E97604
 124 29 85.3 628 2 AB0548
 125 29 85.3 628 2 D90677
 126 29 85.3 628 2 G85527
 127 29 85.3 628 2 G64760
 128 29 85.3 669 2 E71610
 129 29 85.3 700 2 B41897
 130 29 85.3 710 2 A49486
 131 29 85.3 764 2 E95252
 132 29 85.3 766 2 G98117
 133 29 85.3 776 1 A45395
 134 29 85.3 776 2 D98354
 135 29 85.3 776 2 AC2928
 136 29 85.3 778 2 T39560
 137 29 85.3 791 2 T27473
 138 29 85.3 803 2 T39530
 139 29 85.3 1037 2 T50518
 140 29 85.3 1430 2 T34516
 141 29 85.3 1490 2 T47840
 142 29 85.3 1515 2 T52081
 143 29 85.3 2095 2 S29529
 144 29 85.3 73 2 A53237
 145 29 85.3 108 2 J31025
 146 29 85.3 123 2 S31509
 147 29 85.3 127 2 T31159
 148 29 85.3 133 2 C91001
 149 29 85.3 133 2 D85846
 150 29 85.3 156 2 H97334
 151 29 85.3 166 2 T51643
 152 29 85.3 176 2 F84583
 153 29 85.3 188 2 T51271
 154 29 85.3 188 2 T51676
 155 29 85.3 204 2 T51669
 156 29 85.3 204 2 AB0299
 157 29 85.3 205 1 JQ0958
 158 29 85.3 216 2 D96520
 159 29 85.3 218 2 T51681
 160 29 85.3 234 2 T51666
 161 29 85.3 238 2 T46166
 162 29 85.3 240 2 H70091
 163 29 85.3 243 2 T30500
 164 29 85.3 256 2 T49254
 165 29 85.3 261 2 T06650
 166 29 85.3 262 2 A53452
 167 29 85.3 262 2 F83535
 168 29 85.3 265 1 F69296
 169 29 85.3 273 1 JQ2390
 170 29 85.3 278 2 C6383
 171 29 85.3 286 2 H96706
 172 29 85.3 293 2 T09758
 173 29 85.3 295 2 T15151
 174 29 85.3 298 2 G89898
 175 29 85.3 302 2 T24091

cysteine-TRNA liga
 cysteinyl-TRNA syn
 cysteine TRNA synt
 cysteine TRNA synt
 cysteine-TRNA liga
 cysteinyl-TRNA syn
 cysteinyl-TRNA syn
 HBP-G2 (HPK-2) pro
 cysteinyl-TRNA syn
 hypothetical prote
 transcription fact
 brain factor 1 pro
 tryptophan halogen
 hypothetical prote
 Ig heavy chain pre
 hypothetical prote
 acetylactate synth
 ABC transporter (A
 hypothetical prote
 acetylactate synth
 PrpE protein limpo
 probable propionyl
 probable propionyl
 PrpE protein - Esc
 hypothetical prote
 cellulase (EC 3.2.
 ABC transporter, b
 conserved hypoteth
 conserved hypoteth
 outer layer protei
 oligo alginate lya
 oligo alginate lya
 dolichyl-phosphate
 hypothetical prote
 ABC transporter-li
 hypothetical prote
 multi resistance p
 MRP-like ABC trans
 genome polyprotein
 l(3)S12 protein -
 myb-related trans
 hypothetical 12K p
 Ig heavy chain - h
 DNA primase homolo
 hypothetical prote
 unknown protein en
 hypothetical prote
 myb-related trans
 pathogenesis-relat
 hypothetical prote
 myb-related trans
 myb-related trans
 probable luxR-fami
 myb-related protei
 hypothetical prote
 myb-related trans
 MYB27 protein - Ar
 hypothetical prote
 hypothetical prote
 Myb DNA binding pr
 myb-related protei
 phenylalanine hydr
 phenylalanine-4-hy
 p-nitrophenyl phos
 MYB transcription
 probable Myb-like
 probable transcrip
 myb-related protei
 hypothetical prote
 hypothetical prote
 hypothetical prote

82.4 321 2 T47280
 82.4 326 2 H88808
 82.4 333 1 C59812
 82.4 333 2 T09736
 82.4 333 2 T09737
 82.4 335 2 T09737
 82.4 335 2 B98142
 82.4 343 2 T42129
 82.4 346 2 T24803
 82.4 348 2 G69142
 82.4 356 2 A13145
 82.4 358 2 T33417
 82.4 369 1 TVFVAF
 82.4 369 2 I57555
 82.4 370 2 S41035
 82.4 395 2 T46401
 82.4 416 2 T46401
 82.4 425 2 AG2787
 82.4 426 2 H87307
 82.4 429 2 A97567
 82.4 445 2 C56604
 82.4 451 2 T36217
 82.4 463 2 D89937
 82.4 464 2 E89103
 82.4 468 1 GLSOPL
 82.4 468 2 D95137
 82.4 468 2 D98005
 82.4 469 2 AH3271
 82.4 470 1 A27233
 82.4 470 2 H90014
 82.4 472 2 G81866
 82.4 477 2 A10872
 82.4 477 2 D83724
 82.4 477 2 AC1077
 82.4 477 2 A1435
 82.4 478 2 E89790
 82.4 478 2 G95035
 82.4 478 2 C86807
 82.4 478 2 A86677
 82.4 478 2 D97906
 82.4 478 2 AF0153
 82.4 479 2 T39953
 82.4 479 2 E65074
 82.4 479 2 A85946
 82.4 479 2 E91100
 82.4 481 2 H69593
 82.4 482 2 S03395
 82.4 485 2 H81075
 82.4 518 1 G69804
 82.4 520 2 T18124
 82.4 527 2 S53835
 82.4 533 2 D86756
 82.4 571 2 B84469
 82.4 578 2 S55102
 82.4 594 2 E83847
 82.4 617 2 T52499
 82.4 622 2 D90373
 82.4 638 2 G02068
 82.4 646 2 JC7777
 82.4 649 2 S48379
 82.4 687 1 B32382
 82.4 768 2 T18461
 82.4 798 2 S20881
 82.4 849 2 T46253
 82.4 907 2 T15792
 82.4 1012 2 T13603
 82.4 1045 2 S23570
 82.4 1063 2 A33830
 82.4 1063 2 JC4700
 82.4 1150 1 D88556
 82.4 1169 1 S84859
 82.4 1274 2 S28279
 82.4 1365 2 T45031
 82.4 1408 2 T45039

transposase-like p
 protein R09E10.1 f
 ferrichrome ABC tr
 myb-related protei
 ABA-induced myb-re
 dehydration-induce
 hypothetical prote
 probable acyltrans
 hypothetical prote
 GDP-D-mannose dehy
 GDP-mannose 4,6-de
 hypothetical prote
 transforming prote
 c-Maf protein - mo
 hypothetical prote
 long-chain fatty a
 ubiquinol-cytochro
 hypothetical prote
 thymidine kinase (p
 plasmid transfer p
 Glycyl-tRNA synthet
 protein C18B10.4 f
 6-phospho-beta-gal
 6-phospho-beta-gal
 3-isopropylmalate
 beta-galactosidase
 6-phospho-beta-gal
 hypothetical prote
 6-phospho-beta-glu
 beta-glucosidase g
 beta-glucosidase f
 beta-glucosidase f
 6-phospho-beta-glu
 6-phospho-beta-glu
 phospho-beta-glucos
 6-phospho-beta-glu
 bgIA protein - Esc
 6-phospho-beta-glu
 6-phospho-beta-glu
 phospho-beta-galac
 hypothetical prote
 multidrug-efflux t
 probable capsid pr
 NADH2 dehydrogenas
 prophage p12 prote
 hypothetical prote
 PS2 protein - yea
 two-component sens
 ferredoxin oxidore
 hypothetical prote
 white homolog - hu
 ATP binding casses
 glycerol-3-phospha
 ubiquinol-cytochro
 hypothetical prote
 homeotic protein p
 hypothetical prote
 probable N-methyl-
 pol polyprotein ho
 cation efflux syat
 cadmium, zinc, cob
 protein B0464.2 li
 DNA repair protein
 hypothetical prote
 hypothetical prote
 hypothetical prote

249	28	82.4	1494	2	T26452	hypothetical prote	322	79.4	368	2	T03828	myb protein - rice
250	28	82.4	1551	2	T18941	hypothetical prote	323	79.4	374	2	T05891	myb-related protei
251	28	82.4	1557	2	T18412	lipid-binding prot	324	79.4	376	2	T51673	myb-related transc
252	28	82.4	1565	2	AD2135	polyketide synthas	325	79.4	378	2	T51647	myb-related transc
253	28	82.4	2825	2	T14271	Dcc4 protein, stre	326	79.4	388	2	G85147	hypothetical prote
254	28	82.4	4485	2	T08044	dynamin gamma heavy	327	79.4	389	2	T04816	myb-related protei
255	27	79.4	1109	2	D75506	hypothetical prote	328	79.4	395	2	T02989	myb-related protei
256	27	79.4	1113	2	S16254	hypothetical prote	329	79.4	407	2	T27170	hypothetical prote
257	27	79.4	128	2	T51672	myb-related transc	330	79.4	421	1	S24244	myb-related protei
258	27	79.4	130	2	T51684	probable transcrip	331	79.4	421	1	S24244	myb-related protei
259	27	79.4	139	2	B96689	hypothetical prote	332	79.4	422	2	AH2352	hypothetical prote
260	27	79.4	184	2	S54443	prepilin-like prot	333	79.4	429	2	AC2227	hypothetical prote
261	27	79.4	196	2	E82327	MSHA pilin protein	334	79.4	438	2	S71157	cytochrome c bioge
262	27	79.4	203	2	T54420	myb transcripion	335	79.4	490	2	T02545	probable MYB famil
263	27	79.4	205	2	G70304	hypothetical prote	336	79.4	497	2	T27169	hypothetical prote
264	27	79.4	212	2	T51680	myb-related transc	337	79.4	510	1	S43516	carboxypeptidase C
265	27	79.4	212	2	T51646	probable transcrip	338	79.4	517	1	S26606	myb-related protei
266	27	79.4	217	2	T51671	myb-related transc	339	79.4	530	1	G64918	phosphotransferase
267	27	79.4	220	2	T51648	probable transcrip	340	79.4	530	2	F85768	PTS system, maltos
268	27	79.4	228	1	TVMUG1	trichome different	341	79.4	530	2	A99920	PTS system, maltos
269	27	79.4	232	1	JQ0960	myb-related protei	342	79.4	553	2	T06179	myb-related protei
270	27	79.4	236	2	D85096	probable DNA-bindi	343	79.4	553	2	T03762	myb-related transc
271	27	79.4	239	2	T02984	myb-related protei	344	79.4	597	2	S65673	GABA transport pro
272	27	79.4	239	2	T51686	probable transcrip	345	79.4	597	2	T27497	hypothetical prote
273	27	79.4	243	2	T51652	myb-related transc	346	79.4	600	2	T11889	NADH2 dehydrogenas
274	27	79.4	246	2	A96689	hypothetical prote	347	79.4	680	2	D90575	lipoprotein [impor
275	27	79.4	246	2	T51631	probable transcrip	348	79.4	693	2	G82618	pilus biogenesis p
276	27	79.4	248	2	B96608	probable transcrip	349	79.4	697	2	T39512	hypothetical prote
277	27	79.4	249	1	S68688	myb-related protei	350	79.4	745	2	A71448	probable MYB trans
278	27	79.4	249	2	T51687	myb-related transc	351	79.4	795	2	T20939	hypothetical prote
279	27	79.4	251	1	S35729	myb-related protei	352	79.4	809	2	G86603	muramate-Ala ligas
280	27	79.4	255	1	S04899	myb-related protei	353	79.4	809	2	D72022	UDP-N-acetylmurama
281	27	79.4	257	2	T00780	myb-related protei	354	79.4	821	2	AD1507	probable secreted
282	27	79.4	257	2	T51679	myb-related transc	355	79.4	870	2	AB0570	outer membrane ush
283	27	79.4	262	2	T51633	myb-related transc	356	79.4	1367	2	T33819	hypothetical prote
284	27	79.4	267	1	S61506	myb-related protei	357	79.4	1504	2	A33602	DNA-directed DNA p
285	27	79.4	268	1	JQ0961	myb-related protei	358	79.4	1531	1	DVHUAR	multidrug resistan
286	27	79.4	269	1	S58292	probable MYB famil	359	79.4	1581	2	T32963	hypothetical prote
287	27	79.4	273	1	S69189	myb-related protei	360	79.4	2140	2	F95074	serine proteinase,
288	27	79.4	274	1	JQ0957	myb-related protei	361	79.4	2144	2	A97942	metalloproteinase
289	27	79.4	274	2	T05769	myb-related protei	362	79.4	2358	2	T39569	probable alpha-glu
290	27	79.4	275	2	T51651	myb-related transc	363	79.4	2371	2	T43432	alpha-glucan synth
291	27	79.4	276	2	T02985	myb-related protei	364	76.5	40	2	S33400	Ig heavy chain V r
292	27	79.4	277	2	T08554	hypothetical prote	365	76.5	51	2	F83800	hypothetical prote
293	27	79.4	280	2	T00737	myb-related protei	366	76.5	61	2	AI3253	hypothetical prote
294	27	79.4	280	2	T51667	myb-related transc	367	76.5	94	2	T06823	ribosomal protein
295	27	79.4	280	2	T26582	hypothetical prote	368	76.5	100	2	A70875	probable PE protei
296	27	79.4	282	2	T05690	myb-related transc	369	76.5	104	2	AG0706	probable membrane
297	27	79.4	282	2	T51632	myb-related transc	370	76.5	114	2	AH2217	hypothetical prote
298	27	79.4	294	2	T09879	myb-related protei	371	76.5	116	2	T10993	NADH2 dehydrogenas
299	27	79.4	296	2	T06025	transcription fact	372	76.5	116	2	H90626	NADH2 dehydrogenas
300	27	79.4	298	2	H84785	probable MYB famil	373	76.5	117	1	HVCQE1	Ig heavy chain pre
301	27	79.4	302	2	T10033	hypothetical prote	374	76.5	117	1	A71391	NADH2 dehydrogenas
302	27	79.4	310	2	T46035	AtMYB84 - Arabidop	375	76.5	123	1	LABOZ	alpha-lactalbumin
303	27	79.4	311	2	T03827	myb protein homolo	376	76.5	123	2	S74175	alpha-lactalbumin
304	27	79.4	316	1	JQ0956	myb-related protei	377	76.5	128	2	D29504	hypothetical 14K p
305	27	79.4	321	1	S45338	myb-related protei	378	76.5	130	2	D84825	hypothetical prote
306	27	79.4	323	2	T51621	myb-like protein [379	76.5	132	2	AB1767	ATP synthase chain
307	27	79.4	323	2	T51645	myb-related transc	380	76.5	136	2	T38482	hypothetical prote
308	27	79.4	324	2	B85064	MYB-like protein [381	76.5	138	2	B83470	hypothetical prote
309	27	79.4	325	2	T51509	probable transcrip	382	76.5	140	2	S14238	Ig gamma-1 chain p
310	27	79.4	326	2	T49966	myb-related protei	383	76.5	142	1	LABO	alpha-lactalbumin
311	27	79.4	330	2	P96775	hypothetical prote	384	76.5	142	1	LACT	alpha-lactalbumin
312	27	79.4	332	1	S58283	myb-related protei	385	76.5	142	2	S01178	conserved hypothet
313	27	79.4	333	2	T45720	probable transcrip	386	76.5	147	2	AG2901	28K cthf protein (
314	27	79.4	333	2	T51650	probable transcrip	387	76.5	147	2	A97677	hypothetical prote
315	27	79.4	336	2	T51644	probable transcrip	388	76.5	151	2	AE1929	perilucin - Halioti
316	27	79.4	338	2	C64099	drpGlucose 4,6-de	389	76.5	155	2	S78774	perilucin - Halioti
317	27	79.4	338	2	JC8010	single-stranded nu	390	76.5	156	2	H75082	hypothetical prote
318	27	79.4	343	2	T52590	probable transcrip	391	76.5	160	2	T24764	hypothetical prote
319	27	79.4	347	2	T07398	myb-related transc	392	76.5	160	2	A84104	hypothetical prote
320	27	79.4	352	2	T51659	myb-related transc	393	76.5	172	2	G71653	tRNA pseudouridine
321	27	79.4	352	2	D86476	protein F1504.43 [394	76.5	177	2	T30770	hypothetical prote

395	26	76.5	182	2	T16519	hypothetical prote	468	26	76.5	343	2	S09777	hypothetical prote
396	26	76.5	184	2	F42503	C8L protein - vacc	469	26	76.5	344	2	T17077	NADH2 dehydrogen
397	26	76.5	186	2	A00355	probable exported	470	26	76.5	345	2	A97783	tRNA pseudouridine
398	26	76.5	187	2	T22348	hypothetical prote	471	26	76.5	347	2	S47871	NADH2 dehydrogen
399	26	76.5	193	2	B75493	probable molybdopt	472	26	76.5	347	2	AD2201	hypothetical prote
400	26	76.5	195	2	S74714	hypothetical prote	473	26	76.5	349	2	E86590	hypothetical prote
401	26	76.5	200	2	T46222	hypothetical prote	474	26	76.5	349	2	H72033	hypothetical prote
402	26	76.5	201	2	H84012	hypothetical prote	475	26	76.5	353	2	T01978	hypothetical prote
403	26	76.5	209	2	F89963	conserved hypothet	476	26	76.5	363	2	H83893	hypothetical prote
404	26	76.5	209	2	D86882	hypothetical prote	477	26	76.5	367	1	S28471	probable hydro-ly
405	26	76.5	222	2	S58514	grp-binding protei	478	26	76.5	367	2	C82346	perosamine synthas
406	26	76.5	224	2	H97232	uncharacterized me	479	26	76.5	369	2	AE2276	two-component hybr
407	26	76.5	227	2	H89793	hypothetical prote	480	26	76.5	371	2	T32692	hypothetical prote
408	26	76.5	231	2	AC2277	hypothetical prote	481	26	76.5	372	1	D69442	conserved hypothet
409	26	76.5	236	2	S48867	dimethylallyltrans	482	26	76.5	374	2	E82168	probable alpha-1,6
410	26	76.5	236	2	I58002	probable cathepsin	483	26	76.5	388	2	AC1844	periplasmic polyam
411	26	76.5	247	2	S76160	hypothetical prote	484	26	76.5	392	2	G85076	probable reverse t
412	26	76.5	247	2	C82408	hypothetical prote	485	26	76.5	392	2	A82481	probable transcrip
413	26	76.5	248	2	D83691	hypothetical prote	486	26	76.5	393	2	G91155	probable transport
414	26	76.5	255	2	T32072	hypothetical prote	487	26	76.5	393	2	D86001	probable transport
415	26	76.5	260	2	E81194	biotin synthesis p	488	26	76.5	393	2	G65130	hypothetical 43.2K
416	26	76.5	260	2	F81830	conserved hypothet	489	26	76.5	402	2	F83422	conserved hypothet
417	26	76.5	261	2	H81679	conserved hypothet	490	26	76.5	408	2	C96984	probable Mn transp
418	26	76.5	261	2	D71523	probable outer mem	491	26	76.5	413	1	D71083	probable phosphoe
419	26	76.5	261	2	F90506	hypothetical prote	492	26	76.5	416	2	G81258	serine transporter
420	26	76.5	262	2	A80593	probable exported	493	26	76.5	417	1	S67566	probable membrane
421	26	76.5	263	2	B85577	hypothetical prote	494	26	76.5	417	1	F97789	ampG protein limpo
422	26	76.5	263	2	A97726	hypothetical prote	495	26	76.5	420	2	D55018	conserved hypothet
423	26	76.5	266	2	F64810	ybgf protein precu	496	26	76.5	420	2	E37891	conserved hypothet
424	26	76.5	269	2	AF0138	probable exported	497	26	76.5	423	2	G96033	conserved hypothet
425	26	76.5	269	2	T32124	hypothetical prote	498	26	76.5	424	2	B91960	probable inner mem
426	26	76.5	269	2	D69011	hypothetical prote	499	26	76.5	425	2	E97095	MDR-type permease
427	26	76.5	273	2	F71645	hypothetical prote	500	26	76.5	426	2	S51016	sodium-translocati
428	26	76.5	275	2	A81284	prolyl aminopeptida	501	26	76.5	426	2	H82239	conserved hypothet
429	26	76.5	275	2	E95215	exodeoxyribonuclea	502	26	76.5	427	2	F82094	sodium-translocati
430	26	76.5	275	2	A32301	exodeoxyribonuclea	503	26	76.5	463	2	S71624	glucagon-like pept
431	26	76.5	275	2	B98079	exodeoxyribonuclea	504	26	76.5	463	2	I84494	glucagon-like pept
432	26	76.5	277	2	A45018	template activatin	505	26	76.5	463	2	A46172	glucagon-like pept
433	26	76.5	277	2	I64837	Set beta isoform -	506	26	76.5	466	2	G83663	cysteinyI-trNA syn
434	26	76.5	278	2	T21639	hypothetical prote	507	26	76.5	467	2	T21690	hypothetical prote
435	26	76.5	280	2	AH2250	hypothetical prote	508	26	76.5	470	2	T16606	probable serine ca
436	26	76.5	282	2	S00938	str protein - Stap	509	26	76.5	474	2	S07754	NADH2 dehydrogen
437	26	76.5	286	2	S32915	type IV prepilin p	510	26	76.5	476	2	D69400	endonuclease Scel
438	26	76.5	286	2	A53374	type IV prepilin p	511	26	76.5	476	2	A28439	lysine specific pe
439	26	76.5	286	2	G81210	type IV prepilin p	512	26	76.5	477	2	F86670	lysine specific pe
440	26	76.5	286	2	A81788	type IV prepilin l	513	26	76.5	481	2	S56299	hypothetical prote
441	26	76.5	286	2	A55530	megakaryocyte grow	514	26	76.5	484	2	T07782	cytochrome-c oxida
442	26	76.5	288	2	A47654	dichloromethane de	515	26	76.5	489	2	T47747	cysteine-tRNA liga
443	26	76.5	289	2	I51908	Set alpha isoform	516	26	76.5	491	2	T22702	hypothetical prote
444	26	76.5	290	2	I59377	template activatin	517	26	76.5	498	2	AD0978	L-xylose kinase (EC
445	26	76.5	291	2	A25686	ampR protein - Ent	518	26	76.5	502	2	E83353	xylose kinase PA
446	26	76.5	292	2	AH2934	transcription regu	519	26	76.5	504	2	A11960	hypothetical prote
447	26	76.5	292	2	G98347	ampR transcription	520	26	76.5	506	2	A68899	lysine specific pe
448	26	76.5	294	2	B95416	probable beta lact	521	26	76.5	510	2	D96741	hypothetical prote
449	26	76.5	295	2	T16231	hypothetical prote	522	26	76.5	512	2	H86832	hypothetical prote
450	26	76.5	296	2	E83132	transcription regu	523	26	76.5	520	2	B75332	extracellular solu
451	26	76.5	296	2	S24954	regulatory protein	524	26	76.5	521	2	T34482	hypothetical prote
452	26	76.5	307	2	A83391	lipid A biosynthes	525	26	76.5	524	2	C81367	phosphoenolpyruvat
453	26	76.5	309	2	AC2860	transcription regu	526	26	76.5	525	2	F81017	YbhX/YhjW/Yip/Yjd
454	26	76.5	311	2	F90116	transcription regu	527	26	76.5	527	2	H75413	extracellular solu
455	26	76.5	314	2	S58715	guanine nucleotide	528	26	76.5	534	2	S70971	bfpB protein - Esc
456	26	76.5	314	2	S88075	hypothetical prote	529	26	76.5	536	2	T07946	cytochrome-c oxida
457	26	76.5	318	2	T48507	probable GTP-bindi	530	26	76.5	536	2	G95389	probable ABC trans
458	26	76.5	320	2	H90478	hypothetical prote	531	26	76.5	544	2	C95854	probable trehalose
459	26	76.5	322	2	T25966	hypothetical prote	532	26	76.5	545	2	S46151	probable purine nu
460	26	76.5	325	2	T10669	hypothetical prote	533	26	76.5	545	2	A47468	cytochrome-c oxida
461	26	76.5	332	2	T33799	hypothetical prote	534	26	76.5	551	1	A95301	FixN3 cytochrome c
462	26	76.5	335	2	T04029	hypothetical prote	535	26	76.5	552	2	A51027	L-ascorbate oxida
463	26	76.5	335	2	A86464	hypothetical prote	536	26	76.5	562	2	S25725	poly(3-hydroxyalka
464	26	76.5	340	2	S76294	hypothetical prote	537	26	76.5	562	2	AH2975	hypothetical prote
465	26	76.5	342	2	S71773	cysteine proteinase	538	26	76.5	563	2	C98307	opha protein limpo
466	26	76.5	342	2	T09355	hypothetical prote	539	26	76.5	564	2	F59092	hypothetical prote
467	26	76.5	343	2	JC7183	cathepsin Q (EC 3.	540	26	76.5	564	2	T21423	hypothetical prote

541	26	76.5	570	2	E95978	hypothetical prote	614	26	76.5	1150	2	AB0064	probable membrane
542	26	76.5	577	2	D69796	two-component sens	615	26	76.5	1157	1	GNLJLK	pol polyprotein -
543	26	76.5	577	2	T01052	hypothetical prote	616	26	76.5	1159	2	B95370	probable adenylate
544	26	76.5	578	2	S66353	L-ascorbate oxidas	617	26	76.5	1161	2	S18738	pol protein - simi
545	26	76.5	578	2	S30971	hypothetical prote	618	26	76.5	1203	2	F86266	probable phospholi
546	26	76.5	579	2	S11027	L-ascorbate oxidas	619	26	76.5	1213	2	D86384	unknown protein [i
547	26	76.5	581	2	S46742	hypothetical prote	620	26	76.5	1231	2	AC2863	hypothetical prote
548	26	76.5	587	1	KSXVAO	L-ascorbate oxidas	621	26	76.5	1243	2	B97640	sensory transducti
549	26	76.5	592	2	D88712	protein C17H12.4 [622	26	76.5	1266	2	T27024	hypothetical prote
550	26	76.5	598	2	AC0154	probable membrane	623	26	76.5	1277	2	B84517	hypothetical prote
551	26	76.5	598	2	S51456	probable membrane	624	26	76.5	1291	2	E82325	conserved hypothet
552	26	76.5	598	2	S66954	probable membrane	625	26	76.5	1322	2	B71440	hypothetical prote
553	26	76.5	622	2	F71174	hypothetical prote	626	26	76.5	1369	2	T43433	alpha-glucan synth
554	26	76.5	630	2	E96556	hypothetical prote	627	26	76.5	1378	2	T47605	riNG finger-like p
555	26	76.5	630	2	H96770	protein heat shock	628	26	76.5	1529	2	T02730	RNA-directed DNA p
556	26	76.5	632	2	E75057	peptidase PAB1418	629	26	76.5	1581	2	B71636	hypothetical prote
557	26	76.5	634	2	T27465	hypothetical prote	630	26	76.5	1583	2	F97846	hypothetical prote
558	26	76.5	639	1	F69280	iron (II) transpor	631	26	76.5	1587	2	B82012	hypothetical prote
559	26	76.5	648	2	A25047	beta-glucuronidase	632	26	76.5	1611	2	G84493	probable retroelem
560	26	76.5	658	2	T39549	hypothetical prote	633	26	76.5	1747	2	AS4121	collagen alpha-4 c
561	26	76.5	675	2	D65083	murcin-lipoprotein	634	26	76.5	1752	1	S26849	hypothetical prote
562	26	76.5	675	2	D83405	conserved hypothet	635	26	76.5	1768	2	T27023	hypothetical prote
563	26	76.5	692	1	DELVNS	NADH2 dehydrogenas	636	26	76.5	1834	1	JDMU1	DNA-directed RNA p
564	26	76.5	695	1	VH1WV	nucleocapsid prote	637	26	76.5	1840	2	G85422	hypothetical prote
565	26	76.5	695	2	S44049	nucleocapsid prote	638	26	76.5	1841	2	T23979	hypothetical prote
566	26	76.5	705	2	T40451	n-terminal acetyl	639	26	76.5	1943	2	T23986	hypothetical prote
567	26	76.5	705	2	T16088	hypothetical prote	640	26	76.5	2187	2	S60224	polyketide synthas
568	26	76.5	705	2	A35621	spore germination	641	26	76.5	2352	2	T43431	alpha-glucan synth
569	26	76.5	740	2	A96519	protein T2B6.4 [im	642	26	76.5	3175	1	RRWVEV	genome polyprotein
570	26	76.5	745	2	C83011	hypothetical prote	643	26	76.5	3591	1	S21010	filamentous hemagg
571	26	76.5	757	2	T16609	hypothetical prote	644	26	76.5	6486	2	T31076	tyrocidine synthet
572	26	76.5	765	2	E88924	protein R02C2.3 [i	645	25	73.5	54	2	G69733	PBSX prophage ORF
573	26	76.5	772	2	S69577	hypothetical prote	646	25	73.5	54	2	D69949	phage-related prot
574	26	76.5	781	2	AF2516	adenylate cyclase	647	25	73.5	67	2	B98067	hypothetical immun
575	26	76.5	784	2	T45697	hypothetical prote	648	25	73.5	87	4	IMBP12	Ig heavy chain V r
576	26	76.5	786	2	C84163	hypothetical prote	649	25	73.5	95	2	G37262	Ig heavy chain V-I
577	26	76.5	792	2	AB0038	probable outer mem	650	25	73.5	98	2	PL0123	Ig heavy chain V r
578	26	76.5	793	2	T45694	receptor-like prot	651	25	73.5	98	2	PH1143	Ig heavy chain V r
579	26	76.5	821	2	AD1148	probable secreted	652	25	73.5	100	2	D82920	ribosomal protein
580	26	76.5	824	2	F72408	leucine-trNA ligas	653	25	73.5	101	2	S26460	Ig heavy chain V r
581	26	76.5	828	2	D71700	leucine-trNA ligas	654	25	73.5	102	2	PH1277	Ig heavy chain V r
582	26	76.5	838	2	T45699	hypothetical prote	655	25	73.5	102	2	PH1267	Ig heavy chain V r
583	26	76.5	841	2	E71808	probable iron (III	656	25	73.5	102	2	PH1258	Ig heavy chain V r
584	26	76.5	842	2	H64694	iron(III) dicitrat	657	25	73.5	102	2	E75528	hypothetical prote
585	26	76.5	846	2	S13795	neurotactin - fru	658	25	73.5	103	2	S00739	hypothetical prote
586	26	76.5	846	2	S12005	neurotactin - fru	659	25	73.5	103	2	AE2513	hypothetical prote
587	26	76.5	858	2	E72419	flagellar hook-ass	660	25	73.5	104	2	S55728	chitin synthase [E
588	26	76.5	860	1	SYECL	leucine-trNA ligas	661	25	73.5	107	2	T28254	ORF MSV093 probabl
589	26	76.5	860	2	AC0582	leucyl-trNA synth	662	25	73.5	108	2	S69302	hypothetical prote
590	26	76.5	860	2	H90713	leucine trNA synth	663	25	73.5	110	2	PH1655	Ig heavy chain V r
591	26	76.5	860	2	D85564	leucine trNA synth	664	25	73.5	111	2	S25031	Ig heavy chain V r
592	26	76.5	860	2	AF0318	leucine-trNA ligas	665	25	73.5	114	2	S36280	Ig heavy chain V r
593	26	76.5	861	2	H64102	leucine-trNA ligas	666	25	73.5	115	2	S38714	Ig heavy chain V r
594	26	76.5	861	2	T27164	hypothetical prote	667	25	73.5	117	2	S24656	Ig heavy chain V r
595	26	76.5	875	1	A36369	1-phosphatidylinos	668	25	73.5	117	2	S19670	Ig heavy chain V r
596	26	76.5	886	1	GNLJSP	pol polyprotein -	669	25	73.5	117	2	S17079	Ig heavy chain V-g
597	26	76.5	887	2	E82590	leucyl-trNA synth	670	25	73.5	117	2	B27563	Ig heavy chain V r
598	26	76.5	889	2	JC6015	chitin synthase [E	671	25	73.5	117	2	S78486	Ig heavy chain V r
599	26	76.5	894	2	G82260	leucyl-trNA synth	672	25	73.5	118	2	S00700	Ig heavy chain V r
600	26	76.5	899	2	F84477	probable retroelem	673	25	73.5	119	2	S24659	Ig heavy chain V r
601	26	76.5	911	2	JC6016	chitin synthase [E	674	25	73.5	119	2	PL0085	Ig heavy chain V r
602	26	76.5	916	2	JC2315	chitin synthase [E	675	25	73.5	121	1	GVMS11	Ig heavy chain V r
603	26	76.5	930	2	E96600	protein F14J16.20	676	25	73.5	121	2	S24660	Ig heavy chain V r
604	26	76.5	939	2	AF2503	hypothetical prote	677	25	73.5	122	2	S31675	Ig heavy chain V r
605	26	76.5	958	2	S15566	pol protein - simi	678	25	73.5	122	2	A33989	Ig heavy chain V-I
606	26	76.5	960	2	A41638	chitin synthase [E	679	25	73.5	123	2	S20646	Ig heavy chain V r
607	26	76.5	973	2	T01862	hypothetical prote	680	25	73.5	124	2	S06824	Ig heavy chain V r
608	26	76.5	999	2	T19275	hypothetical prote	681	25	73.5	126	2	PH1416	Ig heavy chain V r
609	26	76.5	1010	2	F75134	hypothetical prote	682	25	73.5	126	2	PH1417	Ig heavy chain V r
610	26	76.5	1039	2	E72734	hypothetical prote	683	25	73.5	126	2	PH1418	Ig heavy chain V r
611	26	76.5	1062	2	F89102	protein P3E55.1 [i	684	25	73.5	126	2	PH1419	Ig heavy chain V r
612	26	76.5	1099	2	T16283	hypothetical prote	685	25	73.5	126	2	A83890	hypothetical prote
613	26	76.5	1133	2	S54496	probable membrane	686	25	73.5	127	2	PH1414	Ig heavy chain V r

687	25	73.5	127	2	PH1420	Ig heavy chain v r	760	25	73.5	245	2	AE0888	1-acyl-glycerol-3-
688	25	73.5	127	2	PH1415	Ig heavy chain v r	761	25	73.5	245	2	F85961	1-acyl-sn-glycerol
689	25	73.5	129	2	T16394	hypothetical prote	762	25	73.5	245	2	F91116	1-acyl-sn-glycerol
690	25	73.5	131	1	WMBP14	gene 14 protein -	763	25	73.5	245	2	S20460	1-acylglycerol-3-p
691	25	73.5	131	1	WMBP29	hemolysin - Asperg	764	25	73.5	248	2	T21350	hypothetical prote
692	25	73.5	131	2	S47523	ATP synthase chain	765	25	73.5	248	2	H84008	hypothetical prote
693	25	73.5	132	2	AH1391	Ig heavy chain v r	766	25	73.5	250	2	T25582	hypothetical prote
694	25	73.5	132	2	PH1427	hypothetical prote	767	25	73.5	250	2	F97831	hypothetical prote
695	25	73.5	134	2	D83756	Ig heavy chain v r	768	25	73.5	252	2	AC2226	hypothetical prote
696	25	73.5	136	2	S31587	Ig heavy chain pre	769	25	73.5	252	2	A64492	toxin sensitivity
697	25	73.5	138	1	HWNST7	Ig variable region	770	25	73.5	254	2	C75540	probable histidine
698	25	73.5	139	2	I37781	conserved hypotet	771	25	73.5	257	1	WBPRT5	gene D11 protein -
699	25	73.5	146	2	E69773	Ig variable region	772	25	73.5	261	2	C82067	probable 1-acylgly
700	25	73.5	147	2	I37780	Ig variable region	773	25	73.5	265	2	T12601	NADH2 dehydrogenas
701	25	73.5	150	2	T25581	hypothetical prote	774	25	73.5	265	2	AF2411	stationary phase s
702	25	73.5	151	2	B66047	type III secretion	775	25	73.5	266	2	AF2411	LyA9C - mouse
703	25	73.5	151	2	F91200	sepd protein - Esc	776	25	73.5	266	2	T20806	hypothetical prote
704	25	73.5	151	2	I80310	hypothetical prote	777	25	73.5	266	2	G97831	phosphomethylpyrim
705	25	73.5	154	2	F64026	hypothetical prote	778	25	73.5	267	2	G86782	hypothetical prote
706	25	73.5	157	2	AE2434	hypothetical prote	779	25	73.5	267	2	G95081	hypothetical prote
707	25	73.5	159	2	H71845	hypothetical prote	780	25	73.5	267	2	A97949	hypothetical prote
708	25	73.5	161	1	H70428	conserved hypotet	781	25	73.5	268	2	S51505	cytochrome-c oxida
709	25	73.5	161	2	D72682	hypothetical prote	782	25	73.5	268	2	F64101	prolipo protein dia
710	25	73.5	164	2	S74709	hypothetical prote	783	25	73.5	273	2	T39446	conserved hypotet
711	25	73.5	167	2	T28664	hypothetical prote	784	25	73.5	275	2	T17127	hypothetical prote
712	25	73.5	167	2	D87360	conserved hypotet	785	25	73.5	276	2	A38654	mast cell proteina
713	25	73.5	170	2	F72296	conserved hypotet	786	25	73.5	276	2	G82482	hypothetical prote
714	25	73.5	171	2	AD2457	hypothetical prote	787	25	73.5	276	2	G47301	ViR8 homolog - Bo
715	25	73.5	172	1	C71128	hypothetical prote	788	25	73.5	278	2	H64029	hypothetical prote
716	25	73.5	172	2	A12232	hypothetical prote	789	25	73.5	278	2	D86277	Flu17.8 protein -
717	25	73.5	175	2	S11294	SA85-1.3 protein -	790	25	73.5	282	2	T39471	hypothetical prote
718	25	73.5	175	2	C84987	hypothetical prote	791	25	73.5	282	2	E70553	hypothetical prote
719	25	73.5	176	2	A93136	hypothetical prote	792	25	73.5	285	2	D69975	anti-sigma factor
720	25	73.5	176	2	AB3152	outer membrane lip	793	25	73.5	285	2	T21962	hypothetical prote
721	25	73.5	177	2	D84583	probable pathogene	794	25	73.5	291	2	A32882	ampR protein - Cit
722	25	73.5	179	2	E75035	hypothetical prote	795	25	73.5	291	2	T25825	hypothetical prote
723	25	73.5	183	2	C69860	hypothetical prote	796	25	73.5	292	2	S51045	cumK protein - Pro
724	25	73.5	185	2	AG2026	hypothetical prote	797	25	73.5	292	2	S49164	lysR-type protein
725	25	73.5	186	2	AE1850	hypothetical prote	798	25	73.5	294	2	A48899	regulatory protein
726	25	73.5	186	2	AF2205	hypothetical prote	799	25	73.5	294	2	T34048	hypothetical prote
727	25	73.5	188	2	G69424	conserved hypotet	800	25	73.5	294	2	B97713	hypothetical prote
728	25	73.5	188	2	E90065	hypothetical prote	801	25	73.5	295	2	H98222	hypothetical prote
729	25	73.5	189	2	A12534	transposase all756	802	25	73.5	295	2	AH3063	hypothetical prote
730	25	73.5	194	2	B97727	prolyl endopeptida	803	25	73.5	295	2	S35914	regulatory protein
731	25	73.5	196	2	A26969	retinal retinol-bi	804	25	73.5	296	2	S51746	hypothetical prote
732	25	73.5	199	2	S17777	strg protein - Str	805	25	73.5	296	2	G85627	cell-division prot
733	25	73.5	201	2	S44231	probable bacitraci	806	25	73.5	299	2	B83888	transcription regu
734	25	73.5	203	1	T31684	conserved hypotet	807	25	73.5	300	2	T24547	hypothetical prote
735	25	73.5	205	2	A10967	probable aldehyde	808	25	73.5	302	2	T11675	lactoylglutathione
736	25	73.5	207	2	F95966	probable aldehyde	809	25	73.5	303	2	T06618	hypothetical prote
737	25	73.5	209	2	S77882	dnaa protein homol	810	25	73.5	304	2	S24263	seed storage prote
738	25	73.5	211	1	S40836	formate dehydrogen	811	25	73.5	305	2	AD3063	transcription regu
739	25	73.5	211	2	B91231	formate dehydrogen	812	25	73.5	305	2	D86223	probable transcrip
740	25	73.5	211	2	A86078	formate dehydrogen	813	25	73.5	306	2	AD0637	lipid A biosynthes
741	25	73.5	212	2	T46712	hypothetical prote	814	25	73.5	306	2	AD0807	probable acyltrans
742	25	73.5	213	2	T36345	hypothetical prote	815	25	73.5	306	2	S16888	lipid A biosynthes
743	25	73.5	215	2	A59428	ervatamin B (EC 3.	816	25	73.5	306	2	D85667	lipid A biosynthes
744	25	73.5	222	2	B54898	STX protein - huma	817	25	73.5	306	2	H90807	probable membrane
745	25	73.5	222	2	G72459	hypothetical prote	818	25	73.5	306	2	A10441	hypothetical prote
746	25	73.5	224	2	B89811	conserved hypotet	819	25	73.5	308	2	T48525	cysteine proteinas
747	25	73.5	225	2	B45582	probable 1-acylgly	820	25	73.5	309	2	S41427	selenophosphate sy
748	25	73.5	225	2	T24226	hypothetical prote	821	25	73.5	311	2	H70388	hypothetical prote
749	25	73.5	227	2	F90618	ATP synthase F0 ch	822	25	73.5	313	2	T19503	hypothetical prote
750	25	73.5	228	2	C95262	probable formate d	823	25	73.5	314	2	S41428	cysteine proteinas
751	25	73.5	230	2	I48685	mast cell proteina	824	25	73.5	314	2	D70313	riboflavin kinase
752	25	73.5	232	2	S27670	epoxide hydrolase	825	25	73.5	320	2	T20176	hypothetical prote
753	25	73.5	232	2	T16541	hypothetical prote	826	25	73.5	322	2	S23053	sleepy paired prot
754	25	73.5	233	2	S11292	SA85-1.1 protein -	827	25	73.5	325	2	S59834	probable protein p
755	25	73.5	237	2	A99420	sugar phosphate nu	828	25	73.5	328	2	A35257	replication protei
756	25	73.5	240	2	T00866	hypothetical prote	829	25	73.5	328	2	G85011	probable lauroyl a
757	25	73.5	242	2	T45795	hypothetical prote	830	25	73.5	328	2	D85880	probable heat shoc
758	25	73.5	243	2	AC0083	1-acylglycerol-3-p	831	25	73.5	328	2	B91036	probable heat shoc
759	25	73.5	244	2	B64003	hypothetical prote	832	25	73.5	330	2	C69649	transcription repr

833	25	73.5	330	2	B83902	transcription repr	906	25	73.5	404	2	T25723	hypothetical prote
834	25	73.5	332	2	T41227	hypothetical prote	907	25	73.5	405	2	F82229	probable phosphori
835	25	73.5	332	2	T19457	hypothetical prote	908	25	73.5	406	2	H89006	protein T22P3.11 [
836	25	73.5	332	2	T33310	hypothetical prote	909	25	73.5	411	2	F75439	probable cell wall
837	25	73.5	333	2	PQ0381	hemagglutinin - me	910	25	73.5	413	2	E81013	tryptophan transpo
838	25	73.5	333	2	PQ0377	hemagglutinin - me	911	25	73.5	413	2	D81957	amino-acid transpo
839	25	73.5	333	2	T06516	protein farnesyltr	912	25	73.5	414	2	AG2195	hypothetical prote
840	25	73.5	334	2	B84432	hypothetical prote	913	25	73.5	416	2	JC2544	lactose carrier pr
841	25	73.5	334	2	G86565	CT484 hypothetical	914	25	73.5	417	1	GREC	lactose permease -
842	25	73.5	334	2	D72057	conserved hypotet	915	25	73.5	417	2	H85528	galactoside permea
843	25	73.5	335	2	E71140	hypothetical prote	916	25	73.5	421	2	D90678	galactoside permea
844	25	73.5	335	2	T34296	hypothetical prote	917	25	73.5	421	2	A47713	chitin deacetylase
845	25	73.5	337	2	S26550	NADH2 dehydrogen	918	25	73.5	424	2	F84097	histidinol dehydro
846	25	73.5	337	2	T04035	hypothetical prote	919	25	73.5	425	2	E84631	probable serine ca
847	25	73.5	339	2	H83252	glycosyltransferas	920	25	73.5	428	2	S75037	folyl-polyglutamat
848	25	73.5	340	2	C71266	conserved hypotet	921	25	73.5	428	2	F85849	probable integrase
849	25	73.5	342	2	B96813	hypothetical prote	922	25	73.5	428	2	E91005	probable integrase
850	25	73.5	343	2	H96703	probable RING zinc	923	25	73.5	430	2	E90880	probable enzymes [
851	25	73.5	345	2	E69674	pectate lyase pelB	924	25	73.5	430	2	D85738	probable enzymes y
852	25	73.5	346	2	T11102	NADH2 dehydrogen	925	25	73.5	430	2	F64892	probable membrane
853	25	73.5	346	2	A95324	hypothetical prote	926	25	73.5	431	2	T36570	probable membrane
854	25	73.5	347	2	B58888	NADH2 dehydrogen	927	25	73.5	431	2	C84903	probable cytochrom
855	25	73.5	348	1	S36003	NADH2 dehydrogen	928	25	73.5	436	2	H90773	probable integrase
856	25	73.5	348	2	B58892	NADH2 dehydrogen	929	25	73.5	442	2	AB3556	beta-alanine-pyruv
857	25	73.5	348	2	T11429	NADH2 dehydrogen	930	25	73.5	443	2	S38116	hypothetical prote
858	25	73.5	348	2	G96771	protein choline ki	931	25	73.5	444	2	E85636	integraser for bact
859	25	73.5	349	2	AB1344	ribonucleoside-dip	932	25	73.5	444	2	C82981	probable pyridoxal
860	25	73.5	349	2	AF1714	ribonucleoside-dip	933	25	73.5	446	2	H71490	hypothetical prote
861	25	73.5	349	2	T33948	hypothetical prote	934	25	73.5	447	2	C83890	beta-glucosidase b
862	25	73.5	353	2	H88985	hypothetical prote	935	25	73.5	447	2	G84772	probable serine ca
863	25	73.5	354	2	C97614	protein C50H11.9 [936	25	73.5	450	2	C96947	PTS cellobiose-spe
864	25	73.5	357	2	T25499	hypothetical prote	937	25	73.5	450	2	T21593	hypothetical prote
865	25	73.5	358	2	AB0095	conserved hypotet	938	25	73.5	450	2	D82494	probable oxidoredu
866	25	73.5	359	2	I59403	alpha-2,8-polysial	939	25	73.5	452	2	H84772	probable serine ca
867	25	73.5	359	2	S52425	polysialyltransfer	940	25	73.5	453	2	T30985	hypothetical prote
868	25	73.5	359	2	JC4224	alpha-N-acetylnetr	941	25	73.5	456	2	AE0521	aromatic amino aci
869	25	73.5	361	1	KH8H	aleurain (EC 3.4.2	942	25	73.5	457	1	QRECAA	aromatic amino aci
870	25	73.5	362	1	S12581	cysteine proteinas	943	25	73.5	457	2	D85494	aromatic amino aci
871	25	73.5	362	2	S22502	probable membrane	944	25	73.5	457	2	D90643	amino-terminal ami
872	25	73.5	364	2	A97335	probable cysteine	945	25	73.5	457	2	S47938	phenylalanine-spec
873	25	73.5	365	2	F86413	NADH2 dehydrogen	946	25	73.5	458	2	A85556	phenylalanine-spec
874	25	73.5	367	2	T13813	NADH2 dehydrogen	947	25	73.5	458	2	F90705	phenylalanine-spec
875	25	73.5	367	2	T14228	NADH2 dehydrogen	948	25	73.5	458	2	A39431	phenylalanine tran
876	25	73.5	368	2	T13815	NADH2 dehydrogen	949	25	73.5	458	2	S45424	ALG3 protein - yea
877	25	73.5	368	2	T13795	NADH2 dehydrogen	950	25	73.5	458	2	S75328	DNA-directed DNA p
878	25	73.5	368	2	T14240	NADH2 dehydrogen	951	25	73.5	458	2	A95726	F25A4.34 [imported
879	25	73.5	368	2	A97189	LPS biosynthesis p	952	25	73.5	459	1	KIXEPV	major capsid prote
880	25	73.5	371	2	C97355	uncharacterized pr	953	25	73.5	459	2	C64047	cysteine-tRNA liga
881	25	73.5	375	2	I39169	sialyltransferase	954	25	73.5	459	2	D86656	dipeptidase [impor
882	25	73.5	375	2	I48686	N-glycan alpha 2,8	955	25	73.5	462	2	AH1053	probable exported
883	25	73.5	375	2	A46727	sialyltransferase	956	25	73.5	462	2	A84689	chloroplast membra
884	25	73.5	375	2	AI2041	hypothetical prote	957	25	73.5	464	2	G84986	cysteine-tRNA liga
885	25	73.5	376	1	KHDOP	prestalk cathepsin	958	25	73.5	464	2	AI0572	phenylalanine-spec
886	25	73.5	379	2	S40619	ubiquinol-cytochro	959	25	73.5	464	2	S22697	extensin - Volvox
887	25	73.5	380	2	E69319	flavoprotein reduc	960	25	73.5	465	2	B85358	SERINE CARBOXYPEPT
888	25	73.5	383	2	T47809	polygalacturonase-	961	25	73.5	465	2	AG0415	aromatic amino aci
889	25	73.5	383	2	AG3312	X-Pro dipeptidase	962	25	73.5	469	2	B83270	aromatic amino aci
890	25	73.5	383	2	E97625	Xaa-Pro dipeptidas	963	25	73.5	470	2	A69751	histidine permease
891	25	73.5	383	2	D97911	Xaa-pro dipeptidas	964	25	73.5	471	2	C95067	6-phospho-beta-glu
892	25	73.5	385	2	D97911	hypothetical prote	965	25	73.5	471	2	D96991	6-phospho-beta-glu
893	25	73.5	389	2	E86634	hypothetical prote	966	25	73.5	471	2	AH1114	phospho-beta-gluco
894	25	73.5	391	2	PC4117	replication protei	967	25	73.5	471	2	B97935	6-phospho-beta-glu
895	25	73.5	392	1	S74675	hypothetical prote	968	25	73.5	471	2	AI1475	phospho-beta-gluco
896	25	73.5	393	2	D95894	probable hydrolase	969	25	73.5	472	2	S39719	spore coat polysac
897	25	73.5	394	2	S39739	efflux protein hom	970	25	73.5	473	2	B97073	beta-glucosidase [
898	25	73.5	395	2	T08806	hypothetical prote	971	25	73.5	473	2	F70513	probable PPG prote
899	25	73.5	396	2	E97947	cell division prot	972	25	73.5	473	2	T04218	hypothetical prote
900	25	73.5	397	2	T11777	phosphoglycerate t	973	25	73.5	473	2	S49939	probable membrane
901	25	73.5	398	2	B30565	phospholipase C (E	974	25	73.5	474	2	H65051	6-phospho-beta-glu
902	25	73.5	399	2	B95080	cell division prot	975	25	73.5	474	2	D91075	6-phospho-beta-glu
903	25	73.5	402	1	RSBP18	probable integrase	976	25	73.5	474	2	C85920	6-phospho-beta-glu
904	25	73.5	403	2	H88636	protein W09G12.8 [977	25	73.5	474	2	D84631	probable serine ca
905	25	73.5	404	2	T02282	hypothetical prote	978	25	73.5	475	2	D64751	amino acid permeas

hypothetical prote
probable phosphori
protein T22P3.11 [
probable cell wall
tryptophan transpo
amino-acid transpo
hypothetical prote
lactose carrier pr
lactose permease -
galactoside permea
galactoside permea
chitin deacetylase
histidinol dehydro
probable serine ca
folyl-polyglutamat
probable integrase
probable integrase
probable enzymes [
probable enzymes y
probable membrane
probable membrane
probable cytochrom
beta-alanine-pyruv
hypothetical prote
integraser for bact
probable pyridoxal
hypothetical prote
beta-glucosidase b
probable serine ca
PTS cellobiose-spe
hypothetical prote
probable oxidoredu
probable serine ca
hypothetical prote
aromatic amino aci
aromatic amino aci
aromatic amino aci
amino-terminal ami
phenylalanine-spec
phenylalanine-spec
phenylalanine tran
ALG3 protein - yea
DNA-directed DNA p
F25A4.34 [imported
major capsid prote
cysteine-tRNA liga
dipeptidase [impor
probable exported
chloroplast membra
cysteine-tRNA liga
phenylalanine-spec
extensin - Volvox
SERINE CARBOXYPEPT
aromatic amino aci
aromatic amino aci
histidine permease
6-phospho-beta-glu
6-phospho-beta-glu
6-phospho-beta-glu
phospho-beta-gluco
spore coat polysac
beta-glucosidase [
probable PPG prote
hypothetical prote
probable membrane
6-phospho-beta-glu
6-phospho-beta-glu
6-phospho-beta-glu
amino acid permeas

979 25 73.5 475 2 T47480 hypothetical prote
 980 25 73.5 476 2 T47278 cysteine-tRNA liga
 981 25 73.5 477 2 G86833 6-phospho-beta-glu
 982 25 73.5 477 2 E97073 phospho-beta-gluco
 983 25 73.5 477 2 T45722 hypothetical prote
 984 25 73.5 482 2 C72264 IMP dehydrogenase
 985 25 73.5 483 2 JCS743 matrix metalloprot
 986 25 73.5 484 2 T36427 probable rhamnose
 987 25 73.5 484 2 AE0887 probable membrane
 988 25 73.5 485 2 H90562 mg2+ transport pro
 989 25 73.5 486 2 AF1107 phospho-beta-gluco
 990 25 73.5 486 2 A11468 phospho-beta-gluco
 991 25 73.5 490 1 H70473 IMP dehydrogenase
 992 25 73.5 490 2 S49792 probable membrane
 993 25 73.5 491 2 JE0396 phospho-beta-galac
 994 25 73.5 491 2 A55927 pre-B cell enhanci
 995 25 73.5 491 2 D97311 amino acid tranepo
 996 25 73.5 492 2 G90574 hypothetical prote
 997 25 73.5 493 2 JC8027 type 1 angiotensin
 998 25 73.5 493 2 E71008 hypothetical prote
 999 25 73.5 494 2 AC0133 probable permease
 1000 25 73.5 496 2 H75122 sarcosine oxidase

ALIGNMENTS

RESULT 1
 S41690
 C:Title: cytochrome-c oxidase (EC 1.9.3.1) chain III - Theileria parva mitochondrion
 C:Species: mitochondrion Theileria parva
 C>Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
 C:Accession: S41690; S40135
 R:Kaiaro, A.; Fairlamb, A.H.; Gobright, E.; Nene, V.
 EMBO J. 13, 898-905, 1994
 A:Title: A 7.1 kb linear DNA molecule of Theileria parva has scrambled rDNA sequences an
 A:Reference number: S41689; MUID:94155854; PMID:8112303
 A:Accession: S41690
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-255 <KAI>
 A:Cross-references: UNIPROT:Q36098; UNIPARC:UPI000008BA3A; EMBL:Z23263; NID:G437862; PID
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
 C:Genetics:
 A:Genome: mitochondrion
 A:Genetic code: SGC6
 C:Superfamily: cytochrome-c oxidase chain III
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 100.0%; Score 34; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. NO. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 189 NYWMT 193

RESULT 2
 C86295
 hypothetical protein T24D18.15 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: C86295
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C86295
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-270 <STO>
 A:Cross-references: UNIPROT:Q9S9N0; UNIPARC:UPI00000A5D5F; GB:AE005172; NID:G6587811; PI
 C:Genetics:
 A:Map position: 1

Query Match 91.2%; Score 31; DB 2; Length 270;
 Best Local Similarity 80.0%; Pred. NO. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 240 NYWMT 244

RESULT 3
 E64183
 xylulokinase homolog - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: E64183
 R:Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.P.; Kerlavage, A
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.B.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: E64183
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-511 <TIGR>
 A:Cross-references: UNIPARC:UPI00001685E4; GB:U32791; GB:L42023; NID:G1574662; PIDN:AA02
 C:Superfamily: xylulokinase

Query Match 91.2%; Score 31; DB 2; Length 511;
 Best Local Similarity 80.0%; Pred. NO. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 185 NYWMT 189

RESULT 4
 S73087
 alpha-amylase (EC 3.2.1.1) precursor - Sulfolobus solfataricus
 N:Alternate names: protein c0620
 C:Species: Sulfolobus solfataricus
 C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C:Accession: S73087
 R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
 Mol. Microbiol. 22, 175-191, 1996
 A:Title: Organizational characteristics and information content of an archaeal genome: 1
 A:Reference number: S73076; MUID:97055432; PMID:8899719
 A:Accession: S73087
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-561 <SEN>
 A:Cross-references: UNIPROT:P95867; UNIPARC:UPI0000066A84; EMBL:Y08256; NID:G1707679; PI
 A:Experimental source: strain P2
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
 C:Superfamily: glycosyltrehalose trehalohydrolase
 C:Keywords: glycosidase; hydrolase

Query Match 91.2%; Score 31; DB 2; Length 561;
 Best Local Similarity 80.0%; Pred. NO. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 504 NYWLT 508

RESULT 5

H97012

hypothetical protein CAC0915 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

A:Accession: H97012

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClC

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: H97012

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-606 <KUR>

A:Cross-references: UNIPROT:Q977Y3; UNIPARC:UPI00000D7575; GB:AE001437; PIDN:AAK78891.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0915

Query Match 91.2%; Score 31; DB 2; Length 606;
Best Local Similarity 80.0%; Pred. NO. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

|||:|

Db 96 NYWLT 100

RESULT 6

S68427

chloride channel protein 7 (CLC-7) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

A:Accession: S68427

R:Brandt, S.; Jentsch, T.J.

FEBS Lett. 377, 15-20, 1995

A:Title: CLC-6 and CLC-7 are two novel broadly expressed members of the CLC chloride cha

A:Reference number: S68426; MUID:96130311; PMID:8543009

A:Accession: S68427

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-789 <BRA>

A:Cross-references: UNIPROT:P51799; UNIPARC:UPI000004E54A; EMBL:Z67743; NID:g1177439; PI

C:Genetics:

A:Gene: GDB:CLCN7; CLC-7

A:Cross-references: GDB:3929156

A:Map position: 16p13-16p13

Query Match 91.2%; Score 31; DB 2; Length 789;
Best Local Similarity 80.0%; Pred. NO. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

|||:|

Db 380 NYWLT 384

RESULT 7

S68426

chloride channel protein CLC-7 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

A:Accession: S68426; S72561

R:Brandt, S.; Jentsch, T.J.

FEBS Lett. 377, 15-20, 1995

A:Title: CLC-6 and CLC-7 are two novel broadly expressed members of the CLC chloride cha

A:Reference number: S68426; MUID:96130311; PMID:8543009

A:Accession: S68426
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-802 <BRA>
A:Cross-references: UNIPROT:P51799; UNIPARC:UPI00001796C8; EMBL:Z67744
A:Experimental source: tissue type brain
R:Brandt, S.; Jentsch, T.J.
submitted to the EMBL Data Library, November 1995
A:Description: CLC-6 and CLC-7 are two novel broadly expressed members of the CLC chlor

A:Reference number: S72561

A:Accession: S72561

A:Molecule type: mRNA

A:Residues: 1-414, 'A', 415-528, 'M', 530-802 <BRW>

A:Cross-references: UNIPARC:UPI000004904D; EMBL:Z67744; NID:g1177612; PIDN:CAA91557.1;

C:Genetics:

A:Gene: CLC-7

A:Map position: 16p13

C:Keywords: ion transport; transmembrane protein; voltage-gated ion channel

F:125-142/Domain: transmembrane #status predicted <TM1>

F:170-201/Domain: transmembrane #status predicted <TM2>

F:242-243/Domain: transmembrane #status predicted <TM3>

F:286-310/Domain: transmembrane #status predicted <TM4>

F:325-343/Domain: transmembrane #status predicted <TM5>

F:373-394/Domain: transmembrane #status predicted <TM6>

F:407-432/Domain: transmembrane #status predicted <TM7>

F:485-513/Domain: transmembrane #status predicted <TM8>

F:516-530/Domain: transmembrane #status predicted <TM9>

F:545-563/Domain: transmembrane #status predicted <TM10>

F:573-593/Domain: transmembrane #status predicted <TM11>

F:755-781/Domain: conserved cytosolic domain #status predicted <CCD>

Query Match 91.2%; Score 31; DB 2; Length 802;
Best Local Similarity 80.0%; Pred. NO. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

|||:|

Db 394 NYWLT 398

RESULT 8

T10432

DNA-directed RNA polymerase (EC 2.7.7.6) - Pedicoccus acidilactici (fragment)

C:Species: Pedicoccus acidilactici

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000

A:Accession: T10432

R:Morse, R.; Colline, M.D.; Baledon, J.T.; Reading, S.; Richardson, P.T.

submitted to the EMBL Data Library, June 1995

A:Description: Cloning part of the rpoC gene encoding the B' subunit of the DNA-depende

A:Reference number: Z16792

A:Accession: T10432

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-1055 <MOR>

A:Cross-references: UNIPARC:UPI000016FD00; EMBL:X89232; NID:e984146; PID:e187582

C:Genetics:

A:Gene: rpoC

C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

C:Keywords: nucleotidyltransferase

Query Match 91.2%; Score 31; DB 2; Length 1055;
Best Local Similarity 80.0%; Pred. NO. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

|||:|

Db 499 NYWLT 503

RESULT 9

PH159

Ig heavy chain V region (clone 28F.2B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1159
R:Schitttek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1159
A:Molecule type: DNA
A:Residues: 1-90 <SCH>
A:Cross-references: UNIPROT:Q924Q0; UNIPARC:UPI0000176BC4
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 30; DB 2; Length 90;
Best Local Similarity 80.0%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
DB 23 NYWMT 27

RESULT 10
E90448
hypothetical protein SS02734 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90448
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90448
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: UNIPROT:Q97VA1; UNIPARC:UPI000006482B; GB:AE006641; NID:gi13816059; F
C:Genetics:
A:Gene: SS02734

Query Match 88.2%; Score 30; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
DB 61 NYWMT 65

RESULT 11
H85268
hypothetical protein AT4g23410 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85268
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: H85268
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <STO>
A:Cross-references: UNIPROT:O81737; UNIPARC:UPI00000AA124; GB:NC_001268; NID:g7269189; F
C:Genetics:
A:Gene: AT4G23410
A:Map position: 4

Query Match 88.2%; Score 30; DB 2; Length 234;

Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
DB 126 NYWMT 130

RESULT 12
T05379
hypothetical protein F16G20.110 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05379
R:Bevan, M.; Watson, M.D.; Gibbons, T.; Bartley, J.; Bancroft, I.; Mewes, H.W.; Mayer, K
submitted to the Protein Sequence Database, August 1998
A:Reference number: Z15413
A:Accession: T05379
A:Molecule type: DNA
A:Residues: 1-234 <BEV>
A:Cross-references: UNIPROT:O81737; UNIPARC:UPI00000AA124; EMBL:AL031326
A:Experimental source: cultivar Columbia; BAC clone F16G20
C:Genetics:
A:Map position: 4
A:Introns: 161/3; 200/1
A:Note: F16G20.110

Query Match 88.2%; Score 30; DB 2; Length 234;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
DB 126 NYWMT 130

RESULT 13
NWVZP4
F4 protein - fowlpox virus (strain HP444)
C:Species: fowlpox virus
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JS0224
R:Binns, M.M.; Tomley, F.M.; Campbell, J.; Boursnell, M.E.G.
J. Gen. Virol. 69, 1275-1283, 1988
A:Title: Comparison of a conserved region in fowlpox virus and vaccinia virus genomes an
A:Reference number: JS0220; MUID:88258470; PMID:2838574
A:Accession: JS0224
A:Molecule type: DNA
A:Residues: 1-301 <BIN>
A:Cross-references: UNIPROT:P15912; UNIPARC:UPI0000137F82; GB:D00320; NID:g221401; PIDN:
C:Superfamily: vaccinia virus F4 protein

Query Match 88.2%; Score 30; DB 1; Length 301;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
DB 53 NYWMT 57

RESULT 14
AB1979
ABC transporter ATP-binding protein alr1384 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
C:Accession: AB1979
R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB1979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-361 <KUR>
A;Cross-references: UNIPROT:Q8YX34; UNIPARC:UPI00000CE09F; GB:BA000019; PIDN:BAB73341.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1384

Query Match 88.2%; Score 30; DB 2; Length 361;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 266 NYWMT 270

RESULT 15
T24706
hypothetical protein T08G3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24706
R;Dloyd, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19926
A;Accession: T24706
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-362 <WIL>
A;Cross-references: UNIPROT:Q9XU48; UNIPARC:UPI0000061174; EMBL:Z83236; PIDN:CAB05799.1;
A;Experimental source: clone T08G3
C;Genetics:
A;Gene: CESP.T08G3.10
A;Map position: 5
A;Introns: 100/2; 148/2; 307/2

Query Match 88.2%; Score 30; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 14 NYWMT 18

RESULT 16
JC4039
actin-like protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Oct-2004
C;Accession: JC4039
R;Michaille, J.J.; Gouy, M.; Blanchet, S.; Duret, L.
Gene 154, 205-209, 1995
A;Title: Isolation and characterization of a cDNA encoding a chicken actin-like protein.
A;Reference number: JC4039; MUID:95197003; PMID:7890165
A;Accession: JC4039
A;Molecule type: mRNA
A;Residues: 1-394 <MIC>
A;Cross-references: UNIPROT:PS3488; UNIPARC:UPI0000126054; EMBL:X73971; NID:g806553; PIDN:G806553;
A;Experimental source: embryonic skin
C;Superfamily: Actin

Query Match 88.2%; Score 30; DB 2; Length 394;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 370 NYWMT 374

RESULT 17
F97260
uncharacterized conserved membrane protein CAC2931 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97260
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97260
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-401 <KUR>
A;Cross-references: UNIPROT:Q97F24; UNIPARC:UPI00000CA69A; GB:AE001437; PIDN:AAK80873.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2931

Query Match 88.2%; Score 30; DB 2; Length 401;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 350 NYWMT 354

RESULT 18
H71125
hypothetical protein PH0774 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: H71125
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfukuy, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: H71125
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-410 <KAW>
A;Cross-references: UNIPROT:Q58486; UNIPARC:UPI0000062ED9; GB:AP000003; NID:g3236130; P
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0774

Query Match 88.2%; Score 30; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 101 NYWMT 105

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 101 NYWMT 105

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 101 NYWMT 105

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 101 NYWMT 105

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 410;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 101 NYWMT 105

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 394;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 370 NYWMT 374

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

Query Match 88.2%; Score 30; DB 2; Length 394;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 370 NYWMT 374

RESULT 19
G70216
hypothetical protein BBB03 - Lyme disease spirochete plasmid B/cp26
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70216
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70216

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-449 <KLE>
A;Cross-references: UNIPROT:O50979; UNIPARC:UPI0000056952; GB:AE000792; NID:G3253098; PT
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 88.2%; Score 30; DB 2; Length 449;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||:
Db 315 NYWIT 319

RESULT 20
T01864
hypothetical protein T7M24.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01864
R;Harmon, G.; Langston, Y.; Stoneking, T.; Drone, K.; Ames, M.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of Arabidopsis thaliana T7M24.
A;Reference number: Z14448
A;Accession: T01864
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-533 <HAR>
A;Cross-references: UNIPROT:O81510; UNIPARC:UPI00000A6125; EMBL:AF077408; NID:G3319359;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 92/3; 105/2; 152/3; 268/1; 381/3
A;Note: T7M24.1

Query Match 88.2%; Score 30; DB 2; Length 533;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||:
Db 154 NYWMS 158

RESULT 21
C86366
protein F26F24.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86366
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.W.;
anin, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86366
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-554 <STO>
A;Cross-references: UNIPROT:O49298; UNIPARC:UPI00000482B2; GB:AE005172; NID:G9295687; PT
C;Genetics:
A;Gene: F26F24.2
A;Map position: 1
C;Superfamily: pectinesterase

```
Db      687 NYWMS 691
|||||
RESULT 24
G85607
C:Probable receptor Z1178 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85607; H85658
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85607
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <STO>
A;Cross-references: UNIPROT:Q9LAP1; UNIPARC:UPI00000D2F7E; GB:AE005174; NID:g12513986; F
A;Experimental source: strain O157:H7, substrain EDL933
A;Accession: H85658
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <ST2>
A;Cross-references: UNIPARC:UPI00000D2F7E; GB:AE005174; NID:g12514503; PIDN:AAG55732.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1178; Z1617
C;Superfamily: ferrienterochelin receptor; tonB-dependent receptor amino-terminal homolo

Query Match      88.2%; Score 30; DB 2; Length 696;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
|||||
Db      687 NYWMS 691

RESULT 25
URXLA2
peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog
N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha-amidat
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27715
R;Ohnuye, K.; Kitano, K.; Wada, Y.; Fuchimura, K.; Tanaka, S.; Mizuno, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 150, 1275-1281, 1988
A;Title: Cloning of cDNA encoding a new peptide C-terminal alpha-amidating enzyme having
A;Reference number: A27715; MUID:88134244; PMID:2829895
A;Accession: A27715
A;Molecule type: mRNA
A;Residues: 1-875 <OHS>
A;Cross-references: UNIPROT:P12890; UNIPARC:UPI0000125958; GB:M20191
A;Experimental source: skin
C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of pep
le and dismutates to glyoxylate and the corresponding desglycine peptide alpha-amide. Th
hormones. The other enzyme is peptidyl alpha-amidating enzyme I.
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolo
C;Keywords: copper; glycoprotein; monooxygenase II; oxidoreductase; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;24-39/Domain: propeptide #status predicted <PRO>
F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>
F;133-344/Domain: peptidylglycine monooxygenase I homology <PGM>
F;764-787/Domain: transmembrane #status predicted <TMN>
F;465,662,743/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      88.2%; Score 30; DB 1; Length 875;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
```

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Db      491 NYWVT 495
|||||
RESULT 26
S45298
retinoblastoma-associated protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S45298
R;Reinsteins, R.; Bolton, W.K.; Quinones, J.N.; Mosialos, G.; Sif, S.; Huff, J.L.; Capob
Biochim. Biophys. Acta 1218, 82-86, 1994
A;Title: Characterization of a chicken cDNA encoding the retinoblastoma gene product.
A;Reference number: S45298; MUID:94250698; PMID:8193168
A;Accession: S45298
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-919 <FEI>
A;Cross-references: UNIPROT:Q91016; UNIPARC:UPI000000F0FB; EMBL:U00113; NID:g392056; P
C;Superfamily: retinoblastoma-associated protein

Query Match      88.2%; Score 30; DB 2; Length 919;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
|||||
Db      180 NYWIT 184

RESULT 27
S09583
peptidylglycine monooxygenase (EC 1.14.17.3) B precursor - rat
N;Alternate names: alpha-amidating enzyme type B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 04-Dec-1994
C;Accession: S09583
R;Bertelsen, A.H.; Beaudry, G.A.; Galella, E.A.; Jones, B.N.; Ray, M.L.; Mehta, N.M.
Arch. Biochem. Biophys. 279, 87-96, 1990
A;Title: Cloning and characterization of two alternatively spliced rat alpha-amidating
A;Reference number: S09582; MUID:90247899; PMID:2337358
A;Accession: S09583
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-923 <BER>
A;Cross-references: UNIPARC:UPI000017527B
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolo
C;Keywords: alternative splicing; copper; glycoprotein; monooxygenase; oxidoreductase;
F;135-346/Domain: peptidylglycine monooxygenase I homology <PGM>

Query Match      88.2%; Score 30; DB 2; Length 923;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
|||||
Db      573 NYWVT 577

RESULT 28
S17855
peptidylglycine monooxygenase (EC 1.14.17.3) - African clawed frog
N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S17855
R;Iwawaki, Y.; Kawahara, T.; Shimoi, H.; Suzuki, K.; Ghisalba, O.; Kangawa, K.; Matsuo,
Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin peptidylhydroxyglycine N-
A;Reference number: S17855; MUID:92037609; PMID:1935950
A;Accession: S17855
A;Status: preliminary
A;Molecule type: mRNA
```

A;Residues: 1-935 <IWA>
A;Cross-references: UNIPROT:Q91697; UNIPARC:UPI00000FD952; EMBL:X62771; NID:g64530; PIDN
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: oxidoreductase
F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>

Query Match 88.2%; Score 30; DB 2; Length 935;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
Db 487 NYWMT 491

RESULT 29
URHUAP
Peptidylglycine monooxygenase (EC 1.14.17.3) / peptidylamidoglycolate lyase (EC 4.3.2.5)
N;Alternate names: C-terminal alpha-amidating enzyme; peptidyl alpha-amidating enzyme; P
N;Contains: peptidylamidoglycolate lyase (EC 4.3.2.5); peptidylglycine monooxygenase (EC
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40063; B40063; A39571
R;Eipper, B.A.; Park, L.P.; Dickerson, I.M.; Keutmann, H.T.; Thiele, E.A.; Rodriguez, H.
Mol. Endocrinol. 1, 777-790, 1987
A;Title: Structure of the precursor to an enzyme mediating COOH-terminal amidation in pe
A;Reference number: A40063; MUID:91042563; PMID:3153462
A;Accession: A40063
A;Molecule type: mRNA
A;Residues: 1-972 <EIP>
A;Cross-references: UNIPROT:P10731; UNIPARC:UPI0000125964; GB:M18683; NID:gl63481; PIDN:
A;Accession: B40063
A;Molecule type: protein
A;Residues: 31-45;37-53;64-76;84-97;202-228;230-258;319-339 <EIT>
A;Cross-references: UNIPARC:UPI0000172258; UNIPARC:UPI0000172259; UNIPARC:UPI000017225A;
A;Experimental source: pituitary
R;Katopodis, A.G.; Ping, D.; Smith, C.E.; May, S.W.
Biochemistry 30, 6189-6194, 1991
A;Title: Functional and structural characterization of peptidylamidoglycolate lyase, the
A;Reference number: A39571; MUID:91283459; PMID:2059626
A;Accession: A39571
A;Molecule type: protein
A;Residues: 478-499;544-575;611-630;665-695 <KAT>
A;Cross-references: UNIPARC:UPI000017225F; UNIPARC:UPI0000172260; UNIPARC:UPI0000172261;
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: amidine-lyase; carbon-nitrogen lyase; copper; glycoprotein; monooxygenase; m
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-30/Domain: propeptide #status predicted <PRO>
F;31-477/Product: peptidylglycine monooxygenase I #status predicted <PAM>
F;130-341/Domain: peptidylglycine monooxygenase I homology <PGM>
F;478-972/Product: peptidylamidoglycolate lyase #status predicted <PGL>
F;859-888/Domain: transmembrane #status predicted <TMN>
F;762/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.2%; Score 30; DB 1; Length 972;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
Db 591 NYWMT 595

RESULT 30
URHUAP
Peptidylglycine monooxygenase (EC 1.14.17.3) / peptidylamidoglycolate lyase (EC 4.3.2.5)
N;Alternate names: C-terminal alpha-amidating enzyme; peptidyl alpha-amidating enzyme; P
N;Contains: peptidyl-alpha hydroxyglycine alpha-amidating lyase; peptidylglycine alpha-a
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A35477; JC2418
R;Glauder, J.; Ragg, H.; Rauch, J.; Engels, J.W.
Biochem. Biophys. Res. Commun. 169, 551-558, 1990

A;Title: Human peptidylglycine alpha-amidating monooxygenase: cDNA, cloning and function
A;Reference number: A35477; MUID:90290494; PMID:2357221
A;Accession: A35477
A;Molecule type: mRNA
A;Residues: 1-974 <GLA>
A;Cross-references: UNIPROT:P19021; UNIPARC:UPI000016A5F; GB:M37721; NID:g189594; PIDN:
R;Tateishi, K.; Arakawa, F.; Misumi, Y.; Treston, A.M.; Vos, M.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 205, 282-290, 1994
A;Title: Isolation and functional expression of human pancreatic peptidylglycine alpha-a
A;Reference number: JC2418; MUID:95091738; PMID:7999037
A;Accession: JC2418
A;Molecule type: mRNA
A;Residues: 1-573; 'G', 575-828, 830-896, 898-974 <TAT>
A;Cross-references: UNIPARC:UPI0000172257
C;Genetics:
A;Gene: GDB:PAM
A;Cross-references: GDB:128628; OMIM:170270
A;Map position: 5q15-5q21
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: alternative splicing; amidine-lyase; carbon-nitrogen lyase; copper; glycopro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-30/Domain: propeptide #status predicted <PRO>
F;31-974/Product: peptidylglycine monooxygenase #status predicted <PAM>
F;130-341/Domain: peptidylglycine monooxygenase I homology <PGM>
F;864-887/Domain: transmembrane #status predicted <TMN>
F;762/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.2%; Score 30; DB 1; Length 974;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
Db 591 NYWMT 595

RESULT 31
URHUAP
Peptidylglycine monooxygenase (EC 1.14.17.3) precursor - rat
N;Alternate names: C-terminal alpha-amidating enzyme; peptidyl alpha-amidating enzyme; P
N;Contains: peptidylamidoglycolate lyase (EC 4.3.2.5) [peptidyl-alpha-hydroxyglycine alp
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A32193; B32193; S11333; S09582; B46679; A46679; S11334; S11335; S11336; S11
R;Stoffers, D.A.; Green, C.B.R.; Eipper, B.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 735-739, 1989
A;Title: Alternative mRNA splicing generates multiple forms of peptidyl-glycine alpha-am
A;Reference number: A32193; MUID:89099006; PMID:2911604
A;Accession: A32193
A;Molecule type: mRNA
A;Residues: 1-976 <STO>
A;Cross-references: UNIPROT:P14925; UNIPARC:UPI0000125965; GB:M25732; NID:g206022; PIDN:
A;Accession: B32193
A;Molecule type: mRNA
A;Residues: 1-392,498-976 <ST2>
A;Cross-references: UNIPARC:UPI000002A3AB; GB:M25719; NID:g206024; PIDN:AAA1804.1; PID
A;Experimental source: atrium
R;Kato, I.; Yonekura, H.; Yamamoto, H.; Okamoto, H.
FEBS Lett. 269, 319-323, 1990
A;Title: Isolation and functional expression of pituitary peptidylglycine alpha-amidatin
A;Reference number: S11333; MUID:90382572; PMID:2401356
A;Accession: S11333
A;Molecule type: mRNA
A;Residues: 1-958, 'S', 960-976 <KAT>
A;Cross-references: UNIPARC:UPI0000172263; GB:X59688; GB:X55770; NID:g56842
A;Experimental source: pituitary
R;Bertelsen, A.H.; Beaudry, G.A.; Galella, E.A.; Jones, B.N.; Ray, M.L.; Mehta, N.M.
Arch. Biochem. Biophys. 279, 87-96, 1990
A;Title: Cloning and characterization of two alternatively spliced rat alpha-amidating e
A;Reference number: S09582; MUID:90247899; PMID:2337358
A;Accession: S09582
A;Status: not compared with conceptual translation
A;Molecule type: mRNA

A;Residues: 1-393,499-831,833-886,918-958,'S',960-976 <BER>
A;Cross-references: UNIPARC:UPI0000172264; GB:U52650; GB:L01679; NID:92934921; GB:U52653
R;Husten, B.J.; Tausk, F.A.; Keutmann, H.T.; Eipper, B.A.
J. Biol. Chem. 268, 9709-9717, 1993
A;Title: Use of endoproteases to identify catalytic domains, linker regions, and function
A;Reference number: A46679; MUID:93252847; PMID:8486658
A;Accession: B46679
A;Molecule type: protein
A;Residues: 26-55 <HUS>
A;Cross-references: UNIPARC:UPI000006F2B9
A;Experimental source: rat clone expressed in human embryonic kidney cell line HEK-293
A;Note: sequence extracted from NCBI backbone (NCBI:P:133913)
A;Accession: A46679
A;Molecule type: protein
A;Residues: 376-392,498-504 <H2>
A;Cross-references: UNIPARC:UPI0000073366
A;Experimental source: rat clone expressed in embryonic kidney cell line HEK-293
A;Note: sequence extracted from NCBI backbone (NCBI:P:133914)
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I homolog
C;Keywords: alternative splicing; amidine-lyase; carbon-nitrogen lyase; copper; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-35/Domain: propeptide #status predicted <PRO>
F;36-976/Product: peptidylglycine monooxygenase 1 #status experimental <PAM1>
F;36-900,918-976/Product: peptidylglycine monooxygenase 4 #status experimental <PAM4>
F;36-831,900-976/Product: peptidylglycine monooxygenase 3 #status experimental <PAM3>
F;36-392,498-899,918-976/Product: peptidylglycine monooxygenase 5 #status experimental <PAM5>
F;36-392,498-976/Product: peptidylglycine monooxygenase 2 #status experimental <PAM2>
F;135-346/Domain: peptidylglycine monooxygenase I homology <PGM>
F;863-891/Domain: transmembrane #status predicted <TMN>
F;47-186,81-126,114-131,227-334,293-315/Disulfide bonds: #status experimental
F;79,313,318/Active site: Tyr, Glu, Tyr #status predicted
F;107,108,172/Binding site: copper 1 (His) #status predicted
F;242,244,314/Binding site: copper 2 (His, His, Met) #status predicted
F;765/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.2%; Score 30; DB 1; Length 976;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
594 NYWMT 598

Db

RESULT 32
AB2276
two-component hybrid sensor and regulator alr3761 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2276
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1550 <KUR>
A;Cross-references: UNIPROT:Q8YQ08; UNIPARC:UPI00000CE8D2; GB:BA000019; PIDN:BA075460.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3761

Query Match 88.2%; Score 30; DB 2; Length 1550;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
479 NYWMT 483

Db

RESULT 33
S10789
amylase A-180 - alkaliphilic eubacterium 163-26
C;Species: alkaliphilic eubacterium 163-26
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 15-Oct-1999
C;Accession: S10789
R;Candussio, A.; Schmid, G.; Boeck, A.
Eur. J. Biochem. 191, 177-185, 1990
A;Title: Biochemical and genetic analysis of a maltopentaose-producing amylase from an
A;Reference number: S10789; MUID:90336627; PMID:1696201
A;Accession: S10789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1684 <CAN>
A;Cross-references: UNIPARC:UPI000002CD09; EMBL:X53373; NID:948305; PIDN:CAA37453.1; PIU10789

Query Match 88.2%; Score 30; DB 2; Length 1684;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
375 NYWMT 379

Db

RESULT 34
T30838
cytoplasmic dynein heavy chain - Paramaecium tetraurelia
C;Species: Paramaecium tetraurelia
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30838; PC4341
R;Kandl, K.A.; Forney, J.D.; Asai, D.J.
submitted to the EMBL Data Library, January 1995
A;Description: The dynein genes of Paramaecium: the differential expression of axonemal
A;Reference number: Z20502
A;Accession: T30838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4540 <KAN>
A;Cross-references: UNIPROT:Q27171; UNIPARC:UPI000013CA9; EMBL:U20449; NID:9987228; PIU10789
R;Asai, D.J.; Beckwith, S.M.; Kandl, K.A.; Keating, H.H.; Tjandra, H.; Forney, J.D.
J. Cell Sci. 107, 839-847, 1994
A;Title: The dynein genes of Paramaecium tetraurelia: Sequences adjacent to the catalytic
A;Reference number: PC4340; MUID:94334383; PMID:8056840
A;Accession: PC4341
A;Molecule type: mRNA
A;Residues: 1831-2029 <ASA>
A;Cross-references: UNIPARC:UPI00001775BF
C;Genetics:
A;Genetic code: SGC5
A;Introns: 57/3
C;Superfamily: dynein heavy chain, cytosolic

Query Match 88.2%; Score 30; DB 2; Length 4540;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:
266 NYWMT 270

Db

RESULT 35
S36381
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
A;Accession: S36381; S33396
R;Ansell, K.H.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36376
A;Accession: S36381

A;Molecule type: mRNA
A;Residues: 1-59 <ANS>
A;Cross-references: UNIPARC:UPI000011C623; EMBL:X73012; NID:9295879; PIDN:CAA51498.1; PI
R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A;Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi
A;Reference number: S33391; MUID:93122092; PMID:8419173
A;Accession: S33396
A;Molecule type: mRNA
A;Residues: 3-43 <KET>
A;Cross-references: UNIPARC:UPI0000176EA2; EMBL:X73012
A;Experimental source: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;14-59/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 85.3%; Score 29; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 33 NYWM 36

RESULT 36
S36384
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
A;Accession: S36384; S33399
R;Ansell, K.H.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36376
A;Accession: S36384
A;Molecule type: mRNA
A;Residues: 1-66 <ANS>
A;Cross-references: UNIPARC:UPI000011C629; EMBL:X73020; NID:9295888; PIDN:CAA51504.1; PI
R;Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A;Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi
A;Reference number: S33391; MUID:93122092; PMID:8419173
A;Accession: S33399
A;Molecule type: mRNA
A;Residues: 1-39 <KET>
A;Cross-references: UNIPARC:UPI0000176EA5; EMBL:X73020
A;Experimental source: strain BALB/c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;14-66/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 85.3%; Score 29; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 30 NYWM 33

RESULT 37
G28833
Ig kappa chain V region (HP22.218.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Aug-1996
A;Accession: G28833
R;Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
J. Immunol. 141, 779-784, 1988
A;Title: Alleloneic manipulation of the GAT idiotypic cascade. Immunization of C57BL/6 m
A;Reference number: A92827; MUID:88285674; PMID:3135311
A;Accession: G28833
A;Molecule type: mRNA
A;Residues: 1-89 <COR>

A;Cross-references: UNIPARC:UPI0000176C05
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;6-89/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 22 NYWM 25

RESULT 38
PH1004
Ig heavy chain V region (clone 165.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
A;Accession: PH1004
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1004
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-91 <TYL>
A;Cross-references: UNIPARC:UPI0000176ACD
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 85.3%; Score 29; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 13 NYWM 16

RESULT 39
SI7613
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
A;Accession: SI7613
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: SI7230; MUID:91326098; PMID:1907718
A;Accession: SI7613
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <CLA>
A;Cross-references: UNIPARC:UPI0000176E7A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;8-91/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 24 NYWM 27

RESULT 40
PH1155
Ig heavy chain V region (clone 3D.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1155
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1155
A:Molecule type: DNA
A:Residues: 1-97 <SCH>
A:Cross-references: UNIPROT:Q924Q1; UNIPARC:UPI0000176BC1
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
Db 30 NYWM 33

RESULT 41
PH1106
Ig heavy chain V region (clones V4.2B, V17.2B, V33.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1106
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1106
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI0000176BEF
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
Db 31 NYWM 34

RESULT 42
PH1160
Ig heavy chain V region (clone 7A.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1160
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1160
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176BC5
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
Db 31 NYWM 34

RESULT 43
PH1144
Ig heavy chain V region (clone V2048.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1144
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1144
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q5; UNIPROT:Q924Q8; UNIPROT:Q924Q7; UNIPARC:UPI0000176BBA
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
Db 31 NYWM 34

RESULT 44
PH1151
Ig heavy chain V region (clone 13F.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1151
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1151
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q8; UNIPROT:Q924Q7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924R3; UNIPROT:Q924R2; UNIPARC:UPI0000176BBA
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
Db 31 NYWM 34

RESULT 45
PH1112
Ig heavy chain V region (clone V23.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1112
R:Schitteck, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH112
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:CROSS-references: UNIPROT:Q924R6; UNIPARC:UPI0000176BF2
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
Db 31 NYWM 34

RESULT 46
I60919
HNF-3/fork-head homolog-5 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I60919
R:Clevidence, D.E.; Overdier, D.G.; Tao, W.; Qian, X.; Pani, L.; Lai, E.; Costa, R.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3948-3952, 1993
A:Title: Identification of nine tissue-specific transcription factors of the hepatocyte
A:Reference number: A47450; MUID:93248207; PMID:7683413
A:Accession: I60919
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-101 <RES>
A:CROSS-references: UNIPROT:Q63248; UNIPARC:UPI000012ADDF; GB:L13205; NID:G310158; PIDN:
F:3-94/Domain: fork head DNA-binding domain homology <FHD>

Query Match 85.3%; Score 29; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
Db 75 NYWM 78

RESULT 47
PH0987
Ig heavy chain V region (clone 163.47) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0987
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0987
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <TIL>
A:CROSS-references: UNIPARC:UPI0000176D07
A:Experimental source: B cell, strain [NZB x NZW]P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||

J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26318
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:CROSS-references: UNIPARC:UPI00001769A7; EMBL:X59200
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
Db 19 NYWM 22

RESULT 49
B54743
transcription factor HFK2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C:Accession: B54743
R:Murphy, D.B.; Wiese, S.; Burteind, P.; Schmundt, D.; Mattei, M.G.; Schulz-Schaeffer, W
Genomics 21, 551-557, 1994
A:Title: Human brain factor 1, a new member of the fork head gene family.
A:Reference number: A54743; MUID:95048332; PMID:7959731
A:Accession: B54743
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-109 <MUR>
A:CROSS-references: UNIPARC:UPI000017A1FB; GB:X74143
C:Genetics:
A:Gene: GDB:FKHL2; HBP-2; HFK2
A:CROSS-references: GDB:375747; OMIM:600779
A:Map position: 14q11-14q13
F:8-99/Domain: fork head DNA-binding domain homology <FHD>

Query Match 85.3%; Score 29; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
Db 80 NYWM 83

RESULT 50
MHMS76
Ig heavy chain V-III region (HPC76) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 09-Jul-2004
C:Accession: A02074
R:Bernard, O.; Gough, N.M.
Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980
A:Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between tran
A:Reference number: A02074; MUID:81013937; PMID:6251474
A:Accession: A02074
A:Molecule type: mRNA
A:Residues: 1-111 <BER>

A:Cross-references: UNIPROT:P01804; UNIPARC:UPI0000027247
A>Note: the sequence was also determined from the differentiated gene
A>Note: the sequence of the first 197 residues of the C region was also determined and d
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-94/Domain: immunoglobulin homology <IMM>
F:17-92/Disulfide bonds: #status predicted

Query Match 85.3%; Score 29; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
26 NYWM 29

Search completed: May 11, 2006, 16:38:03
Job time : 17.377 secs

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GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 46.2295 Seconds
(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-1

Perfect score: 34

Sequence: 1 NYWMT 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	209	Q7XB55_9VIRI	Q7xb55 closterium
2	34	100.0	255	Q36098_THEPA	Q36098 theileria p
3	34	100.0	430	Q8XI47_CLOPE	Q8xi47 clostridium
4	34	100.0	479	Q5PQK9_RAT	Q5pqk9 rattus norv
5	34	100.0	481	Q831B5_ENTFA	Q831b5 enterococu
6	34	100.0	1441	Q9LK63_ARATH	Q9lk63 arabidopsis
7	34	100.0	1466	Q8VZZ4_ARATH	Q8vzza arabidopsis
8	31	91.2	116	Q9XPH9_CHEMY	Q9xph9 chelonias my
9	31	91.2	154	Q7QJP6_ANOGA	Q7qjp6 anopheles g
10	31	91.2	208	Q7P812_FUSNV	Q7p812 fusobacteri
11	31	91.2	229	Q88T17_LACPL	Q88t17 lactobacill
12	31	91.2	270	Q9S9N0_ARATH	Q9s9n0 arabidopsis
13	31	91.2	281	Q66BH8_YERPS	Q66bh8 yersinia ps
14	31	91.2	293	Q8ZZ19_PYRAE	Q8zz19 pyrobaculum
15	31	91.2	296	Q811M6_ENTABE	Q811m6 enterobacte
16	31	91.2	348	Q5QHV5_LETAM	Q5qhv5 leishmania
17	31	91.2	348	Q4QB87_LETMA	Q4qb87 leishmania
18	31	91.2	349	Q86FT0_LEITA	Q86ft0 leishmania
19	31	91.2	354	Q4HUH3_GIBZE	Q4huh3 gibberella
20	31	91.2	364	Q8PTH4_METMA	Q8pth4 methanosarc
21	31	91.2	401	Q5B017_EMENI	Q5b017 aspergillus
22	31	91.2	423	Q6AE08_LEITXX	Q6ae08 leifsonia x
23	31	91.2	447	Q7UY34_RHOBA	Q7uy34 rhodopirell
24	31	91.2	453	Q9BRN4_HUMAN	Q9brn4 homo sapien
25	31	91.2	454	Q59NK9_CANAL	Q59nk9 candida alb
26	31	91.2	455	Q5XXG4_GEOKA	Q5xxg4 geobacillus
27	31	91.2	489	Q9CL71_PASMU	Q9cl71 pasteurella
28	31	91.2	493	1 XYL8_HAEIN	P44401 haemophilus
29	31	91.2	493	Q30495_PSEFL	O30495 pseudomonas
30	31	91.2	493	Q4ZTP8_PSESE	Q4ztp8 pseudomonas
31	31	91.2	493	Q882C6_PSESM	Q882c6 pseudomonas

32	31	91.2	495	2	Q4ITN3_AZOVI	Q4itn3 azotobacter
33	31	91.2	503	2	Q7N5I9_PHOLL	Q7n5i9 photorhabdu
34	31	91.2	511	2	Q4QLI1_HAB18	Q4qli1 haemophilus
35	31	91.2	520	2	Q8RNR2_LEGPN	Q8rnr2 legionella
36	31	91.2	520	2	Q5WTT7_LEGPL	Q5wt77 legionella
37	31	91.2	520	2	Q5X211_LEGPA	Q5x211 legionella
38	31	91.2	520	2	Q5ZSK3_LEGPH	Q5zsk3 legionella
39	31	91.2	534	2	Q4QQA0_DROME	Q4qqa0 drosophila
40	31	91.2	534	2	Q4VST4_DROME	Q4vst4 drosophila
41	31	91.2	539	2	Q9VJ03_DROME	Q9vj03 drosophila
42	31	91.2	561	2	Q6MMW1_BDEBA	Q6mmw1 bdellovibri
43	31	91.2	561	2	P95867_SULSO	P95867 sulfolobus
44	31	91.2	606	2	Q977Y3_CLOAB	Q977y3 clostridium
45	31	91.2	716	2	Q8R2A7_9VIRU	Q8rqv7 canine minu
46	31	91.2	716	2	Q8QAV7_VIRU	Q8qav7 canine minu
47	31	91.2	749	2	Q8DE10_VIBVU	Q8de10 vibrio vuln
48	31	91.2	749	2	Q7MPN5_VIBVU	Q7mpn5 vibrio vuln
49	31	91.2	758	2	Q4VXY0_HUMAN	Q4vxy0 homo sapien
50	31	91.2	762	1	GLGB_NEIDE	Q9rg15 neisseria d
51	31	91.2	776	2	Q4S9H6_TETNG	Q4s9h6 tetraodon n
52	31	91.2	802	2	Q5ZL60_CHICK	Q5z160 gallus gall
53	31	91.2	803	1	CLCN7_MOUSE	O70496 mus musculu
54	31	91.2	803	1	CLCN7_RAT	P51799 rattus norv
55	31	91.2	803	2	Q6RUT3_MOUSE	P6rut3 mus musculu
56	31	91.2	805	1	CLCN7_HUMAN	P51798 homo sapien
57	31	91.2	805	2	Q4UOX5_RABIT	Q4uox5 oryctolagus
58	31	91.2	809	2	Q4PKH3_BOVIN	Q4pkh3 bos taurus
59	31	91.2	812	2	Q6GRY8_HUMAN	Q96ty8 homo sapien
60	31	91.2	904	2	Q87JH7_VIBPA	Q87jh7 vibrio para
61	31	91.2	1047	2	Q55PA9_DICDI	Q55fa9 dictyosteli
62	31	91.2	1055	1	RPOC_PEDAC	P77917 pediococcus
63	31	91.2	1121	2	Q4P7M9_USTMA	Q4p7m9 ustilago ma
64	31	91.2	1217	2	Q5FM96_LACJO	Q5fm96 lactobacill
65	31	91.2	1224	2	Q74L94_LACJO	Q74l94 lactobacill
66	31	91.2	2158	2	Q9RR50_VIBCH	Q9rr50 vibrio chol
67	31	91.2	2413	2	Q9PDB0_VIBCH	Q9fdb0 vibrio chol
68	31	91.2	3271	2	Q7N1E4_PHOLL	Q7nie4 photorhabdu
69	30	88.2	62	2	Q74P76_BACCL	Q74p76 bacillus ce
70	30	88.2	100	2	Q736W0_BACCL	Q736w0 bacillus ce
71	30	88.2	101	2	Q97VA1_SULSO	Q97va1 sulfolobus
72	30	88.2	105	2	Q6B715_RABIT	Q6b715 oryctolagus
73	30	88.2	115	2	Q9P8V1_ASHGO	Q9p8v1 ashbya goss
74	30	88.2	122	2	Q6SX65_HCMV	Q6sxb6 human cytom
75	30	88.2	122	2	Q6SXB6_HCMV	Q6sxb6 human cytom
76	30	88.2	127	2	Q5DHN3_SCHJA	Q5dhn3 schistosoma
77	30	88.2	196	2	Q5HZA9_RAT	Q5hza9 rattus norv
78	30	88.2	196	2	Q9D8V1_MOUSE	Q9d8v1 mus musculu
79	30	88.2	219	2	Q54MP3_DICDI	Q54mp3 dictyosteli
80	30	88.2	223	1	CLPP2_GLUOX	Q5tqt4 gluconobact
81	30	88.2	226	2	Q946Y2_ORYSA	Q946y2 oryza sativ
82	30	88.2	234	2	Q81737_ARATH	Q81737 arabidopsis
83	30	88.2	241	2	Q88T15_LACPL	Q88t15 lactobacill
84	30	88.2	260	2	Q6PA76_XENLA	Q6pa76 xenopus lae
85	30	88.2	267	2	Q6HMX4_BACHK	Q6hmx4 bacillus th
86	30	88.2	267	2	Q81CJ7_BACCR	Q81cj7 bacillus ce
87	30	88.2	267	2	Q81PP5_BACAN	Q81pp5 bacillus an
88	30	88.2	267	2	Q63AI7_BACCZ	Q63ai7 bacillus ce
89	30	88.2	281	2	Q84WP6_ARATH	Q84wf6 arabidopsis
90	30	88.2	292	2	Q709M9_9ENTR	Q709m9 citrobacter
91	30	88.2	301	1	V130_FOWPV	P15912 fowlpox vir
92	30	88.2	301	2	Q70H28_FOWPV	Q70h28 fowlpox vir
93	30	88.2	309	2	Q7CFB1_STRP5	Q7cfb1 streptococc
94	30	88.2	309	2	Q8E143_STRP5	Q8e143 streptococc
95	30	88.2	309	2	Q8E6J7_STRP3	Q8e6j7 streptococc
96	30	88.2	309	2	Q8E1U3_STRP8	Q8e1u3 streptococc
97	30	88.2	312	2	Q878G5_STRP3	Q878g5 streptococc
98	30	88.2	312	2	Q9A0S3_STRPY	Q9a0s3 streptococc
99	30	88.2	314	2	Q4NT55_9DELT	Q4nt55 anaeromyxob
100	30	88.2	319	2	Q5XD25_STRP6	Q5xd25 streptococc
101	30	88.2	329	2	Q5C405_SCHJA	Q5c405 schistosoma
102	30	88.2	331	2	Q5FL87_CANGA	Q5fl87 candida gla
103	30	88.2	339	2	Q754N9_ASHGO	Q754n9 ashbya goss
104	30	88.2	339	2	Q81Y98_HUMAN	Q81y98 homo sapien

105 30 88.2 351 2 Q50RC6 ENTHI Q50rc6 entamoeba h 178 29 85.3 75 2 Q85KH4_9HYME 2085KH4_9HYME
 106 30 88.2 Q8XU48 CAEEL Q8xu48 caenorhabdi 179 29 85.3 85 2 Q4VC96_9AVES 204VC96_9AVES
 107 30 88.2 Q8YX34_ANASP Q8yx34 anabaena sp 180 29 85.3 93 2 Q03477_METTY 003477_METTY
 108 30 88.2 Q74LE1_LACJO Q74le1 lactobacilli 181 29 85.3 93 2 Q20906_METAE 020906_METAE
 109 30 88.2 Q6PI31_MOUSE Q6pi31 mus musculus 182 29 85.3 95 2 Q5C3B9_SCHJA 05C3B9_SCHJA
 110 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 183 29 85.3 95 2 Q20907_METTY 020907_METTY
 111 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 184 29 85.3 96 2 Q20899_9AVES 020899_9AVES
 112 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 185 29 85.3 96 2 Q20904_METTS 020904_METTS
 113 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 186 29 85.3 97 2 Q20900_9AVES 020900_9AVES
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 122 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 195 29 85.3 111 1 HV35_MOUSE 10111 HV35_MOUSE
 123 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 196 29 85.3 111 2 Q59Y16_CANAL 059Y16_CANAL
 124 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 197 29 85.3 111 2 Q59YX3_CANAL 059YX3_CANAL
 125 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 198 29 85.3 112 2 Q4QTC6_9PASS 04QTC6_9PASS
 126 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 199 29 85.3 112 2 Q8LUC7_9FURN 08LUC7_9FURN
 127 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 200 29 85.3 112 2 Q8LY69_9FURN 08LY69_9FURN
 128 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 201 29 85.3 112 2 Q9T825_9PASS 09T825_9PASS
 129 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 202 29 85.3 113 1 HV27_MOUSE 10111 HV27_MOUSE
 130 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 203 29 85.3 113 1 HV28_MOUSE 10111 HV28_MOUSE
 131 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 204 29 85.3 113 1 HV30_MOUSE 10111 HV30_MOUSE
 132 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 205 29 85.3 113 1 HV31_MOUSE 10111 HV31_MOUSE
 133 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 206 29 85.3 113 1 HV34_MOUSE 10111 HV34_MOUSE
 134 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 207 29 85.3 113 1 HV33_MOUSE 10111 HV33_MOUSE
 135 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 208 29 85.3 115 1 HV33_MOUSE 10111 HV33_MOUSE
 136 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 209 29 85.3 115 1 HV33_MOUSE 10111 HV33_MOUSE
 137 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 210 29 85.3 116 2 Q6DK56_9SAUR 06DK56_9SAUR
 138 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 211 29 85.3 118 2 Q93B84_HUMAN 093B84_HUMAN
 139 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 212 29 85.3 121 2 Q4ZBY4_CAUD 04ZBY4_CAUD
 140 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 213 29 85.3 123 2 Q8N287_HUMAN 08N287_HUMAN
 141 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 214 29 85.3 123 2 Q47794_ENTFA 047794_ENTFA
 142 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 215 29 85.3 125 2 Q4Q052_LEIMA 04Q052_LEIMA
 143 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 216 29 85.3 128 2 Q7T6W8_9REOV 07T6W8_9REOV
 144 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 217 29 85.3 130 2 Q6NVU8_HUMAN 06NVU8_HUMAN
 145 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 218 29 85.3 133 2 Q5DC51_SCHJA 05DC51_SCHJA
 146 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 219 29 85.3 133 2 Q6EB45_CAMJE 06EB45_CAMJE
 147 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 220 29 85.3 136 2 Q9GM39_MACFA 09GM39_MACFA
 148 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 221 29 85.3 142 2 Q4NLA2_9MICC 04NLA2_9MICC
 149 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 222 29 85.3 143 2 Q6RC33_DROSE 06RC33_DROSE
 150 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 223 29 85.3 144 2 Q6RC44_DROMA 06RC44_DROMA
 151 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 224 29 85.3 144 2 Q6RC43_DROMA 06RC43_DROMA
 152 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 225 29 85.3 144 2 Q6RC42_DROMA 06RC42_DROMA
 153 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 226 29 85.3 144 2 Q6RC41_DROMA 06RC41_DROMA
 154 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 227 29 85.3 146 2 Q4XBL3_PLACH 04XBL3_PLACH
 155 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 228 29 85.3 146 2 Q88KJ6_PSEPK 088KJ6_PSEPK
 156 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 229 29 85.3 148 2 Q9DALL_MOUSE 09DALL_MOUSE
 157 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 230 29 85.3 149 2 Q7T6W5_9REOV 07T6W5_9REOV
 158 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 231 29 85.3 151 2 Q8TW2_METKA 08TW2_METKA
 159 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 232 29 85.3 151 2 Q9FFY3_ARATH 09FFY3_ARATH
 160 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 233 29 85.3 163 2 Q9LH32_ARATH 09LH32_ARATH
 161 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 234 29 85.3 167 2 Q800K2_ORYLA 0800K2_ORYLA
 162 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 235 29 85.3 168 2 Q95QA9_CAEL 095QA9_CAEL
 163 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 236 29 85.3 168 2 Q4ZB07_9VIRU 04ZB07_9VIRU
 164 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 237 29 85.3 172 2 Q8H1U2_MONBE 08H1U2_MONBE
 165 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 238 29 85.3 178 2 Q4LERO_9REOV 04LERO_9REOV
 166 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 239 29 85.3 187 2 Q800K3_ORYLA 0800K3_ORYLA
 167 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 240 29 85.3 187 2 Q4TAU2_TETNG 04TAU2_TETNG
 168 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 241 29 85.3 203 2 Q4G2D6_TRIVA 04G2D6_TRIVA
 169 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 242 29 85.3 204 2 Q5VZD2_CNPV 05VZD2_CNPV
 170 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 243 29 85.3 207 2 Q5L8L6_BACFN 05L8L6_BACFN
 171 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 244 29 85.3 208 2 Q968M9_PLAVI 0968M9_PLAVI
 172 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 245 29 85.3 209 2 Q968M6_PLAVI 0968M6_PLAVI
 173 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 246 29 85.3 214 2 Q576P9_BRUAB 0576P9_BRUAB
 174 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 247 29 85.3 214 2 Q89464_MYCLE 089464_MYCLE
 175 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 248 29 85.3 214 2 Q8FUQ3_BRUSU 08FUQ3_BRUSU
 176 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 249 29 85.3 214 2 Q8YDF6_BRUME 08YDF6_BRUME
 177 30 88.2 Q8P131_MOUSE Q8p131 mus musculus 250 29 85.3 216 2 Q6W537_ANOGA 06W537_ANOGA

Q85kh4 schletterer
 Q4vc96 cevx cyanop
 O03477 metallura t
 O20906 metallura a
 Q5c3e9 schisoma
 O20907 metallura t
 O20899 metallura w
 O20904 metallura t
 O20900 metallura w
 O20901 metallura b
 O20902 metallura p
 O20903 metallura o
 O20905 metallura e
 O20908 metallura t
 O20909 metallura t
 O21857 metallura t
 Q63248 rattus norv
 P01804 mus musculu
 Q59y16 candida alb
 Q59yx3 candida alb
 Q4gtc5 lepidothrix
 Q8luc7 glyphorynch
 Q8ly69 glyphorynch
 Q9t825 pipra pipra
 P01796 mus musculu
 P01797 mus musculu
 P01798 mus musculu
 P01799 mus musculu
 P01800 mus musculu
 P01803 mus musculu
 P01801 mus musculu
 P01802 mus musculu
 Q6dk56 chinemys re
 Q9h3b4 homo sapien
 Q8zb4 bacterioph
 Q8n287 homo sapien
 Q47794 enterococu
 Q4q052 leishmania
 Q7t6w8 equine rota
 Q6nvu8 homo sapien
 Q5dc51 schisoma
 Q6eb45 campylobact
 Q9gm39 macaca fasc
 Q4nla2 athrobacte
 Q6rc33 drosophila
 Q6rc44 drosophila
 Q6rc43 drosophila
 Q6rc42 drosophila
 Q4xbl3 plasmodium
 Q88kj6 pseudomonas
 Q9dal1 mus musculu
 Q7t6w5 equine rota
 Q8tw2 methanopyru
 Q9ffy3 arabidopsis
 Q9lh32 arabidopsis
 Q800k2 oryzias lat
 Q95qa9 caenorhabdi
 Q4zbq7 bacterioph
 Q8h1u2 monosiga br
 Q4lero equine rota
 Q800k3 oryzias lat
 Q4tau2 tetraodon n
 Q4g2d6 trichomonas
 Q6vzd2 canarypox v
 Q5l8l6 bacteroides
 Q968m9 plasmodium
 Q968m6 plasmodium
 Q576f9 brucella ab
 Q89464 mycobacteri
 Q8fuq3 brucella su
 Q8ydf6 brucella me
 Q6w537 anopheles g

251	29	85.3	217	2	Q4FPD6_9RICK	Q4fpd6 candidatus	324	29	85.3	305	2	Q58AD9_9BURK	Q58ad9 ralstonia m
252	29	85.3	219	2	Q92RD1_RHINE	Q92rd1 rhizobium m	325	29	85.3	306	1	Q5UBC_BACSU	Q45462 bacillus eu
253	29	85.3	220	1	CLPP_BACFR	Q64nd2 bacteroides	326	29	85.3	307	2	Q5TW03_ANOGA	Q5tw03 anopheles g
254	29	85.3	221	1	CLPP_BACTN	Q8ai29 bacteroides	327	29	85.3	308	2	Q8BWM4_MYCPE	Q8bwm4 mycoplasma
255	29	85.3	222	1	CLPP_PORGI	Q7mx09 porphyromon	328	29	85.3	310	2	Q566W3_BRARE	Q566w3 brachydanio
256	29	85.3	224	1	FOXGC_HUMAN	Q14488 homo sapien	329	29	85.3	310	2	Q4T255_TETNG	Q4t255 tetraodon n
257	29	85.3	225	2	Q9NAF1_CABEL	Q9naf1 caenorhabd1	330	29	85.3	312	2	Q59T29_CANAL	Q59t29 candida alb
258	29	85.3	228	2	Q7WJG4_BORPA	Q7wjg4 bordetella	331	29	85.3	312	2	Q59T58_CANAL	Q59t58 candida alb
259	29	85.3	229	2	Q9GN92_DROSI	Q9gm92 drosophila	332	29	85.3	315	2	Q4HAP7_9DEIO	Q4hap7 deinococcus
260	29	85.3	229	2	Q9GN93_DROSI	Q9gm93 drosophila	333	29	85.3	318	2	Q8IT15_9METZ	Q8it15 mnemiopsis
261	29	85.3	229	2	Q9GN11_DROSI	Q9gn11 drosophila	334	29	85.3	321	2	Q9WVL7_THEMA	Q9wvl7 thermotoga
262	29	85.3	229	2	Q9GPE4_DROSI	Q9gpe4 drosophila	335	29	85.3	324	2	Q9FV9_9ARATH	Q9fv9 arabidopsis
263	29	85.3	229	2	Q9GPE5_DROSI	Q9gpe5 drosophila	336	29	85.3	327	2	Q9RDE9_DEIRA	Q9rde9 deinococcus
264	29	85.3	229	2	Q7WOP2_BORBR	Q7wop2 bordetella	337	29	85.3	331	2	Q72AK1_DESVH	Q72ak1 desulfovibr
265	29	85.3	229	2	Q7WET4_BORBR	Q7wet4 bordetella	338	29	85.3	333	2	Q6NW50_BRARE	Q6nw50 brachydanio
266	29	85.3	231	2	Q6WHQ2_BPKV4	Q6whq2 bacterioph	339	29	85.3	334	2	Q8NLW1_CORGL	Q8nlw1 corynebacte
267	29	85.3	231	2	Q6YQV4_ONYPE	Q6yvq4 onion yello	340	29	85.3	339	2	Q5DFU1_SCHJA	Q5dfu1 schistosoma
268	29	85.3	234	1	A29AB_DROME	Q46197 drosophila	341	29	85.3	340	2	Q7P6Q3_FUSNV	Q7p6q3 fusobacteri
269	29	85.3	234	1	A29AB_DROSI	Q9u968 drosophila	342	29	85.3	341	2	Q6MPQ3_BDEBA	Q6mpq3 bdellovibri
270	29	85.3	234	1	Q6GUY7_DROME	Q6guy7 drosophila	343	29	85.3	342	2	Q19258_CABEL	Q19258 caenorhabd1
271	29	85.3	234	2	Q6GUY6_DROME	Q6guy6 drosophila	344	29	85.3	343	2	Q9N880_PLAVI	Q9n880 plasmodium
272	29	85.3	234	2	Q6GUY8_DROME	Q6guy8 drosophila	345	29	85.3	344	2	Q7Y9C0_9SAUR	Q7y9c0 typanocryp
273	29	85.3	234	2	Q6GUZ1_DROME	Q6guz1 drosophila	346	29	85.3	344	2	Q674C8_9CORV	Q674c8 telophoru
274	29	85.3	236	1	YAIH_LACLA	Q9cjb2 lactococcus	347	29	85.3	346	2	Q61981_CABEL	Q61981 caenorhabd1
275	29	85.3	236	2	Q8DXH4_STRAS	Q8dxh4 streptococ	348	29	85.3	346	2	Q69X98_ORYSA	Q69x98 oryza sativ
276	29	85.3	238	2	Q5ISQ9_MACFA	Q5isq9 macaca fasc	349	29	85.3	346	2	Q56T02_PHAPA	Q56t02 pharomachru
277	29	85.3	238	2	Q7T6W1_9REOV	Q7t6w1 equine rota	350	29	85.3	346	2	Q56T04_PHAHA	Q56t04 pharomachru
278	29	85.3	239	2	Q8P216_STRP3	Q8p216 streptococ	351	29	85.3	346	2	Q5IAM9_METTY	Q5iam9 metallura t
279	29	85.3	239	2	Q7CNK4_STRP8	Q7cnk4 streptococ	352	29	85.3	346	2	Q5IAN0_METFA	Q5ian0 metallura a
280	29	85.3	239	2	Q7T6W3_9REOV	Q7t6w3 equine rota	353	29	85.3	346	2	Q5IAQ2_9AVES	Q5iaq2 ensifera en
281	29	85.3	242	2	Q80897_HP23	Q80897 human papil	354	29	85.3	346	2	Q6WR68_9AVES	Q6wr68 neomorphus
282	29	85.3	246	1	Y495_SYNY3	Q55185 synchocycat	355	29	85.3	346	2	Q8HJRE_9PASS	Q8hje2 eminia lepi
283	29	85.3	246	2	Q8RQV4_DEIRA	Q8rvq4 deinococcus	356	29	85.3	346	2	Q8SIQ6_9SYLV	Q8siq6 cisticola f
284	29	85.3	248	2	Q66270_9SPHN	Q66270 erythromicr	357	29	85.3	346	2	Q8HK61_9FURN	Q8hk61 glyphorynch
285	29	85.3	251	2	Q82990_9SPHN	Q82990 erythroba	358	29	85.3	349	2	Q9KVB1_VIRCH	Q9kvb1 vibrio chol
286	29	85.3	255	2	Q6PC11_ACIAD	Q6fc11 actinobact	359	29	85.3	351	2	Q5AY08_EMENI	Q5ay08 aspergillus
287	29	85.3	256	2	Q8PWE0_METWA	Q8pwe0 methanobac	360	29	85.3	351	2	Q7Q0P8_ANOGA	Q7q0p8 anopheles g
288	29	85.3	259	1	LPXA_CHRVI	Q46481 chromatium	361	29	85.3	355	2	Q4UQF9_XANCP	Q4uqf9 xanthomonas
289	29	85.3	260	2	Q8MXW9_DUGJA	Q8mxw9 dugesia jap	362	29	85.3	355	2	Q8PC20_XANCP	Q8pc20 xanthomonas
290	29	85.3	262	2	Q9LXW0_ARATH	Q9lxw0 arabidopsis	363	29	85.3	356	2	Q7YTB3_SACKO	Q7ytb3 saccoglossu
291	29	85.3	265	2	Q5YKJ4_MOCFA	Q5yvji4 nocardia fa	364	29	85.3	365	2	Q5W0Z9_HUMAN	Q5w0z9 homo sapien
292	29	85.3	270	2	Q22510_CABEL	Q22510 caenorhabd1	365	29	85.3	368	2	Q8VCL6_MOUSE	Q8vc16 mus musculu
293	29	85.3	271	2	Q573M6_9BACT	Q573m6 uncultured	366	29	85.3	368	2	Q9D3Q8_MOUSE	Q9d3q8 mus musculu
294	29	85.3	271	2	Q7VK16_HELBP	Q7vk16 helicobacte	367	29	85.3	372	2	Q6SEW9_9BACT	Q6sew9 uncultured
295	29	85.3	272	2	Q8SLI7_TETNG	Q8sl17 tetraodon n	368	29	85.3	374	2	Q5SR52_CRYNE	Q5sr52 cryptococcu
296	29	85.3	274	2	Q8Y5E8_LISMO	Q8y5e8 listeria mo	369	29	85.3	375	2	Q6SH42_9BACT	Q6sh42 uncultured
297	29	85.3	277	2	Q7LXP7_LISMF	Q7lxp7 listeria in	370	29	85.3	377	2	Q6LXG3_CABER	Q6lxg3 caenorhabd1
298	29	85.3	277	2	Q929Q3_LISIN	Q929q3 listeria in	371	29	85.3	380	2	Q36232_WILSA	Q36232 williopsis
299	29	85.3	279	2	Q619H6_CABER	Q619h6 caenorhabd1	372	29	85.3	380	2	Q8A342_BACTN	Q8a342 bacteroides
300	29	85.3	279	2	Q66778_9REOV	Q66778 equine rota	373	29	85.3	380	2	Q5NII4_FRATT	Q5nii4 franciella
301	29	85.3	279	2	Q66778_9REOV	Q66778 equine rota	374	29	85.3	380	2	Q5Y5T1_MOUSE	Q5y5t1 mus musculu
302	29	85.3	279	2	Q66779_9REOV	Q66779 equine rota	375	29	85.3	382	2	Q9I0R2_PSEAB	Q9i0r2 pseudomonas
303	29	85.3	279	2	Q66780_9REOV	Q66780 equine rota	376	29	85.3	383	2	P74616_SYNY3	P74616 synchocyst
304	29	85.3	279	2	Q6SKR7_9REOV	Q6skr7 human rotav	377	29	85.3	387	1	QIN_AVTIS3	Q56260 avian sarco
305	29	85.3	283	1	YDAU_ECOLI	Q6xk5 brachydanio	378	29	85.3	388	2	Q5A1R9_CANAL	Q5a1r9 candida alb
306	29	85.3	285	1	Q6NDX5_BRARE	Q6ndx5 escherichia	379	29	85.3	392	1	FOXQ1_RAT	Q63244 rattus norv
307	29	85.3	285	2	Q627K9_ORYSA	Q627k9 oryza sativ	380	29	85.3	395	2	Q5LUB4_SILPO	Q5lub4 silicibacte
308	29	85.3	288	2	Q5PA65_NEIG1	Q5fa65 neisseria g	381	29	85.3	395	2	Q7SX57_AVTIS3	Q7sx57 avian sarco
309	29	85.3	289	2	Q9JUY3_NEIMA	Q9juy3 neisseria m	382	29	85.3	396	2	Q4NJP3_9MICC	Q4njp3 arthrobacte
310	29	85.3	291	2	Q5NT8_ANOGA	Q5nt8 anopheles g	383	29	85.3	400	1	FOXQ1_MOUSE	Q70220 mus musculu
311	29	85.3	291	2	Q83ZC9_ECOLI	Q83zc9 escherichia	384	29	85.3	400	1	Q9JLN7_RATRT	Q9jln7 rattus ratt
312	29	85.3	295	2	Q7SL67_ORYSA	Q7sl67 oryza sativ	385	29	85.3	400	2	Q9JJ18_MOUSE	Q9jj18 mus musculu
313	29	85.3	295	2	Q5FA38_NEIG1	Q5fa38 neisseria g	386	29	85.3	402	2	Q61733_BRAFL	Q61733 branchiosto
314	29	85.3	295	2	Q9JWJ1_NEIMA	Q9jw11 neisseria m	387	29	85.3	403	1	FOXQ1_HUMAN	Q9c009 homo sapien
315	29	85.3	295	2	Q9K0I7_NEIME	Q9k0i7 neisseria m	388	29	85.3	403	2	Q5VW73_HUMAN	Q5v73 homo sapien
316	29	85.3	298	2	Q5XLY9_9REOV	Q5xly9 equine rota	389	29	85.3	406	2	Q8DC10_VIBVO	Q8dc10 vibrio vuln
317	29	85.3	299	2	Q5XLZ0_9REOV	Q5xlz0 equine rota	390	29	85.3	406	2	Q7MHC8_VIBVU	Q7mhc8 vibrio vuln
318	29	85.3	299	2	Q5XLZ1_9REOV	Q5xlz1 equine rota	391	29	85.3	407	2	Q9N476_CABEL	Q9n476 caenorhabd1
319	29	85.3	299	2	Q5XLZ2_9REOV	Q5xlz2 equine rota	392	29	85.3	408	2	Q8T4L2_BRUMA	Q8t4l2 brugia mala
320	29	85.3	299	2	Q5XLZ3_9REOV	Q5xlz3 equine rota	393	29	85.3	409	2	Q6KZK0_PICTO	Q6kzk0 picophilus
321	29	85.3	301	2	Q7Q864_ANOGA	Q7q864 anopheles g	394	29	85.3	416	2	Q6GCU8_STAAS	Q6gcu8 staphylococ
322	29	85.3	301	2	Q6NWA9_BRARE	Q6nwa9 brachydanio	395	29	85.3	416	2	Q6GK8_STAAR	Q6gk8 staphylococ
323	29	85.3	304	2	Q9F3R8_9BURK	Q9f3r8 cupriavidus	396	29	85.3	416	2	Q5HJ5_STAAC	Q5hj5 staphylococ

397	29	85.3	416	2	Q7A1Y3 STAAW	Q7A1Y3 staphylococ	470	29	85.3	465	1	SVC_BURMA	Q62j37 burkholderi
398	29	85.3	416	2	Q7A814 STAAW	Q7A814 staphylococ	471	29	85.3	465	1	SVC_BURPS	Q63se8 burkholderi
399	29	85.3	416	2	Q9X43 STAAW	Q9X43 staphylococ	472	29	85.3	465	1	SVC_METCA	Q60bq8 methylococ
400	29	85.3	418	2	Q6MBC_BEBBA	Q6mmb6 bdeliovibri	473	29	85.3	465	1	SVC_NITEU	Q82Y45 nitrosomona
401	29	85.3	420	2	Q73862 BRARE	Q73862 brachydanio	474	29	85.3	466	2	Q4LMF8_BBURK	Q4lmf8 burkholderi
402	29	85.3	420	2	Q568V0 BRARE	Q568v0 brachydanio	475	29	85.3	466	1	SVC_BACSK	Q5wt3 bacillus cl
403	29	85.3	421	2	Q54M16 DICDI	Q54m16 dictyosteli	476	29	85.3	466	1	SVC_STAAC	Q5hies staphylococ
404	29	85.3	424	2	Q7PVV5 ANOGA	Q7pvv5 anopheles g	477	29	85.3	466	1	SVC_STAAC	Q932g0 staphylococ
405	29	85.3	424	2	Q9P4L5 ECOLI	Q9f4l5 escherichia	478	29	85.3	466	1	SVC_STAAN	Q95w73 staphylococ
406	29	85.3	425	1	Y677_MYCPN	P75l15 mycoplasma	479	29	85.3	466	1	SVC_STAAR	Q95jd9 staphylococ
407	29	85.3	434	2	Q64ME1 BACFR	Q64mz1 bacteroides	480	29	85.3	466	1	SVC_STAAS	Q95pvr8 staphylococ
408	29	85.3	435	2	Q894Q8 CLOTE	Q894q8 clostridium	481	29	85.3	466	1	SVC_STAAW	Q8nxy7 staphylococ
409	29	85.3	436	2	Q9YHC5 XENLA	Q9yhc5 xenopus lae	482	29	85.3	466	1	SVC_STAEP	Q8ctul1 staphylococ
410	29	85.3	437	2	Q8TIR1 METAC	Q8tir1 methanosarc	483	29	85.3	466	1	SVC_STAEP	Q5hmr3 staphylococ
411	29	85.3	438	2	Q9GG38 9ILILI	Q9gg38 enhalus aco	484	29	85.3	466	2	SVC_STAEO	Q6N096 homo sapien
412	29	85.3	443	2	Q6W1Z9 RHISN	Q6w1z9 rhizobium s	485	29	85.3	466	2	Q4L319_STAHL	Q4l319 staphylococ
413	29	85.3	444	2	Q6QNM9 PHACH	Q6qnm9 phanerochaet	486	29	85.3	467	2	Q4H319_CIOIN	Q4h319 ciona intes
414	29	85.3	445	1	S1P2_DROME	P32031 drosophila	487	29	85.3	468	1	SVC_OCEIH	Q8nt29 oceanobacil
415	29	85.3	446	2	Q7IWY8 9DIPT	Q7iwy8 drosophila	488	29	85.3	468	2	Q6N0G9 RHOPA	Q6n0g9 rhodopsedo
416	29	85.3	446	2	Q7IWZ3 DRONS	Q7iww3 drosophila	489	29	85.3	469	1	FOXGA_HUMAN	P55316 homo sapien
417	29	85.3	446	2	Q7IWZ6 9DIPT	Q7iww6 drosophila	490	29	85.3	470	1	SVC_ENTFA	Q839v5 enterococcu
418	29	85.3	446	2	Q7IWZ9 9DIPT	Q7iww9 drosophila	491	29	85.3	470	1	SVC_LACUO	Q74l26 lactobacill
419	29	85.3	446	2	Q7IXO6 9DIPT	Q7ix06 drosophila	492	29	85.3	471	1	SVC_LISMP	Q724h3 listeria mo
420	29	85.3	446	2	Q9T4B3 9DIPT	Q9t4b3 drosophila	493	29	85.3	471	1	SVC_LISMO	Q9yab1 listeria mo
421	29	85.3	446	2	Q9T4V1 9DIPT	Q9t4v1 drosophila	494	29	85.3	473	1	SVC_ACIAO	Q6fc71 acinetobact
422	29	85.3	446	2	Q8TB08 9DIPT	Q8tb08 drosophila	495	29	85.3	477	1	C1112_MOUSE	Q9cyu6 mus musculu
423	29	85.3	446	2	Q8TB09 9DIPT	Q8tb09 drosophila	496	29	85.3	477	1	FOXGB_HUMAN	P55315 homo sapien
424	29	85.3	446	2	Q9TB10 9DIPT	Q9tb10 drosophila	497	29	85.3	477	2	Q5FM34_LACAC	Q5fm34 lactobacill
425	29	85.3	446	2	Q9TB11 9DIPT	Q9tb11 drosophila	498	29	85.3	480	1	FOXGB_RAT	Q90939 rattus norv
426	29	85.3	446	2	Q9TB12 9DIPT	Q9tb12 drosophila	499	29	85.3	480	2	Q803R2_BRARE	Q803r2 brachydanio
427	29	85.3	446	2	Q9TB13 9DIPT	Q9tb13 drosophila	500	29	85.3	481	1	FOXGB_MOUSE	Q60987 mus musculu
428	29	85.3	446	2	Q9TB15 9DIPT	Q9tb15 drosophila	501	29	85.3	482	1	Q5CQ42_CRYPV	Q5cq42 cryptospori
429	29	85.3	446	2	Q9TB16 9DIPT	Q9tb16 drosophila	502	29	85.3	484	2	Q7PX00_ANOGA	Q7pxq0 anopheles g
430	29	85.3	446	2	Q9TB17 9DIPT	Q9tb17 drosophila	503	29	85.3	486	2	Q5HZY6_MOUSE	Q5hzy6 mus musculu
431	29	85.3	446	2	Q9TB18 9DIPT	Q9tb18 drosophila	504	29	85.3	487	2	Q80Z17_MOUSE	Q80z17 mus musculu
432	29	85.3	446	2	Q9TB20_DROIM	Q9tb20 drosophila	505	29	85.3	489	2	Q86XT7_HUMAN	Q86xt7 homo sapien
433	29	85.3	446	2	Q7V8F2 PROMM	Q7v8f2 prochloroco	506	29	85.3	500	2	Q5CEW8_CRYHO	Q5cew8 cryptospori
434	29	85.3	447	1	SVC_SFRA3	Q8e7f2 streptococc	507	29	85.3	504	2	Q9AA21_CAUCR	Q9aa21 caulobacter
435	29	85.3	447	1	SVC_SFRA5	Q8a1z4 streptococc	508	29	85.3	509	2	Q5DNC4_9HILA	Q5dnc4 leptorhynch
436	29	85.3	447	1	SVC_SFRAU	Q8dwa9 streptococc	509	29	85.3	512	2	Q62095_CABEL	Q62095 caenorhabdi
437	29	85.3	447	1	SVC_SFRP3	Q8x5t7 streptococc	510	29	85.3	517	2	Q9P8G4_NAPHY	Q9p8g4 corioliopsis
438	29	85.3	447	1	SVC_SFRP6	Q5x9w5 streptococc	511	29	85.3	520	1	LAC2_AGABI	Q12542 agarius bi
439	29	85.3	447	1	SVC_SFRP8	Q8znd1 streptococc	512	29	85.3	520	2	Q6CAE9_YARLI	Q6cae9 yarrowia li
440	29	85.3	447	1	SVC_SFRPN	Q9t825 streptococc	513	29	85.3	521	2	Q90312_9PHYC	Q90312 chlorella v
441	29	85.3	447	1	SVC_SFRPY	Q9xzx9 streptococc	514	29	85.3	522	2	Q3RGE6_CIOCL	Q3rge6 clostridium
442	29	85.3	447	1	SVC_SFRR6	Q8dqe8 streptococc	515	29	85.3	528	2	Q8NID5_NAPHY	Q8nid5 trameetes sp
443	29	85.3	447	1	SVC_SFRT1	Q5mlw6 streptococc	516	29	85.3	536	2	Q4V5E0_DROME	Q4v5e0 drosophila
444	29	85.3	447	1	SVC_SFRT2	Q5mf6 streptococc	517	29	85.3	537	2	Q4S9B1_TETNG	Q4s9b1 tetraodon n
445	29	85.3	447	1	Q6BDS7_9ODON	Q6bds7 orthetrum t	518	29	85.3	549	2	Q4SKL4_TETNG	Q4skl4 tetraodon n
446	29	85.3	448	1	SVC_LACLA	Q9cej0 lactococcus	519	29	85.3	550	2	Q4WF04_ASPFU	Q4wf04 aspergillus
447	29	85.3	451	1	FOXGB_CHICK	Q90964 gallus gall	520	29	85.3	550	2	Q60V54_CAEBR	Q60v54 caenorhabdi
448	29	85.3	451	2	Q8S295_DROME	Q8sz95 drosophila	521	29	85.3	550	2	Q88UP7_LACPL	Q88up7 lactobacill
449	29	85.3	458	1	CHIT3_DROME	Q9w5u2 drosophila	522	29	85.3	552	2	Q88YT2_LACPL	Q88yt2 lactobacill
450	29	85.3	459	1	SVC_SHEON	Q8g522 shewanella	523	29	85.3	571	2	Q8CK43_KULLA	Q8ck43 kluyveromyc
451	29	85.3	460	1	SVC1_CORGL	Q8nmr7 corynebacte	524	29	85.3	573	2	Q8D523_VIBVU	Q8d523 vibrio vuln
452	29	85.3	460	1	SVC_BRAJA	Q8nmp8 bradyrhizob	525	29	85.3	573	2	Q29216_LISIN	Q29216 listeria in
453	29	85.3	460	2	Q62ISO_CAEER	Q62150 caenorhabdi	526	29	85.3	573	2	Q7MBV6_VIBVY	Q7mbv6 vibrio vuln
454	29	85.3	461	1	SVC_AZOSE	Q5plh8 azarcus sp	527	29	85.3	587	2	Q4YSX0_PLABE	Q4ysx0 plasmodium
455	29	85.3	461	1	SVC_ECO57	Q8xct9 escherichia	528	29	85.3	591	1	LAC1_CRYPA	Q03966 cryptonectr
456	29	85.3	461	1	SVC_ECOL6	Q8fk44 escherichia	529	29	85.3	591	2	Q6CX94_KULLA	Q6cx94 kluyveromyc
457	29	85.3	461	1	SVC_ECOLI	P21888 escherichia	530	29	85.3	591	2	Q6QNN1_PHACH	Q6qnn1 phanerochaet
458	29	85.3	461	1	SVC_ERMCT	Q6d2ea erwinia car	531	29	85.3	591	2	Q6QNN2_PHACH	Q6qnn2 phanerochaet
459	29	85.3	461	1	SVC_FHOLL	Q7n085 photorhabdu	532	29	85.3	592	2	Q4TNE1_9SPHN	Q4tne1 erythrobaet
460	29	85.3	461	1	SVC_SALPA	Q5pce2 salmonella	533	29	85.3	593	1	D8BD_VIBVU	Q8bdzo vibrio vuln
461	29	85.3	461	1	SVC_SALTY	Q8zrp6 salmonella	534	29	85.3	596	2	Q8NLR6_CORGL	Q8nlr6 corynebacte
462	29	85.3	461	1	SVC_SALTY	Q8xr68 salmonella	535	29	85.3	597	2	Q8UDT3_AGRTS	Q8udt3 agrobacteri
463	29	85.3	461	1	SVC_SHIFL	Q8zmc27 shigella fl	536	29	85.3	599	2	Q6G2T4_BARHE	Q6g2t4 bartonella
464	29	85.3	461	1	SVC_YERPE	Q8zcc0 yersinia pe	537	29	85.3	602	2	Q5KZHO_GROKA	Q5kzho geobacillus
465	29	85.3	461	1	SVC_YERPS	Q66dk9 yersinia ps	538	29	85.3	604	1	YFIC_BACSU	P54719 bacillus su
466	29	85.3	461	2	Q22525_CABEL	Q22525 caenorhabdi	539	29	85.3	606	2	Q3VPM6_DROME	Q9vnm6 drosophila
467	29	85.3	461	2	Q57S29_SALCH	Q57s29 salmonella	540	29	85.3	608	2	P74356_SNYI3	P74356 synecocyst
468	29	85.3	463	1	SVC1_CORDI	Q6nfc3 corynebacte	541	29	85.3	617	2	Q4MYE8_THEPA	Q4mye8 theileria p
469	29	85.3	463	1	SVC_CAUCR	Q9aay2 caulobacter	542	29	85.3	617	2	Q8FM03_CORBP	Q8fm03 corynebacte

543	29	85.3	618	2	Q7CY08	agrobacteri	616	29	85.3	900	2	Q4UWK8	XANCP	Q4uwk8	xanthonas
544	29	85.3	620	2	Q6M1Y6	corynebacte	617	29	85.3	902	2	Q55Z28	CRYNE	Q55z28	cryptococcu
545	29	85.3	620	2	Q5RDU0	pongo pygma	618	29	85.3	902	2	Q5KNE4	CRYNE	Q5kne4	cryptococcu
546	29	85.3	628	1	P77495	eschericchia	619	29	85.3	909	2	Q62233	ORYSA	Q62233	oryza sativ
547	29	85.3	628	1	PRPE	SALTY	620	29	85.3	916	2	Q9RHT4	PSRFL	Q9rht4	pseudomonas
548	29	85.3	628	2	Q575T3	salmonella	621	29	85.3	980	2	Q74EH0	GEOSL	Q74eh0	geobacter s
549	29	85.3	628	2	Q5PFW9	salmonella	622	29	85.3	991	2	Q848A4	STRHY	Q848a4	streptomyce
550	29	85.3	628	2	Q7N1D7	photorhabdu	623	29	85.3	997	2	Q4Y642	PLACH	Q4y642	plasmodium
551	29	85.3	628	2	Q8FXH0	eschericchia	624	29	85.3	998	2	Q4YBR1	PLABE	Q4ybr1	plasmodium
552	29	85.3	628	2	Q8X692	eschericchia	625	29	85.3	1037	2	Q7FB56	ARATH	Q7fb56	arabidopsis
553	29	85.3	628	2	Q8Z902	salmonella	626	29	85.3	1064	2	Q8LLJ6	OCHDN	Q8llj6	ochromonas
554	29	85.3	629	2	Q7W5L4	bordetella	627	29	85.3	1120	2	Q4NOD1	THEPA	Q4nod1	theileria p
555	29	85.3	629	2	Q7WD50	bordetella	628	29	85.3	1135	2	Q7X904	ORYSA	Q7x904	oryza sativ
556	29	85.3	630	2	Q5NXJ6	azobarcus sp	629	29	85.3	1143	2	Q54WNO	DICDI	Q54wn0	dictyostelli
557	29	85.3	631	2	P94903	lysoabacter	630	29	85.3	1194	2	Q60YCH	CAEBR	Q60ych	caenorhabdi
558	29	85.3	631	2	Q4SMP4	tetradon n	631	29	85.3	1208	2	Q5R7B9	VIBF1	Q5r7b9	vibriio fisc
559	29	85.3	632	2	Q8XZ86	ralstonia s	632	29	85.3	1226	2	Q7MXJ9	PORGI	Q7mxj9	porphyromon
560	29	85.3	638	2	Q8JU13	lumpy skin	633	29	85.3	1227	2	Q6LMZA	PHOPR	Q6lmza	photobacter
561	29	85.3	638	2	Q91MY0	lumpy skin	634	29	85.3	1241	2	Q5BFP0	EMENI	Q5bfp0	aspergillus
562	29	85.3	639	2	Q8JTX0	lumpy skin	635	29	85.3	1318	2	Q7F9Y7	ORYSA	Q7f9y7	oryza sativ
563	29	85.3	645	2	Q8V3R9	swinepox vl	636	29	85.3	1325	2	Q8GU63	ORYSA	Q8gu63	oryza sativ
564	29	85.3	649	2	Q33459	pseudomonas	637	29	85.3	1326	2	Q4UPN2	XANCP	Q4upn2	xanthonas
565	29	85.3	651	2	Q9UBU4	tetrahymena	638	29	85.3	1326	2	Q8P449	XANCP	Q8p449	xanthonas
566	29	85.3	655	2	Q89EF6	bradyrhizob	639	29	85.3	1367	2	Q6Z9H4	CAEBR	Q6z9h4	caenorhabdi
567	29	85.3	663	2	Q7RHQ0	plasmodium	640	29	85.3	1376	2	Q23590	CABEL	Q23590	caenorhabdi
568	29	85.3	664	2	Q8LIG5	oryza sativ	641	29	85.3	1470	2	Q9M1C7	ARATH	Q9m1c7	arabidopsis
569	29	85.3	669	2	Q96218	plasmodium	642	29	85.3	1493	2	Q8LGU0	ARATH	Q8lgu0	arabidopsis
570	29	85.3	675	2	Q97AJ6	cafetetia r	643	29	85.3	1493	2	Q84E55	ORYSA	Q84e55	oryza sativ
571	29	85.3	697	2	Q7QDT2	anopheles g	644	29	85.3	1493	2	Q9LK62	ARATH	Q9lk62	arabidopsis
572	29	85.3	700	1	GUNA	PAELA	645	29	85.3	1514	2	Q75Q02	9BRAS	Q75q02	thlaapi cae
573	29	85.3	700	2	Q08672	TRYRA	646	29	85.3	1514	2	Q9LK64	ARATH	Q9lk64	arabidopsis
574	29	85.3	707	2	Q98JY6	rhizobium l	647	29	85.3	1515	2	Q24510	ARATH	Q24510	arabidopsis
575	29	85.3	710	2	Q97UH5	sulfolobus	648	29	85.3	1555	2	Q9U0N0	PLAF7	Q9u0n0	plasmodium
576	29	85.3	719	2	Q5CSB7	cryptospori	649	29	85.3	1574	2	Q8GU62	ORYSA	Q8gu62	oryza sativ
577	29	85.3	724	2	Q9K5L5	actinoplane	650	29	85.3	1619	2	Q83CA2	THEPA	Q83ca2	coxiella bu
578	29	85.3	726	2	Q5B9H5	EMENI	651	29	85.3	1631	2	Q4N618	THEPA	Q4n618	theileria p
579	29	85.3	728	2	Q4SKL9	tetragon n	652	29	85.3	1669	2	Q9W1A8	DROME	Q9w1a8	drosophila
580	29	85.3	730	2	Q4PFD8	ustilago ma	653	29	85.3	1778	2	Q55P04	CRYNE	Q55p04	cryptococcu
581	29	85.3	731	2	Q7S9Z8	neurospora	654	29	85.3	1778	2	Q5KEF3	CRYNE	Q5kef3	cryptococcu
582	29	85.3	754	2	Q7F9Y8	oryza sativ	655	29	85.3	1832	2	Q9KI28	POLCB	Q9ki28	polyangium
583	29	85.3	761	2	Q9KWT4	sphingomona	656	29	85.3	1832	2	Q9L8C8	POLCB	Q9l8c8	polyangium
584	29	85.3	764	2	Q8DN23	STRR6	657	29	85.3	1852	2	Q6RKJ1	GIBMO	Q6rkj1	gibberella
585	29	85.3	764	2	Q97N95	STRPN	658	29	85.3	1874	2	Q5IUZ3	MAGGR	Q5iuz3	magnaporthe
586	29	85.3	776	1	VP4	ROTEH	659	29	85.3	2009	2	Q9P855	GIBFU	Q9p855	gibberella
587	29	85.3	776	1	VP4	ROTH6	660	29	85.3	2095	1	RRPL	TOSV	P37800	toscana vir
588	29	85.3	776	2	Q8UBJ1	agrobacteri	661	29	85.3	2172	2	Q7X4R4	STRHY	Q7x4r4	streptomyce
589	29	85.3	776	2	Q86176	equine rota	662	29	85.3	2286	2	Q7PL80	DROME	Q7pl80	drosophila
590	29	85.3	776	2	Q86186	equine rota	663	29	85.3	2396	2	Q8SA91	MAIZE	Q8sa91	zea mays (m
591	29	85.3	776	2	Q86186	equine rota	664	29	85.3	2516	2	Q9RN43	PHOLU	Q9rn43	photorhabdu
592	29	85.3	776	2	Q98167	lapine rota	665	29	85.3	2525	2	Q7N7Y9	PHOLL	Q7n7y9	photorhabdu
593	29	85.3	776	2	Q98168	lapine rota	666	29	85.3	3913	2	Q4U919	THEAN	Q4u919	theileria a
594	29	85.3	776	2	Q98169	lapine rota	667	29	85.3	3928	2	Q4N1R4	THEPA	Q4n1r4	theileria p
595	29	85.3	776	2	Q98635	equine rota	668	29	85.3	4464	2	Q7RL36	PLAYO	Q7rl36	plasmodium
596	29	85.3	776	2	Q998M5	equine rota	669	29	85.3	38	2	Q4XR58	PLACH	Q4xr58	leptospiira
597	29	85.3	776	2	Q998M6	equine rota	670	29	85.3	54	2	Q4XR58	PLACH	Q4xr58	leptospiira
598	29	85.3	776	2	Q998M7	equine rota	671	29	85.3	105	2	Q99CNO	9HIV1	Q99cno	human immun
599	29	85.3	778	1	PMTY	SCHPO	672	29	85.3	108	1	TGB2	PVSP	P16651	potato viru
600	29	85.3	783	2	Q4SGF9	TETNG	673	29	85.3	110	2	Q9VG00	DROME	Q9vg00	drosophila
601	29	85.3	785	2	Q8ZTY7	PYRAE	674	29	85.3	111	2	Q849D2	STRVN	Q849d2	streptomyce
602	29	85.3	791	2	Q9NA27	CABEL	675	29	85.3	112	2	Q8MPU0	CABEL	Q8mpu0	caenorhabdi
603	29	85.3	797	2	Q4ILE2	GIBBEZ	676	29	85.3	113	2	Q75UW3	9ACTO	Q75uw3	planomonosp
604	29	85.3	802	2	Q7XN74	ORYSA	677	29	85.3	113	2	Q75UW7	9ACTO	Q75uw7	nonomuraea
605	29	85.3	804	2	Q82P57	STRAY	678	29	85.3	113	2	Q75UW9	9ACTO	Q75uw9	kitasatospo
606	29	85.3	809	2	Q4HMP9	CAMLA	679	29	85.3	113	2	Q75UX0	KIBAR	Q75ux0	kibdelospor
607	29	85.3	816	1	SYL	XANCP	680	29	85.3	113	2	Q75UX1	KIBAR	Q75ux1	kibdelospor
608	29	85.3	844	2	Q4FNRO	GRICK	681	29	85.3	113	2	Q75UX3	9ACTO	Q75ux3	catenulopla
609	29	85.3	853	2	Q86P51	DROME	682	29	85.3	113	2	Q75UX4	AMYOR	Q75ux4	amycolatops
610	29	85.3	853	2	Q9VVG5	drosophila	683	29	85.3	113	2	Q75UX6	9ACTO	Q75ux6	actinoplane
611	29	85.3	872	2	Q6CDD1	YARLI	684	29	85.3	113	2				
612	29	85.3	876	2	Q7MVD7	PORGI	685	29	85.3	113	2				
613	29	85.3	880	1	SYL	XANAC	686	29	85.3	113	2				
614	29	85.3	880	2	Q5GX18	XANOR	687	29	85.3	113	2				
615	29	85.3	889	2	Q7UYD6	RHOBA	688	29	85.3	113	2				

689	28	82.4	118	2	Q7UM72_RHOBA	Q7um72 rhodopirell	762	28	82.4	239	2	Q7XM98_ORYSA	Q7xm98 oryza sativ
690	28	82.4	127	2	Q85868_SPHAR	Q85868 sphingomona	763	28	82.4	240	2	Q45592_BACSU	Q45592 bacillus su
691	28	82.4	130	2	Q8S417_MALZE	Q8s417 zea mays (m	764	28	82.4	242	2	Q4JL76_ORYSA	Q4jl76 oryza sativ
692	28	82.4	133	2	Q7ACE3_ECO57	Q7ace2 escherichia	765	28	82.4	242	2	Q5NK12_ORYSA	Q5nki2 oryza sativ
693	28	82.4	135	2	Q9EYC4_ECO57	Q9eyc4 escherichia	766	28	82.4	243	2	Q94CJ3_ARATH	Q94cj3 arabidopsis
694	28	82.4	136	2	P92986_ARATH	P92986 arabidopsis	767	28	82.4	243	2	Q8RAU8_THETN	Q8rau8 thermoanaer
695	28	82.4	139	2	Q8KD00_CHLTE	Q8kd00 chlorobium	768	28	82.4	243	2	Q87KS7_VIBPA	Q87ks7 vibrio para
696	28	82.4	143	2	Q8X688_ECO57	Q8x688 escherichia	769	28	82.4	243	2	Q9YMH8_NPVLd	Q9ymh8 lymantria d
697	28	82.4	147	2	Q7Y307_9CAUD	Q7y307 stx1 conve	770	28	82.4	256	1	SURE_PORGI	Q7mt32 porphyromon
698	28	82.4	148	2	Q96F36_RHILo	Q96f36 rhizobium l	771	28	82.4	256	2	Q94IG1_ARAGE	Q94igi1 arabis gumm
699	28	82.4	151	2	Q84U45_9ASPA	Q84u45 dendrobium	772	28	82.4	256	2	Q9LX82_ARATH	Q9lx82 arabidopsis
700	28	82.4	152	2	Q83DC5_C0XBA	Q83dc5 coxiella bu	773	28	82.4	256	2	Q4TSU1_9SPHN	Q4tsu1 erythroba
701	28	82.4	156	2	Q97DD6_CLOAB	Q97dd6 clostridium	774	28	82.4	258	2	Q74LF8_LACJO	Q74lf8 lactobacill
702	28	82.4	157	2	Q710P4_ORYSA	Q710p4 oryza sativ	775	28	82.4	261	2	Q6R074_ARATH	Q6r074 arabidopsis
703	28	82.4	159	2	Q88MJ3_PSEPK	Q88mj3 pseudomonas	776	28	82.4	261	2	Q9T0G9_ARATH	Q9t0g9 arabidopsis
704	28	82.4	162	2	Q6LGF5_PROPR	Q6lgf5 photobacter	777	28	82.4	261	2	Q4JL77_AZOVl	Q4jl77 azotobacter
705	28	82.4	165	2	Q8S3Y9_SORBI	Q8s3y9 sorghum bic	778	28	82.4	262	1	PH4H_PSEAE	Q6emj5 pseudomonas
706	28	82.4	166	2	Q9ZTE8_ARATH	Q9zte8 arabidopsis	779	28	82.4	262	2	Q6EMJ5_PSEPU	Q6emj5 pseudomonas
707	28	82.4	168	2	Q4PIX5_DROME	Q4pix5 drosophila	780	28	82.4	263	2	Q88EH3_PSEPK	Q88eh3 pseudomonas
708	28	82.4	168	2	Q6U398_LACPL	Q6u398 lactobacill	781	28	82.4	263	2	Q4KG96_PSEF5	Q4kg96 pseudomonas
709	28	82.4	169	2	Q5WEM5_BACSK	Q5wem5 bacillus cl	782	28	82.4	265	2	Q29873_ARCFU	Q29873 archaeeoglob
710	28	82.4	170	2	Q4JL86_ARATH	Q4jl86 arabidopsis	783	28	82.4	265	2	Q4ZQ55_PSESY	Q4zq55 pseudomonas
711	28	82.4	172	2	Q4JL80_ORYSA	Q4jl80 oryza sativ	784	28	82.4	265	2	Q885L0_PSESM	Q885l0 pseudomonas
712	28	82.4	175	2	Q3ATE4_EMENI	Q3ate4 aspergillus	785	28	82.4	265	2	Q4T126_TETNG	Q4t126 tetraodon n
713	28	82.4	176	2	Q39186_ARATH	Q39186 arabidopsis	786	28	82.4	267	2	Q7XB39_VITVI	Q7xb39 vitis vinif
714	28	82.4	177	2	Q4JL77_ORYSA	Q4jl77 oryza sativ	787	28	82.4	269	2	Q9LK14_ARATH	Q9lk14 arabidopsis
715	28	82.4	182	2	Q9S0U9_HYACU	Q9s0u9 hyaloraphid	788	28	82.4	269	2	Q6QAD8_ARATH	Q6qad8 arabidopsis
716	28	82.4	183	2	Q8S3Y6_SORBI	Q8s3y6 sorghum bic	789	28	82.4	273	2	Q94IF8_ARATH	Q94if8 arabidopsis
717	28	82.4	183	2	Q32803_9LACT	Q32803 lactococcus	790	28	82.4	273	2	Q94IF6_ARATH	Q94if6 arabidopsis
718	28	82.4	185	2	Q677Q1_9VIRU	Q677q1 lymphocyti	791	28	82.4	273	2	Q94IF7_ARATH	Q94if7 arabidopsis
719	28	82.4	186	2	Q9LTD2_ARATH	Q9ltd2 arabidopsis	792	28	82.4	273	2	Q94IF9_ARATH	Q94if9 arabidopsis
720	28	82.4	187	2	Q5DGZ3_SCHJA	Q5dgz3 schistosoma	793	28	82.4	273	2	Q39028_ARATH	Q39028 arabidopsis
721	28	82.4	188	2	Q9LES5_ARATH	Q9les5 arabidopsis	794	28	82.4	273	2	Q93V20_ARATH	Q93v20 arabidopsis
722	28	82.4	188	2	Q9ZTD0_ARATH	Q9ztd0 arabidopsis	795	28	82.4	273	2	Q93V46_ARATH	Q93v46 arabidopsis
723	28	82.4	190	2	Q70RD2_GERHY	Q70rd2 gerbera hyb	796	28	82.4	273	2	Q73TB4_MYCPA	Q73tb4 mycobacteri
724	28	82.4	192	2	Q67YJ3_ARATH	Q67yj3 arabidopsis	797	28	82.4	276	2	Q9LUR5_ARATH	Q9lru5 arabidopsis
725	28	82.4	194	2	Q669J8_YERPS	Q669j8 yersinia ps	798	28	82.4	276	2	Q56UT4_ORYSA	Q56ut4 oryza sativ
726	28	82.4	202	2	Q7U4E0_SYNXP	Q7u4e0 synechococ	799	28	82.4	276	2	Q81C00_BACCR	Q81c00 bacillus ce
727	28	82.4	204	2	Q9ZTD3_ARATH	Q9ztd3 arabidopsis	800	28	82.4	278	2	Q9FRI3_ARATH	Q9fri3 arabidopsis
728	28	82.4	204	2	Q8ZDV6_YERPE	Q8zdv6 yersinia pe	801	28	82.4	283	2	Q94FU0_ARATH	Q94fu0 arabidopsis
729	28	82.4	205	2	P81391_ANTMA	P81391 antirrhinum	802	28	82.4	285	2	Q9ARI8_ORYSA	Q9ari8 oryza sativ
730	28	82.4	210	2	Q5JL15_ORYSA	Q5jl15 oryza sativ	803	28	82.4	286	2	Q8H257_ROSIA	Q8h257 goessypioide
731	28	82.4	212	2	Q61ZT8_METMP	Q61zt8 methanococ	804	28	82.4	286	2	Q9C9G7_ARATH	Q9c9g7 arabidopsis
732	28	82.4	212	2	Q9IVQ1_9HIV1	Q9ivq1 human immu	805	28	82.4	287	2	Q8H261_GOSHI	Q8h261 goessypium h
733	28	82.4	213	2	Q8CLA3_YERPE	Q8cla3 yersinia pe	806	28	82.4	287	2	Q8H260_GOSHI	Q8h260 goessypium h
734	28	82.4	214	2	Q4JL85_ARATH	Q4jl85 arabidopsis	807	28	82.4	287	2	Q8H259_ROSIA	Q8h259 goessypium r
735	28	82.4	215	2	Q96Y57_SULTO	Q96y57 sulfotobus	808	28	82.4	287	2	Q8H258_ROSIA	Q8h258 goessypium h
736	28	82.4	216	2	Q9FNW0_ARATH	Q9fnw0 arabidopsis	809	28	82.4	289	2	Q6K949_ORYSA	Q6k949 oryza sativ
737	28	82.4	218	2	Q9ZTC6_ARATH	Q9ztc6 arabidopsis	810	28	82.4	290	2	Q6C225_YARLI	Q6c225 yarrowia li
738	28	82.4	220	2	Q9PEV3_ORYSA	Q9pev3 oryza sativ	811	28	82.4	291	2	Q67L38_SYMTH	Q67l38 symbiobacte
739	28	82.4	220	2	Q4FPC8_9RICK	Q4fpc8 candidatus	812	28	82.4	293	2	Q49020_GOSHI	Q49020 goessypium h
740	28	82.4	221	2	Q6TGS1_ORYSA	Q6tgs1 oryza sativ	813	28	82.4	293	2	Q94JN4_GOSHI	Q94jnn4 goessypium h
741	28	82.4	223	2	Q94IG0_9BRAS	Q94ig0 crucihimala	814	28	82.4	293	2	Q94JN5_GOSHI	Q94jnn5 goessypium h
742	28	82.4	225	2	Q85QS3_9INSE	Q85qs3 tricholepid	815	28	82.4	293	2	Q93V35_ORYSA	Q93v35 oryza sativ
743	28	82.4	226	2	Q4JL82_ARATH	Q4jl82 arabidopsis	816	28	82.4	294	2	Q21876_CAEEL	Q21876 caenorhabdi
744	28	82.4	226	2	Q5XE59_STRP6	Q5xe59 streptococ	817	28	82.4	295	2	Q76681_CAEEL	Q76681 caenorhabdi
745	28	82.4	226	2	Q9AIR1_STRPY	Q9air1 streptococ	818	28	82.4	295	2	Q9GYT8_CAEEL	Q9gyt8 caenorhabdi
746	28	82.4	226	2	Q7CNN0_STRP8	Q7cnn0 streptococ	819	28	82.4	297	2	Q51KFS_CAEER	Q51kf5 caenorhabdi
747	28	82.4	226	2	Q7CFJ3_STRP3	Q7cfj3 streptococ	820	28	82.4	298	1	XERC_STAAM	P67630 staphylococ
748	28	82.4	228	2	Q5VNN2_ORYSA	Q5vnn2 oryza sativ	821	28	82.4	298	1	XERC_STAAN	P67631 staphylococ
749	28	82.4	229	2	Q8PS53_METMA	Q8ps53 methanosarc	822	28	82.4	298	1	XERC_STAAU	Q8kjf6 staphylococ
750	28	82.4	229	2	Q8TLU3_METAC	Q8tlu3 methanosarc	823	28	82.4	298	1	XERC_STAAW	Q8nwz8 staphylococ
751	28	82.4	231	2	Q8S100_SIVCZ	Q8s100 chimpanzee	824	28	82.4	298	2	Q8H5F5_ORYSA	Q8h5f5 oryza sativ
752	28	82.4	232	2	Q43576_HUMAN	Q43576 homo sapien	825	28	82.4	298	2	Q6G9W1_STAAS	Q6g9w1 staphylococ
753	28	82.4	232	2	Q4V3R9_DROME	Q4v3r9 drosophila	826	28	82.4	298	2	Q5GH13_STAAR	Q5gh13 staphylococ
754	28	82.4	234	2	Q8H6Y7_PHYIN	Q8h6y7 phytophthor	827	28	82.4	298	2	Q5HG10_STAAC	Q5hg10 staphylococ
755	28	82.4	234	2	Q50069_ARATH	Q50069 arabidopsis	828	28	82.4	299	2	Q9A256_9CAUD	Q9az56 lactococcus
756	28	82.4	235	2	Q9FN86_ARATH	Q9fn86 arabidopsis	829	28	82.4	299	2	Q4HH25_CAMCO	Q4hh25 campylobact
757	28	82.4	235	2	Q7BUA2_ECOLI	Q7bua2 escherichia	830	28	82.4	300	2	Q5DX30_CAEEL	Q5dx30 caenorhabdi
758	28	82.4	235	2	Q8E9G1_SHEON	Q8e9g1 shewanella	831	28	82.4	300	2	Q5I141_9VIRU	Q5i141 microplatis
759	28	82.4	237	2	Q53NK6_ORYSA	Q53nk6 oryza sativ	832	28	82.4	307	2	Q9FGY3_ARATH	Q9fyg3 arabidopsis
760	28	82.4	238	2	Q9SCP1_ARATH	Q9scp1 arabidopsis	833	28	82.4	308	2	Q7Q863_ANOGA	Q7q863 anopheles g
761	28	82.4	239	2	Q7Y4K9_9CAUD	Q7y4k9 streptococ	834	28	82.4	308	2	Q72QC6_LEPIC	Q72qc6 leptospira

835	28	82.4	309	2	Q4TUT0_9SPHN	Q4tj0 erythroba	908	28	82.4	395	1	YNK2_CABEL	P34553 caenorhabdi
836	28	82.4	309	2	Q4TLR2_9SPHN	Q4tlr2 erythroba	909	28	82.4	395	2	Q84AT9_9ENTR	Q84at9 buchmera ap
837	28	82.4	316	2	Q504L8_XENTR	Q504l8 xenopus tro	910	28	82.4	395	2	Q4RJS5_TETNG	Q4rjs5 tetraodon n
838	28	82.4	317	2	Q6CRM6_KLULA	Q6crm6 kluyveromyc	911	28	82.4	399	1	Y507_PASMU	Q9cnc5 pasteurella
839	28	82.4	317	2	Q70J49_HAEIN	Q70j49 haemophilus	912	28	82.4	399	2	Q7PKZ7_ANOGA	Q9pkz7 anopheles g
840	28	82.4	317	2	Q8PES1_LEPIN	Q8fes1 leptospira	913	28	82.4	399	2	Q5LT80_SILPO	Q5lt80 silicibacte
841	28	82.4	320	2	Q4UBJ9_SULAC	Q4ubj9 sulfolobus	914	28	82.4	399	2	Q6F8R0_ACIAD	Q6fkr7 acinetobact
842	28	82.4	321	2	Q9M232_ARATH	Q9m232 arabidopsis	915	28	82.4	401	1	ASSY_SYNEL	Q8dky7 synechococ
843	28	82.4	322	2	Q8LTP9_9CAUD	Q8ltp9 lactococcus	916	28	82.4	403	1	MAF_HUMAN	Q75444 homo sapien
844	28	82.4	322	2	Q9AYV5_BPTU2	Q9ayv5 lactococcus	917	28	82.4	407	2	Q9V4M0_DROME	Q9v4m0 drosophila
845	28	82.4	323	2	Q6R095_ARATH	Q6r095 arabidopsis	918	28	82.4	407	2	Q98397_9PARA	Q98397 meales vir
846	28	82.4	323	2	Q9LDB1_ARATH	Q9ldeb1 arabidopsis	919	28	82.4	416	2	Q9NT30_HUMAN	Q9nt30 homo sapien
847	28	82.4	324	2	Q9W6B1_BRARE	Q9w6b1 brachydanio	920	28	82.4	416	2	Q4K094_STRPN	Q4k094 streptococ
848	28	82.4	325	2	Q6NZW9_BRARE	Q6nzw9 brachydanio	921	28	82.4	416	2	Q4K0D5_STRPN	Q4k0d5 streptococ
849	28	82.4	327	2	Q4V3L3_DROME	Q4v3l3 drosophila	922	28	82.4	416	2	Q5WY86_LEGPL	Q5wy86 legionella
850	28	82.4	327	2	Q98UK4_BRARE	Q98uk4 brachydanio	923	28	82.4	416	2	Q5X6T1_LEGPA	Q5x6t1 legionella
851	28	82.4	332	2	Q82937_ECO57	Q82937 escherichia	924	28	82.4	416	2	Q5ZXB0_LSGPH	Q5zxb0 legionella
852	28	82.4	332	2	Q799R6_ECOLI	Q799r6 escherichia	925	28	82.4	419	2	Q5AHCI_CANAL	Q5ahci candida alb
853	28	82.4	332	2	Q6HU51_BACHK	Q6hjs1 bacillus th	926	28	82.4	419	2	Q4PPG6_9RICK	Q4ppg6 candidatus
854	28	82.4	333	2	Q39551_CRAPL	Q39551 craterostig	927	28	82.4	421	2	Q5OU13_ENTHI	Q5ou13 entamoeba h
855	28	82.4	333	2	Q39550_CRAPL	Q39550 craterostig	928	28	82.4	423	2	Q8R1U5_MOUSE	Q8r1u5 mus musculu
856	28	82.4	333	2	Q34933_BACSU	Q34933 bacillus su	929	28	82.4	424	2	Q8DJ55_SYNEL	Q8djs5 synechococ
857	28	82.4	334	2	Q8XM97_CLOPE	Q8xm97 clostridium	930	28	82.4	425	2	Q8UEN8_AGR75	Q8uen8 agrobacteri
858	28	82.4	335	2	Q39552_CRAPL	Q39552 craterostig	931	28	82.4	426	2	Q6SQS9_DBRHA	Q6sq99 debaryomyce
859	28	82.4	335	2	Q7QCV7_AGR75	Q7qcv7 agrobacteri	932	28	82.4	426	2	Q9AAW9_CAUCR	Q9aaw9 caulobacter
860	28	82.4	335	2	Q8R0S5_MOUSE	Q8r0s5 mus musculu	933	28	82.4	428	2	Q5AR60_EMENI	Q5ar60 aspergillus
861	28	82.4	337	2	Q5YXN9_NOCFA	Q5yxn9 nocardia fa	934	28	82.4	429	2	Q7CYP2_AGR75	Q7cyp2 agrobacteri
862	28	82.4	340	2	Q9FM05_ARATH	Q9fm05 arabidopsis	935	28	82.4	431	2	Q8C0R6_MOUSE	Q8c0r6 mus musculu
863	28	82.4	341	2	Q5B804_EMENI	Q5b804 aspergillus	936	28	82.4	431	2	Q6AXB8_MOUSE	Q6axb8 mus musculu
864	28	82.4	341	2	Q9PTR4_ORYSA	Q9ptr4 oryza sativ	937	28	82.4	433	2	Q4ZRM3_PSESY	Q4zrm3 pseudomonas
865	28	82.4	341	2	Q6XRA0_9BACT	Q6xra0 uncultured	938	28	82.4	433	2	Q87ZT8_PSESM	Q87zt8 pseudomonas
866	28	82.4	341	2	Q880A3_PSESM	Q880a3 pseudomonas	939	28	82.4	437	2	Q4I4Q8_GIBZE	Q4i4q8 gibberella
867	28	82.4	343	2	Q9ZGU3_ECO57	Q9zgu3 escherichia	940	28	82.4	440	2	Q5AHP7_CANAL	Q5ahp7 candida alb
868	28	82.4	345	2	Q73TT4_MYCPA	Q73tt4 mycobacteri	941	28	82.4	440	2	Q623B2_CAEBR	Q623b2 caenorhabdi
869	28	82.4	346	2	Q4WV05_ASPPU	Q4wv05 aspergillus	942	28	82.4	444	2	Q5LR78_MAGGR	Q5l7r78 magnaporthe
870	28	82.4	346	2	P92019_CABEL	P92019 caenorhabdi	943	28	82.4	445	2	Q86548_BHV4	Q86548 bovine herp
871	28	82.4	348	2	Q26433_METHH	Q26433 methanobact	944	28	82.4	445	2	Q99D10_BHV4	Q99d10 bovine herp
872	28	82.4	349	2	Q5T839_ANOGA	Q5t839 anopheles g	945	28	82.4	449	2	Q5H9J6_HUMAN	Q5h9j6 homo sapien
873	28	82.4	351	2	Q8F8J6_LEPIN	Q8f8j6 leptospira	946	28	82.4	451	2	Q9X8D0_STRCO	Q9x8d0 streptomyce
874	28	82.4	356	2	Q8U6L8_AGR75	Q8u6l8 agrobacteri	947	28	82.4	451	2	Q7UX64_RHOBA	Q7ux64 rhodospirell
875	28	82.4	356	2	Q87PN3_VIBPA	Q87pn3 vibrio para	948	28	82.4	454	2	Q8Q0S3_METMA	Q8q0s3 methanosarc
876	28	82.4	357	2	Q837D7_ENTFA	Q837d7 enterococcu	949	28	82.4	456	2	Q5GH22_SMIMA	Q5gh22 emanthopsis
877	28	82.4	357	2	Q72N28_LEPIC	Q72n28 leptospira	950	28	82.4	457	2	Q5CVG6_CRYPV	Q5cvg6 cryptospori
878	28	82.4	358	2	Q9FYX4_LYCES	Q9fyx4 lycopersico	951	28	82.4	457	2	Q5CKG6_CRYPV	Q5ckg6 cryptospori
879	28	82.4	358	2	Q6UDM3_9HERP	Q6udm3 psittacid h	952	28	82.4	460	2	Q9VS33_DROME	Q9vs33 drosophila
880	28	82.4	358	2	Q789F2_CHICK	Q789f2 gallus gall	953	28	82.4	462	2	Q6PP77_HUMAN	Q6pp77 homo sapien
881	28	82.4	359	2	Q789F3_CHICK	Q789f3 gallus gall	954	28	82.4	463	1	SYG_STAAC	Q5hfj5 staphylococ
882	28	82.4	361	2	Q7QXK6_ANOGA	Q7qxk6 anopheles g	955	28	82.4	463	1	SYG_STAAN	P67034 staphylococ
883	28	82.4	369	1	MAF_AVISA4	P23091 avian muscu	956	28	82.4	463	1	SYG_STAAN	P99129 staphylococ
884	28	82.4	369	1	MAF_RAT	P54844 rattus norv	957	28	82.4	463	1	SYG_STAAR	Q6g9d5 staphylococ
885	28	82.4	369	1	MAF_RAT	Q7nh46 gloebacter	958	28	82.4	463	1	SYG_STAAS	Q6g902 staphylococ
886	28	82.4	369	1	MAF_RAT	Q92171 gallus gall	959	28	82.4	463	1	SYG_STAAP	P67035 staphylococ
887	28	82.4	370	1	MAF_MOUSE	P54843 mus musculu	960	28	82.4	463	1	SYG_STAAP	Q8cad5 staphylococ
888	28	82.4	370	2	Q7IA33_HUMAN	Q7ia33 homo sapien	961	28	82.4	463	1	SYG_STAEP	Q8mny2 staphylococ
889	28	82.4	370	2	Q6KC09_TETNG	Q6kc09 tetraodon n	962	28	82.4	463	2	Q4L6R5_STAHL	P67034 staphylococ
890	28	82.4	371	2	Q5K021_ORYLA	Q5k021 oryza lat	963	28	82.4	464	2	Q4QG22_LEIMA	Q4qg22 leishmania
891	28	82.4	371	2	Q6KC07_FUGRU	Q6kc07 fuqu rubrip	964	28	82.4	464	2	Q6W6H0_STRHB	P61546 lactococcus
892	28	82.4	373	2	Q6G147_HUMAN	Q6g147 homo sapien	965	28	82.4	468	1	LACG_LACIA	P11546 lactococcus
893	28	82.4	373	2	Q8AB77_BACTN	Q8ab77 bacteroides	966	28	82.4	468	1	LACG_STRMU	P50978 streptococ
894	28	82.4	376	2	Q4MW44_BACCE	Q4mw44 bacillus ce	967	28	82.4	468	2	Q9EV38_STRGN	Q9ev38 streptococ
895	28	82.4	376	2	Q73CJ0_BACC1	Q73cj0 bacillus ce	968	28	82.4	468	2	Q5X9Y7_STRP6	Q5x9y7 streptococ
896	28	82.4	379	2	Q9VX89_DROME	Q9vx89 drosophila	969	28	82.4	468	2	Q9Y118_STRPY	Q9y118 streptococ
897	28	82.4	379	2	Q6HMH8_BACHK	Q6hmh8 bacillus th	970	28	82.4	468	2	Q8DPP6_STRR6	Q8dpp6 streptococ
898	28	82.4	380	2	Q83CT6_COXBU	Q83ct6 coxiella bu	971	28	82.4	468	2	Q8E4S2_STRR3	Q8e4s2 streptococ
899	28	82.4	380	2	Q4QT62_MOUSE	Q4qy62 mus musculu	972	28	82.4	468	2	Q8KSV1_STRP3	Q8k5v1 streptococ
900	28	82.4	381	2	Q8D9B2_VIBVU	Q8d9b2 vibrio vuln	973	28	82.4	468	2	Q8NZEI_STRP8	Q8nzei streptococ
901	28	82.4	381	2	Q7ML28_VIBVY	Q7ml28 vibrio vuln	974	28	82.4	468	2	Q97QL9_STRPN	Q97ql9 streptococ
902	28	82.4	383	2	Q81QV0_BACAN	Q8lqv0 bacillus an	975	28	82.4	469	1	BGL1_BACSU	P40740 bacillus su
903	28	82.4	390	2	Q61J58_CAEBR	Q61j58 caenorhabdi	976	28	82.4	469	1	LEU2_BRUMS	Q8y1c9 brucella me
904	28	82.4	392	2	Q4IKZ3_GIBZE	Q4ikz3 gibberella	977	28	82.4	469	1	LEU2_BRUSU	Q8fyg9 brucella su
905	28	82.4	392	2	Q8KPS7_SYNP7	Q8kps7 synechococ	978	28	82.4	469	2	Q57AZO_BRUAB	Q57azo brucella ab
906	28	82.4	392	2	Q5NSA1_SYNP6	Q5nsa1 synechococ	979	28	82.4	469	2	Q4L868_STAHL	Q4l868 staphylococ
907	28	82.4	393	2	Q605V3_METCA	Q605v3 methylococc	980	28	82.4	469	2	Q65D37_BACLD	Q65d37 bacillus ll

981 28 82.4 470 1 LACG STAAM P67767 staphylococ
 982 28 82.4 470 1 LACG STAAN P67768 staphylococ
 983 28 82.4 470 1 LACG STAAU P11175 staphylococ
 984 28 82.4 470 1 LACG STAAW P67769 staphylococ
 985 28 82.4 470 1 LACG STAPB Q8cnf8 staphylococ
 986 28 82.4 470 2 Q6G7C5 STAAS Q6G7C5 staphylococ
 987 28 82.4 470 2 Q6GEP0 STAEQ Q6gep0 staphylococ
 988 28 82.4 470 2 Q5HM41 STAEQ Q5hm41 staphylococ
 989 28 82.4 470 2 Q5HE1C STAAC Q5he1c staphylococ
 990 28 82.4 472 2 Q9JTM6 NEIMA Q9jtm6 neisseria m
 991 28 82.4 475 2 Q6ERZI ORISA Q6erzi oryza sativ
 992 28 82.4 475 2 Q5FMF4 LACAC Q5fmf4 lactobacill
 993 28 82.4 476 2 Q838Z1 ENTFA Q838z1 enterococcu
 994 28 82.4 476 2 Q8FZ40 BRUSU Q8fz40 brucella su
 995 28 82.4 477 2 Q57K64 SALCH Q57k64 salmonella
 996 28 82.4 477 2 Q5WBD7 BACSK Q5wbd7 bacillus cl
 997 28 82.4 477 2 Q8Z3X2 SALT1 Q8z3x2 salmonella
 998 28 82.4 477 2 Q8ZM78 SALT1 Q8zm78 salmonella
 999 28 82.4 477 2 Q5PJG8 SALPA Q5pjg8 salmonella
 1000 28 82.4 477 2 Q725F1 LISMF Q725f1 listeria mo

ALIGNMENTS

RESULT 1
 Q7XB55_9VIRI PRELIMINARY; PRT; 209 AA.
 AC Q7XB55;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Sexual cell division-inducing pheromone.
 GN Name=scdip-1;
 OS Clostridium ehrenbergii.
 OC Eukaryota; Viridiplantae; Streptophyta; Zygnemophyceae; Desmidiaceae;
 OC Closteriaceae; Closterium.
 OX NCBI_TaxID=102165;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Fukumoto R., Sekimoto H., Fujii T.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB066448; BAC80145.1; -; mRNA.
 DR GO; GO:0000910; P:cytokinesis; IEA.
 DR InterPro; IPR001412; TRNA-synt_1.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
 KW Cell division.
 SQ SEQUENCE 209 AA; 23200 MW; D80ECC48B3B05EDD CRC64;

Query Match 100.0%; Score 34; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

Qy 1 NYWMT 5
 |||||
 Db 190 NYWMT 194

RESULT 2
 Q36098_THEPA PRELIMINARY; PRT; 255 AA.
 ID Q36098_THEPA
 AC Q36098;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Cytochrome oxidase subunit III.
 GN Name=colII;
 OS Theileria parva.
 OG Mitochondrion.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94155854; PubMed=8112303;
 RA Kairo A., Fairlamb A., Gobright E., Nene V.;
 RT "A 7.1 kb linear DNA molecule of Theileria parva has scrambled rDNA
 sequences and open reading frames for mitochondrially-encoded
 proteins.";
 RL EMBO J. 13:898-905(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Nene M.;
 RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 223263; CAAB0799.1; -; Genomic_DNA.
 DR PIR; S41690; S41690.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000298; CytC_oxdse_III.
 DR PROSITE; PS50253; COX3; 1.
 KW Mitochondrion.
 SQ SEQUENCE 255 AA; 29890 MW; A3FF61D44A28844 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

Qy 1 NYWMT 5
 |||||
 Db 189 NYWMT 193

RESULT 3
 Q8XI47_CLOPE PRELIMINARY; PRT; 430 AA.
 ID Q8XI47;
 AC Q8XI47;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Probable nitrate extrusion protein.
 GN Name=narK; OrderedLocustNames=CPE2274;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.0224937999;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; BA000016; BAB81980.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome.
 SQ SEQUENCE 430 AA; 45530 MW; 7264A7433ADAD1DEC CRC64;

Query Match 100.0%; Score 34; DB 2; Length 430;
 Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;

Qy 1 NYWMT 5
 |||||
 Db 269 NYWMT 273

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RESULT 4
Q5POK9 RAT PRELIMINARY; PRT; 479 AA.
AC Q5POK9
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087137; AAH87137.1; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;

Query Match 100.0%; Score 34; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 50 NYWMT 54

RESULT 5
Q831B5 ENTFA PRELIMINARY; PRT; 481 AA.
AC Q831B5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycosyl hydrolase, family 1.
GN OrderedLocNames=EF2597;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074(2003).
DR EMBL; AF016955; AAO82307.1; -; Genomic_DNA.
DR HSSP; P11546; IPBG.
DR TIGR; EF2597; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 481 AA; 54978 MW; CF9250BAD786F1B0 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 177 NYWMT 181

RESULT 6
Q9LK63 ARATH PRELIMINARY; PRT; 1441 AA.
ID Q9LK63_ARATH PRELIMINARY; PRT; 1441 AA.
AC Q9LK63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Multidrug resistance-associated protein (MRP); ABC-transporter.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 Fl, TAC
RT and BAC clones."
RL DNA Res. 7:217-221(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000375; BAB01400.1; -; Genomic_DNA.
DR HSSP; P26361; IROW.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.

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DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; F:transport; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR011527; ABC membrane 1.
 DR InterPro; IPR001140; ABC TM transp.
 DR InterPro; IPR003439; ABC transp_like.
 DR Pfam; PF00664; ABC membrane; 2.
 DR Pfam; PF00005; ABC trans; 2.
 DR ProDom; PD000006; ABC transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS0929; ABC TMIF; 2.
 DR PROSITE; PS0211; ABC TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 SQ SEQUENCE 1441 AA; 161588 MW; 452E811289748EE8 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 1441;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 918 NYWMT 922

RESULT 7
 Q8VZ24 ARATH PRELIMINARY; PRT; 1466 AA.
 ID Q8VZ24;
 AC Q8VZ24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE ATP-binding cassette transporter KRPP6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Forestier C.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY052368; AAL14776.1; -; mRNA.
 DR HSP; P26361; IRW.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; F:transport; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR011527; ABC membrane 1.
 DR InterPro; IPR001140; ABC TM transp.
 DR InterPro; IPR003439; ABC transp_like.
 DR Pfam; PF00664; ABC membrane; 2.
 DR Pfam; PF00005; ABC trans; 2.
 DR ProDom; PD000006; ABC transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS0929; ABC TMIF; 2.
 DR PROSITE; PS0211; ABC TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 DR ATP-binding.
 SQ SEQUENCE 1466 AA; 164378 MW; 8C90CF66FF07F0E8 CRC64;

Query Match 100.0%; Score 34; DB 2; Length 1466;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 918 NYWMT 922

RESULT 8
 Q9XPH9 CHEMY PRELIMINARY; PRT; 116 AA.
 ID Q9XPH9;
 AC Q9XPH9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).
 OS Chelonia mydas (Green sea-turtle) (Chelonia agassizi).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Chelonioidea; Cheloniidae; Chelonia.
 OX NCBI_TaxID=8469;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99297345; PubMed=10368956;
 RA Kumazawa Y., Nishida M.;
 RT "Complete mitochondrial DNA sequences of the green turtle and blue-tailed mole skink: statistical evidence for archosaurian affinity of turtles.";
 RL Mol. Biol. Evol. 16:784-792(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96073446; PubMed=7476123;
 RA Kumazawa Y., Nishida M.;
 RT "Variations in mitochondrial tRNA gene organization of reptiles as phylogenetic markers.";
 RL Mol. Biol. Evol. 12:759-772(1995).
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 DE -!- SIMILARITY: Belongs to the complex I subunit 3 family.
 DR EMBL; AB012104; BAA79204.1; -; Genomic DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR InterPro; IPR000440; Oxidored q4.
 DR Pfam; PF00507; Oxidored q4; 1.
 DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 116 AA; 13428 MW; 2455CB3A43D8D291 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 116;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 22 NYWMT 26

RESULT 9
 Q7QJP6 ANOGA PRELIMINARY; PRT; 154 AA.
 ID Q7QJP6 ANOGA PRELIMINARY; PRT; 154 AA.
 AC Q7QJP6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000009346 (fragment).
 GN ORFNames=ENSANG00000006995;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 EG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation,";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB0100807; EAA04373.2; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
 DR GO; GO:0006518; P:peptide metabolism; IEA.
 DR InterPro; IPR000720; P:aminoxigenase.
 DR PRINTS; PR00790; PAMONOXGNASE.
 FT NON_TER 154
 SQ SEQUENCE 154 AA; 17391 MW; 0494469270C12B8A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 154;
 Best Local Similarity 80.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 150 NYWLT 154

RESULT 10

Q7P812 FUSNV
 ID Q7P812 FUSNV PRELIMINARY; PRT; 208 AA.
 AC Q7P812;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=FNV2330;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OC NCBI_TaxID=209882;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 49256;
 RA Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haselkorn R., Overbeek R., Kyrpides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB0100001; EAA25286.1; -; Genomic_DNA.
 DR Hypothetical protein.
 SQ SEQUENCE 208 AA; 23770 MW; E80DD1059D4CA443 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 208;
 Best Local Similarity 80.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 124 NYWLT 128

RESULT 11

Q88T17 LACPL
 ID Q88T17 LACPL PRELIMINARY; PRT; 229 AA.
 AC Q88T17;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Integral membrane protein.
 GN OrderedLocusNames=lp_3192;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OC NCBI_TaxID=1590;

RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RX Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100.1990-1995(2003).
 DR EMBL; AL935261; CAD65341.1; -; Genomic_DNA.
 DR InterPro; IPR010699; DUF1275.
 DR Pfam; PF06912; DUF1275; 1.
 KW Complete proteome.
 SQ SEQUENCE 229 AA; 25108 MW; 7800DD69FAEA047CC CRC64;

Query Match 91.2%; Score 31; DB 2; Length 229;
 Best Local Similarity 80.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 160 NYWLT 164

RESULT 12

Q9S9N0 ARATH
 ID Q9S9N0 ARATH PRELIMINARY; PRT; 270 AA.
 AC Q9S9N0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T24D18.15 protein.
 GN Name=T24D18.15;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
 RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hwang B., Koo T., Li J., Liu A., Vaysberg M., Altati H., Brooks S.,
 RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
 RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
 RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP Theologis;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC010924; AAF18502.1; -; Genomic_DNA.
 DR PIR; C86295; C86295.
 DR GO; GO:0005789; C:endoplasmic reticulum membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006506; P:GPI anchor biosynthesis; IEA.
 DR InterPro; IPR009580; PIG-F__mfrase.
 DR Pfam; PF06699; PIG-F; 1.
 SQ SEQUENCE 270 AA; 30170 MW; 8C9244973A594ABE CRC64;

Query Match 91.2%; Score 31; DB 2; Length 270;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 240 NYWLT 244

RESULT 13

Q66B8_YERPS

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ID Q66BH8 YERPS PRELIMINARY; PRT; 281 AA.
AC Q66BH8.
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative phage protein.
GN OrderedLocusNames=YPTB1793;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH21032.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 281 AA; 31586 MW; 46A99A36FA705666 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 281;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 32 NYWLT 36

RESULT 14
Q8ZZ19 PYRAE
ID Q8ZZ19 PYRAE PRELIMINARY; PRT; 293 AA.
AC Q8ZZ19.
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE02239.
GN OrderedLocusNames=PAE02239;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009757; AAL62650.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 33722 MW; 9CAF37897566C86A CRC64;

Query Match 91.2%; Score 31; DB 2; Length 293;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 3 NYWLT 7

RESULT 15
Q8L1M6_ENTAE

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ID Q8L1M6 ENTAE PRELIMINARY; PRT; 296 AA.
AC Q8L1M6.
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Transcriptional activator protein AmpR.
GN Name=ampR;
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=type strain: CIP 60.86;
RA Benzerara Y., Rottman M.M., Arlet G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
DR EMBL; AJ487977; CAD32302.1; -; Genomic_DNA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH 1; 1.
DR PRINTS; PR00039; HTH_LysR.
DR PROSITE; PS50931; HTH_LYSR; 1.
DR DNA-binding; Transcription regulation.
KW DNA-binding; Transcription; IEA.
SQ SEQUENCE 296 AA; 33018 MW; BE48A5C6AB100280 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 296;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 263 NYWLT 267

RESULT 16
Q5QHV5 LEIAM
ID Q5QHV5 LEIAM PRELIMINARY; PRT; 348 AA.
AC Q5QHV5.
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Rbp38p.
OS Leishmania amazonensis.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5659;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MHOM/BR/73/M2269;
RA Siqueira Neto J.L., Fernandez M.F., Cano M.I.N.;
RT "The protein component of LagT2 (Leishmania amazonensis G-strand
RT telomeric complex 2).";
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485300; AAR90345.1; -; Genomic_DNA.
SQ SEQUENCE 348 AA; 39824 MW; 5A35BF491D0718E1 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 348;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 289 NYWLT 293

RESULT 17
Q4QB87_LEIMA
ID Q4QB87_LEIMA PRELIMINARY; PRT; 348 AA.

```


AC Q4QB87;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DE Hypothetical protein.
 GN ORFNames=FGL1385.1;
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Mitochondrial RNA binding protein, putative.
 GN ORFNames=LmjP23.0760;
 OS Leishmania major.
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
 RA Bianchetti G., Buchy M., Bothe G., Brusch C., Carloni L.,
 RA Duesterhoeft A., Forzy M., Gabel C., Goffeau A., Hilbert H.,
 RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
 RA Fumelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
 RA Tosato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
 RA Rajandream M., and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: C7005262; CAJ04428.1; -; Genomic DNA.
 SQ SEQUENCE 348 AA; 39734 MW; 78708D3FE24EC001 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 348;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 289 NYWLT 293
 RESULT 19
 ID Q86PT0_LEITA PRELIMINARY; PRT; 349 AA.
 AC Q86PT0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE Mitochondrial RNA-binding protein RBP38.
 GN Name=RBP38;
 OS Leishmania tarentolae (Sauroleishmania tarentolae).
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
 OC lizard Leishmania.
 OX NCBI_TaxID=5689;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22680906; PubMed=12796301; DOI=10.1128/EC.2.3.560-568.2003;
 RA Sbicego S., Alfonso J.D., Estevez A.M., Rubio M.A., Kang X.,
 RA Turk C.W., Peris M., Simpson L.;
 RT "RBP38, a novel RNA-binding protein from trypanosomatid mitochondria,
 RT modulates RNA stability.";
 RL Eukaryot. Cell 2:560-568(2003).
 DR EMBL: AY187286; AAO39844.1; -; Genomic DNA.
 SQ SEQUENCE 349 AA; 39953 MW; 44P8158365C8E6F9 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 349;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 290 NYWLT 294
 RESULT 19
 ID Q4HUH3_GIBZE PRELIMINARY; PRT; 354 AA.
 AC Q4HUH3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FGL1385.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=PH-1;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rogov P., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talman J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACM01000465; EAA78698.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 354 AA; 39403 MW; B1B79DF53BCF234D CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 354;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 164 NYWLT 168
 RESULT 20
 ID Q8PTH4_METMA PRELIMINARY; PRT; 364 AA.
 AC Q8PTH4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein MM2741.
 GN OrderedLocNames=MM2741;
 OS Methanosarcina mazel (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OX NCBI_TaxID=2209;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=1215824;
 RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wier A., Baeumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazel: evidence for lateral gene

RT transfer between Bacteria and Archaea.;"
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
 DR EMBL; AE013521; AM32437.1; -; Genomic_DNA.

KW Complete proteome.
 SQ SEQUENCE 364 AA; 43180 MW; 4157BEC23CF2C0DB CRC64;

Query Match 91.2%; Score 31; DB 2; Length 364;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 13 NYWLT 17

RESULT 21

Q5B017 EMENI PRELIMINARY;
 AC Q5B017 EMENI PRELIMINARY; PRT; 401 AA.
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=AN5943.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FGSC A4;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zalnoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.

RT "Genome Sequence of Aspergillus nidulans.;"
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAC01000101; EAA57806.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 401 AA; 44645 MW; 4421C5EF509A583C CRC64;

Query Match 91.2%; Score 31; DB 2; Length 401;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 193 NYWLT 197

RESULT 22

Q6AE08_LEIXX

ID Q6AE08_LEIXX PRELIMINARY; PRT; 423 AA.
 AC Q6AE08_LEIXX PRELIMINARY; PRT; 423 AA.
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Membrane efflux protein (Fosmidomycin resistance).
 GN Name=fer; OrderedLocusNames=Lxx15890;
 OS Leifsonia xylii (subsp. xylii).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Microbacteriaceae; Leifsonia.
 OX NCBI_TaxID=59736;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CTCB07;
 RC PubMed=15305603;
 RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
 RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
 RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorzy H.A.,
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.B., Lemos E.G.M.,
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
 "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
 xylii subsp. xylii.;"
 RL Mol. Plant Microbe Interact. 17:827-836(2004).
 DR EMBL; AB016822; AAT9388.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0046677; P:response to antibiotic; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS.1.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF07690; MFS.1; 1.
 DR PROSITE; PS50850; MFS; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 423 AA; 43604 MW; 8BE597DC8A32F93B CRC64;

Query Match 91.2%; Score 31; DB 2; Length 423;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||||
 Db 111 NYWLT 115

RESULT 23

Q7UY34_RHOBA PRELIMINARY;
 AC Q7UY34_RHOBA PRELIMINARY; PRT; 447 AA.
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB913;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firellula.
 OX NCBI_TaxID=1117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=1;
 EX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gleckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firellula sp.

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RT strain 1.";
DR Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
RL EMBL; BX294134; CAD71814.1; -; Genomic_DNA.
DR InterPro; IPR006311; Tat.
DR TIGRPFAMS; TIGR01409; TAT signal seq; 1.
KW Complete proteome; Hypothetical_protein.
SQ SEQUENCE 447 AA; 50329 MW; 518ACF2E330094B06 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 447;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 332 NYWLT 336

RESULT 24
Q9BRN4 HUMAN PRELIMINARY; PRT; 453 AA.
AC Q9BRN4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CLCN7 protein (fragment).
GN Names=CLCN7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Faxon A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006158; AA06158.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0005821; P:chloride-gated chloride channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR00644; CBS.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_Clc; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
FT NON_TER 1
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SQ SEQUENCE 453 AA; 50306 MW; C0415EAE07EA41BD CRC64;

Query Match          91.2%; Score 31; DB 2; Length 453;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 44 NYWLT 48

RESULT 25
Q59NK9 CANAL PRELIMINARY; PRT; 454 AA.
AC Q59NK9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Ca019.6606;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T., Davis R.W., Scherer S.;
RA "The diploid genome sequence of Candida albicans.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL; AACQ01000204; EAK92073.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 454 AA; 51731 MW; A69ECDF7893B914D CRC64;

Query Match          91.2%; Score 31; DB 2; Length 454;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 136 NYWLT 140

RESULT 26
Q5KXG4 GEOKA PRELIMINARY; PRT; 455 AA.
AC Q5KXG4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Beta-glucosidase (EC 3.2.1.21).
GN Ordered locus Names=GK2337;
OS Geobacillus kaustophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTA426;
RX PubMed=15576355; DOI=10.1093/nar/gkh970;
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RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
RA Mateui S., Uchiyama I.,
RT "Thermoadaptation trait revealed by the genome sequence of
RT thermophilic Geobacillus kaustophilus." ;
RL Nucleic Acids Res. 32:6292-6303 (2004).
DR EMBL; BA000043; BAD76622.1; -; Genomic DNA.
DR GO; GO:0008422; F:beta-glucosidase activity; IEA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; UNKNOWN_1.
KW Complete proteome; GLYCOSIDase; Hydrolase;
SQ SEQUENCE 455 AA; 52703 MW; F50EF72209531CFB CRC64;

Query Match 91.2%; Score 31; DB 2; Length 455;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 159 NYWLT 163

RESULT 27
Q9CLV1 PASMU PRELIMINARY; PRT; 489 AA.
AC Q9CLV1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PM1371.
GN OrderedLocusNames=PM1371;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70." ;
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
CC -!- SIMILARITY: Belongs to the FGGY kinase family.
DR EMBL; AE006175; AAK03455.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004856; F:xylulokinase activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR GO; GO:0005997; F:xylulose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR Pfam; PF02782; FGGY_C; 1.
DR Pfam; PF00370; FGGY_N; 1.
DR TIGRFAMs; TIGR01312; XylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; UNKNOWN 1.
DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN 1.
KW Complete proteome; Hypothetical protein; Kinase; Transferase.
SQ SEQUENCE 489 AA; 53936 MW; 54D2E90B4B543CB0 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 489;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 163 NYWLT 167

RESULT 28
Q9CLV1 PASMU PRELIMINARY; PRT; 493 AA.
AC Q9CLV1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Xylulose kinase (EC 2.7.1.17) (Xylulokinase).
GN Name=xylB; OrderedLocusNames=H1113;
OS Haemophilus influenzae;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Science 269:496-512 (1995).
CC -!- CATALYTIC ACTIVITY: ATP + D-xylulose = ADP + D-xylulose 5-
CC phosphate.
CC -!- SIMILARITY: Belongs to the FGGY kinase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; U32791; AAC22767.1; ALT_INIT; Genomic_DNA.
DR TIGR; H1113; -
DR InterPro; IPR000577; FGGY_kin.
DR PANTHER; PTHR10196; FGGY_kin; 1.
DR Pfam; PF02782; FGGY_C; 1.
DR Pfam; PF00370; FGGY_N; 1.
DR TIGRFAMs; TIGR01312; XylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
KW Carbohydrate metabolism; Complete proteome; Kinase; Transferase;
KW Xylulose metabolism.
SQ SEQUENCE 493 AA; 54804 MW; 0F7C72AEB26FEDD6 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 493;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 167 NYWLT 171

RESULT 29
Q30495 PSEFL PRELIMINARY; PRT; 493 AA.
AC Q30495;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xylulose kinase.
GN Name=mtly;
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.

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OX NCBI_TaxID=294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM50106;
RX MEDLINE=97236441; PubMed=91116029;
RA Brunker P., Altenbuchner J., Kulbe K.D., Mattes R.;
RT "Cloning, nucleotide sequence and expression of a mannitol
RT dehydrogenase gene from Pseudomonas fluorescens DSM 50106 in
RT Escherichia coli.";
RL Biochim. Biophys. Acta 1351:157-167 (1997).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=DSM50106;
RX MEDLINE=98121321; PubMed=9461423; DOI=10.1016/S0378-1119(97)00574-X;
RA Brunker P., Altenbuchner J., Mattes R.;
RT "Structure and function of the genes involved in mannitol, arabinol
RT and glucitol utilization from Pseudomonas fluorescens DSM50106.";
RL Gene 206:117-126 (1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM50106;
RA Bruenker P., Altenbuchner J., Mattes R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the FGGY kinase family.
DR EMBL: AF007800; AAC04473.1; -; Genomic_DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0004856; F:xylulokinase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0005997; P:xylulose metabolism; IEA.
DR InterPro: IPR000577; FGGY_kin.
DR InterPro: IPR001680; WD40.
DR InterPro: IPR006000; Xylulokinase.
DR Pfam: PF02782; FGGY_C; 1.
DR Pfam: PF00370; FGGY_N; 1.
DR TIGRfam: TIGR01312; XylB; 1.
DR PROSITE: PS00933; FGGY_KINASES_1; FALSE NEG.
DR PROSITE: PS00445; FGGY_KINASES_2; UNKNOWN_1.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Kinase; Transferase.
SQ SEQUENCE 493 AA; 52057 MW; 6E66792F8E5B5C65 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 493;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 168 NYWLT 172

RESULT 30
Q4ZTP8_PSESY Q4ZTP8_PSESY PRELIMINARY; PRT; 493 AA.
AC Q4ZTP8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Xylulokinase.
GN ORFNames=Psyr_2435;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA Nolan M., Goltman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000.";

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RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the FGGY kinase family.
DR EMBL: CF000075; AY37474.1; -; Genomic_DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR InterPro: IPR012282; Cytochrome_c_R.
DR InterPro: IPR000577; FGGY_kin.
DR InterPro: IPR006000; Xylulokinase.
DR Pfam: PF02782; FGGY_C; 1.
DR Pfam: PF00370; FGGY_N; 1.
DR TIGRfam: TIGR01312; XylB; 1.
DR PROSITE: PS00445; FGGY_KINASES_2; UNKNOWN_1.
KW Kinase; Transferase.
SQ SEQUENCE 493 AA; 52619 MW; 1CE24D3DE7E0C7A8 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 493;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 163 NYWLT 167

RESULT 31
Q882C6_PSESM Q882C6_PSESM PRELIMINARY; PRT; 493 AA.
AC Q882C6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xylulokinase.
GN Name=xylB; OrderedLocustNames=PSPT02702;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Daviden T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
CC -!- SIMILARITY: Belongs to the FGGY kinase family.
DR EMBL: AE016853; AA056204.1; -; Genomic_DNA.
DR TIGR: PSPT02702; -.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0004856; F:xylulokinase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0005997; P:xylulose metabolism; IEA.
DR InterPro: IPR000577; FGGY_kin.
DR InterPro: IPR006000; Xylulokinase.
DR Pfam: PF02782; FGGY_C; 1.

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DR Pfam; PF00370; FGGY_N; 1.
DR TIGRFAMs; TIGR01312; XylB; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
KW Complete proteome; Kinase; Transferrase.
SQ SEQUENCE 493 AA; 52729 MW; D47DC977396E201D CRC64;

  Query Match          91.2%; Score 31; DB 2; Length 493;
  Best Local Similarity 80.0%; Pred. No. 1.9e+03;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 163 NYWLT 167

RESULT 32
Q4ITN3_AZOVI
ID Q4ITN3_AZOVI PRELIMINARY; PRT; 495 AA.
AC Q4ITN3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Xylulokinase.
GN ORFNames=AvinDRAFT_1115;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RA DOE Joint Genome Institute;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAU03000016; EAM04110.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 495 AA; 53351 MW; B8EB9B186E91D370 CRC64;

  Query Match          91.2%; Score 31; DB 2; Length 495;
  Best Local Similarity 80.0%; Pred. No. 2e+03;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 163 NYWLT 167

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RESULT 33
Q7N5I9_PHOLL
ID Q7N5I9_PHOLL PRELIMINARY; PRT; 503 AA.
AC Q7N5I9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xylulose kinase.
GN Name=xylB; OrderedLocNames=plu1959;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Deroo S., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571865; CAE14252.1; -; Genomic_DNA.
DR Photolist; plu1959; -;
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004856; F:xylulokinase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005996; P:monosaccharide metabolism; IEA.
DR GO; GO:0005987; P:xylulose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR006000; Xylulokinase.
DR Pfam; PF02782; FGGY_C; 1.
DR TIGRFAMs; TIGR01312; XylB; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 503 AA; 55030 MW; C6393157DF42794F CRC64;

  Query Match          91.2%; Score 31; DB 2; Length 503;
  Best Local Similarity 80.0%; Pred. No. 2e+03;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 165 NYWLT 169

RESULT 34
Q4QLI1_HAE18
ID Q4QLI1_HAE18 PRELIMINARY; PRT; 511 AA.
AC Q4QLI1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Xylulose kinase (EC 2.7.1.17).
GN Name=xylB; OrderedLocNames=NTH11277;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20.";
RL J. Bacteriol. 187:4627-4636(2005).

```

CC -1- SIMILARITY: Belongs to the FGGY kinase family.
 DR ENBL; CP000057; AAX88116.1; -, Genomic_DNA.
 DR InterPro; IPR000577; FGGY_kin.
 DR InterPro; IPR006000; Xylulokinase.
 DR Pfam; PF02782; FGGY_C; 1.
 DR Pfam; PF00370; FGGY_N; 1.
 DR TIGRFAMs; TIGR01312; XylB; 1.
 DR PROSITE; PS00933; FGGY_KINASES_1; UNKNOWN_1.
 DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
 KW Complete proteome; Kinase; Transferase.
 SQ SEQUENCE 511 AA; 56779 MW; A60A996AA82EB4F7 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 511;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||:|
 Db 185 NYWLT 189

RESULT 35

Q8RN2 LEGPN
 ID Q8RN2_LEGPN PRELIMINARY; PRT; 520 AA.
 AC Q8RN2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein lprN.
 GN Name=lprN;
 OS Legionella pneumophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=446;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22060681; PubMed=12065505;
 RX DOI=10.1128/JAI.70.7.3637-3648.2002;
 RA Rankin S., Li Z., Isberg R.R.;
 RT "Macrophage-induced genes of Legionella pneumophila; protection from
 RT reactive intermediates and solute imbalance during intracellular
 RT growth.";

RL Infect. Immun. 70:3637-3648(2002).

[2]

RN NUCLEOTIDE SEQUENCE.
 RP Chien M., Morozova I., Chen J., Shuman H.A., Russo J.J.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

[3]

RN NUCLEOTIDE SEQUENCE.
 RA Rankin S., Li Z., Isberg R.R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AF480909; AAM00608.1; -, Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003423; OEP.

DR InterPro; IPR010131; RND_outer_NodT.

DR Pfam; PF02321; OEP; 2.

DR TIGRFAMs; TIGR01845; RND_outer_NodT; 1.

KW Hypothetical protein.

SQ SEQUENCE 520 AA; 57302 MW; B8570F881E5DD6D6 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 520;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||:|
 Db 34 NYWLT 38

RESULT 36

Q5WTT7 LEGPL
 ID Q5WTT7_LEGPL PRELIMINARY; PRT; 520 AA.
 AC Q5WTT7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein lprN.
 GN Name=lprN; OrderedLocusNames=lp12436;
 OS Legionella pneumophila (strain Lens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=297245;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15467720; DOI=10.1038/ngl1447;
 RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
 RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
 RA Etienne J., Glaser P., Buchrieser C.;
 RT "Evidence in the Legionella pneumophila genome for exploitation of
 RT host cell functions and high genome plasticity.";

RL Nat. Genet. 36:1165-1173(2004).

DR ENBL; CR628337; CAH16676.1; -, Genomic_DNA.

DR LegioList; lp12436; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008289; F:lipid binding; IEA.

DR GO; GO:0005215; P:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003423; OEP.

DR InterPro; IPR010131; RND_outer_NodT.

DR Pfam; PF02321; OEP; 2.

DR TIGRFAMs; TIGR01845; RND_outer_NodT; 1.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 520 AA; 57166 MW; 2662545AE794EA96 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 520;

Best Local Similarity 80.0%; Pred. No. 2e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 |||:|
 Db 34 NYWLT 38

RESULT 37

Q5X211 LEGPA
 ID Q5X211_LEGPA PRELIMINARY; PRT; 520 AA.
 AC Q5X211;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein lprN.
 GN Name=lprN; OrderedLocusNames=lp2582;
 OS Legionella pneumophila (strain Paris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=297246;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX PubMed=15467720; DOI=10.1038/ngl1447;

RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,

RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,

RA Etienne J., Glaser P., Buchrieser C.;

RT "Evidence in the Legionella pneumophila genome for exploitation of

RT host cell functions and high genome plasticity.";

RL Nat. Genet. 36:1165-1173(2004).

DR ENBL; CR628336; CAH13735.1; -, Genomic_DNA.

DR LegioList; lp2582; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0008289; F:lipid binding; IEA.

DR GO; GO:0005215; P:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003423; OEP.

DR InterPro; IPR010131; RND_outer_NodT.

```

DR Pfam; PF02321; OBP; 2.
KW TIGRFAMs; TIGR01845; RND outer_NodT; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 520 AA; 57343 MW; FE3672F01ADFFA82 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 520;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 34 NYWLT 38

RESULT 38
Q5ZSK3 LEGPH
ID Q5ZSK3 LEGPH PRELIMINARY; PRT; 520 AA.
AC Q5ZSK3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Outer membrane efflux protein (RND multidrug efflux).
GN OrderedLocusNames=lpq2514;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asanani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steshenko V., Park S.H., Zhao B., Tepitskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Gerlinger-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella pneumophila.";
RL Science 305:1966-1968 (2004).
DR EMBL; AE017354; AAU28574.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OBP; 2.
DR TIGRFAMs; TIGR01845; RND_outer_NodT; 1.
KW Complete proteome.
SQ SEQUENCE 520 AA; 57302 MW; B8570F881E5DD6D6 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 520;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 34 NYWLT 38

RESULT 39
Q4QQA0 DROME
ID Q4QQA0 DROME PRELIMINARY; PRT; 534 AA.
AC Q4QQA0;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE IP11809p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Celniker S.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT023516; AAY84916.1; -; mRNA.
SQ SEQUENCE 534 AA; 59133 MW; 7942562EFAA5172 CRC64;

Query Match          91.2%; Score 31; DB 2; Length 534;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 526 NYWLT 530

RESULT 40
Q4V5T4 DROME
ID Q4V5T4 DROME PRELIMINARY; PRT; 536 AA.
AC Q4V5T4;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE IP11909p (Fragment).
GN Name=CG10700;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Celniker S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT022572; AAY54988.1; -; mRNA.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF00070; Pyr_redox; 2.
DR Pfam; PF00355; Rieske; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 536 AA; 59165 MW; 7C4523630EA851AE CRC64;

Query Match          91.2%; Score 31; DB 2; Length 536;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 528 NYWLT 532

RESULT 41
Q9VJ03 DROME
ID Q9VJ03 DROME PRELIMINARY; PRT; 539 AA.
AC Q9VJ03;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TReMBLrel. 26, Last annotation update)
DE CG10700-PA.
GN Name=CG10700; ORFNames=CG10700;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.D.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN (2)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN (3)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN (4)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richer J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a

RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN (5)
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RN NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003661; AAF53755.1; -; Genomic DNA.
 DR Ensembl; CG10700; *Drosophila melanogaster*.
 DR FlyBase; Fggn0032754; CG10700.
 DR GO; GO:0015036; P:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0008118; P:electron transport; IEA.
 DR InterPro; IPR001327; FAD pyr_redox.
 DR InterPro; IPR000103; Pyridine redox_2.
 DR InterPro; IPR001100; Pyr redox.
 DR InterPro; IPR005806; Rieske reg.
 DR Pfam; PF00070; Pyr_redox; 2.
 DR Pfam; PF00355; Rieske; 1.
 DR PRINTS; PR00368; PDPNR.
 DR PRINTS; PR00411; PNDRTASEI.
 DR PRINTS; PR00469; PNDRTASEII.
 SQ SEQUENCE 539 AA; 59872 MW; C66441DFA787784E CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 539;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYWMT 5
 DB 531 NYWLT 535
 RESULT 42
 Q6MMW1 BDEBA PRELIMINARY; PRT; 546 AA.
 AC Q6MMW1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Probable cytochrome C-type biogenesis protein precursor.
 GN Ordered locus names=Bdl606;
 OS *Bdellovibrio bacteriovorus*.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN (1)
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of *Bdellovibrio bacteriovorus* from a
 genomic perspective.";
 RL Science 303:689-692(2004).
 DR EMBL; BX842650; CAE79483.1; -; Genomic DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008535; P:cytochrome c oxidase complex assembly; IEA.
 DR InterPro; IPR002541; Cytc_asm.
 DR Pfam; PF01578; Cytochrom C_asm; 1.
 KW Complete proteome; Signal.
 FT SIGNAL 1
 SQ SEQUENCE 546 AA; 60976 MW; 041540128A4A97A6 CRC64;
 Query Match 91.2%; Score 31; DB 2; Length 546;
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||:|

Db 366 NYWLT 370

RESULT 43

ID P95867_SULSO PRELIMINARY; PRT; 561 AA.

AC P95867;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)

DE Orf c06020 protein (Malto-oligosyltrehalose trehalohydrolase) (Trez) (EC 3.2.1.141).

DE (EC 3.2.1.141).

GN Name=orf c06020; Synonyms=trez; OrderedLocusNames=SSO2093;

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus

OX NCBI_TaxID=2287;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=P2;

RX MEDLINE=97055432; PubMed=8999719;

RA Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y., Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T., Doolittle W.F., Ragan M.A., Charlebois R.L.;

RA "Organizational characteristics and information content of an archaeal genome: 156 kb of sequence from Sulfolobus solfataricus P2.";

RT Mol. Microbiol. 22:175-191(1996).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awevez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erasuo G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X., Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RA "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

RL EMBL; Y08256; CA69503.1; -; Genomic_DNA.

DR EMBL; AE006815; AAK42272.1; -; Genomic_DNA.

DR PIR; S73087; S73087.

DR HSSP; Q55088; 1EH9.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR004193; Glyco_hydro_13N.

DR Pfam; PF00128; Alpha-amylase; 1.

DR Pfam; PF02922; Isoamylase_N; 1.

KW Complete proteome.

SQ SEQUENCE 561 AA; 64370 MW; B00E403020F6B242 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 561;

Best Local Similarity 80.0%; Pred. No. 2.2e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||:|

Db 504 NYWLT 508

RESULT 44

ID Q977Y3_CLOAB PRELIMINARY; PRT; 606 AA.

AC Q977Y3;

DT 01-OCT-2001 (TRENBLrel. 18, Created)

DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Endoglucanase A (Endo-1,4-beta-glucanase) (Cellulase A), secreted;

DE dockerin domain.

GN OrderedLocusNames=CAC0915;

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1488;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 824 / DSM 792 / VOM B-1787;

RX MEDLINE=21359325; PubMed=11466286;

RX DOI=10.1128/JB.183.16.4823-4838.2001;

RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;

RA "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

RT J. Bacteriol. 183:4823-4838(2001).

RL EMBL; AE007607; AAK78891.1; -; Genomic_DNA.

DR PIR; H97012; H97012.

DR HSSP; P38686; 1DAV.

DR GO; GO:0000272; P:polysaccharide catabolism; IEA.

DR InterPro; IPR002105; Dockerin_1.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00404; Dockerin_1; 2.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.

KW Complete proteome.

SQ SEQUENCE 606 AA; 66777 MW; EC00E082846F4CDB CRC64;

Query Match 91.2%; Score 31; DB 2; Length 606;

Best Local Similarity 80.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||:|

Db 96 NYWLT 100

RESULT 45

ID Q5R2A7_9VIRU PRELIMINARY; PRT; 716 AA.

AC Q5R2A7;

DT 01-FEB-2005 (TRENBLrel. 29, Created)

DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)

DE Non structural protein 1.

GN Name=NS1;

OS Canine minute virus.

OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Bocavirus.

OX NCBI_TaxID=329639;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HM-6;

RX PubMed=15550767; DOI=10.1007/s11262-004-7430-3;

RA Ohshima T., Kishi M., Mochizuki M.;

RT "Sequence analysis of an asian isolate of minute virus of canines (canine parvovirus type 1).";

RL Virus Genes 29:291-296(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HM-6;

RA Ohshima T., Kishi M., Mochizuki M.;

RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB158475; BAD72954.1; -; Genomic DNA.

DR GO; GO:0019079; P:viral genome replication; IEA.

DR InterPro; IPR001257; Parvo_NSI.

DR Pfam; PF01057; Parvo_NSI; 1.

SQ SEQUENCE 716 AA; 81914 MW; 5A0AFE2C40262C99 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 716;

Best Local Similarity 80.0%; Pred. No. 2.8e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 266 NYWLT 270

RESULT 46

ID Q8QQV7_VIVRU PRELIMINARY; PRT; 716 AA.
AC Q8QQV7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Non structural protein 1.
OS Canine minute virus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Bocavirus.
OX NCBI_TaxID=329639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22329668; PubMed=12441065; DOI=10.1006/viro.2002.1674;
RA Schwartz D., Green B., Carmichael L.E., Parrish C.R.;
RT "The canine minute virus (minute virus of canines) is a distinct
RT parvovirus that is most similar to bovine parvovirus.";
RL Virology 302:219-223(2002).
DR EMBL; AF495467; AM15964.1; -; Genomic DNA.
DR GO; GO:0019079; P:Viral genome replication; IEA.
DR InterPro; IPR001257; Parvo NS1.
DR Pfam; PF01057; Parvo NS1; 1.
SQ SEQUENCE 716 AA; 81900 MW; 98C9CA9AAF197A8F CRC64;

Query Match 91.2%; Score 31; DB 2; Length 716;
Best Local Similarity 80.0%; Pred. NO. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 266 NYWLT 270

RESULT 47

ID Q8DE10_VIVVU PRELIMINARY; PRT; 749 AA.
AC Q8DE10;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical wbfB-like protein.
GN OrderedLocusNames=VV10795;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016799; AA009299.1; -; Genomic_DNA.
DR InterPro; IPR010344; DUF940_lipo.
DR Pfam; PF06082; DUF940; 1.
KW Complete proteome.
SQ SEQUENCE 749 AA; 84260 MW; 9749843B2AF57EAS CRC64;

Query Match 91.2%; Score 31; DB 2; Length 749;
Best Local Similarity 80.0%; Pred. NO. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 476 NYWLT 480

RESULT 48

ID Q7MPN5_VIBVY PRELIMINARY; PRT; 749 AA.
AC Q7MPN5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VV0328.
GN OrderedLocusNames=VV0328;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14656985; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; BA000037; BAC93092.1; -; Genomic_DNA.
DR InterPro; IPR010344; DUF940_lipo.
DR Pfam; PF06082; DUF940; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 749 AA; 84142 MW; A002F7EF2B24EFC CRC64;

Query Match 91.2%; Score 31; DB 2; Length 749;
Best Local Similarity 80.0%; Pred. NO. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 476 NYWLT 480

RESULT 49

ID Q4VXY0_HUMAN PRELIMINARY; PRT; 758 AA.
AC Q4VXY0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTTHUMP00000041762 (Fragment).
GN Name=CLCN7; ORFNames=LA16c-390B6.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Martin S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031600; CAB53065.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 758 AA; 83808 MW; C66C7E0008596040 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 758;
Best Local Similarity 80.0%; Pred. NO. 2.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 349 NYWLT 353

RESULT 50

ID GLGB_NEIDE STANDARD; PRT; 762 AA.

```
AC Q9RQ15;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
DE enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-
DE transferase).
DE Name=glbB;
GN Neisseria denitrificans.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Bergeriella.
OX NCBI_TaxID=494;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 14686; PubMed=10407163;
RX MEDLINE=99337488;
RA Buettcher V., Quanz M., Willmitzer L.;
RT "Molecular cloning, functional expression and purification of a glucan
RT branching enzyme from Neisseria denitrificans.";
RL Biochim. Biophys. Acta 1432:406-412(1999).
CC -!- FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
CC linkages in glycogen by scission of a 1,4-alpha-linked
CC oligosaccharide from growing alpha-1,4-glucan chains and the
CC subsequent attachment of the oligosaccharide to the alpha-1,6
CC position (By similarity).
CC -!- CATALYTIC ACTIVITY: Transfers a segment of a 1,4-alpha-D-glucan
CC chain to a primary hydroxy group in a similar glucan chain.
CC -!- PATHWAY: Glycogen biosynthesis; third step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF102867; AAF04747.1; -; Genomic_DNA.
DR HSP; F07762; IM7X.
DR HAMAP; MF_00685; -; 1.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006407; GlbB.
DR InterPro; IPR004193; Glyco_hydro_13N.
DR PANTHER; PTHR10357:SP34; GlbB; 1.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02922; Isoamylase N; 1.
DR TIGRFAMs; TIGR01515; branching_enzym; 1.
KW Glycogen biosynthesis; Glycosyltransferase; Transferase.
FT ACT_SITE 312 312 By similarity.
FT ACT_SITE 347 347 By similarity.
FT ACT_SITE 352 352 By similarity.
FT ACT_SITE 415 415 By similarity.
FT ACT_SITE 417 417 By similarity.
FT ACT_SITE 470 470 By similarity.
FT ACT_SITE 534 534 By similarity.
FT ACT_SITE 535 535 By similarity.
SQ SEQUENCE 762 AA; 86367 MW; 9922F80406DE3E3 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 762;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 272 NYWLT 276
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Search completed: May 11, 2006, 16:37:51
Job time : 77.2295 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:37 ; Search time 11.5574 Seconds
(without alignments)
35.767 Million cell updates/sec

Title: US-10-808-538-1

Perfect score: 34

Sequence: 1 NYWMT 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfileai.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	5	2	US-09-155-106-1
2	34	100.0	122	2	US-09-155-106-18
3	34	100.0	122	2	US-09-155-106-19
4	34	100.0	122	2	US-09-155-106-20
5	34	100.0	122	2	US-09-155-106-26
6	34	100.0	122	2	US-09-155-106-32
7	34	100.0	151	2	US-09-564-329A-15
8	34	100.0	151	2	US-09-563-620-15
9	34	100.0	151	2	US-09-855-632-15
10	34	100.0	151	2	US-09-934-773-15
11	34	100.0	151	2	US-09-855-153-15
12	34	100.0	151	2	US-10-224-720-15
13	34	100.0	489	2	US-09-134-000C-5481
14	31	91.2	79	2	US-09-248-796A-27215
15	31	91.2	241	2	US-09-540-236-2821
16	31	91.2	762	2	US-09-579-365-2
17	31	91.2	762	2	US-09-807-063-2
18	31	91.2	861	2	US-09-949-016-11001
19	30	88.2	100	2	US-09-840-459-36
20	30	88.2	100	2	US-09-497-625A-36
21	30	88.2	160	2	US-08-845-381B-76
22	30	88.2	209	2	US-08-845-381B-75
23	30	88.2	247	2	US-09-270-767-36941
24	30	88.2	247	2	US-09-270-767-52158
25	30	88.2	298	2	US-09-318-661-2
26	30	88.2	298	2	US-09-883-758-2
27	30	88.2	347	2	US-08-845-381B-74
28	30	88.2	347	2	US-08-845-381B-74
29	30	88.2	347	2	US-08-845-381B-74
30	30	88.2	347	2	US-08-845-381B-74
31	30	88.2	347	2	US-08-845-381B-74
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Sequence 6655, Ap
Sequence 7396, Ap
Sequence 73, Appl
Sequence 2, Appl
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Sequence 2, Appl
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Sequence 16, Appl
Sequence 17, Appl
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Sequence 2, Appl
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Sequence 5047, Ap
Sequence 15, Appl
Sequence 6055, Ap
Sequence 15, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 16, Appl
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Sequence 16, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 4, Appl
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Sequence 1, Appl
Sequence 4, Appl
Sequence 9, Appl
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Sequence 2, Appl
Sequence 28, Appl
Sequence 2, Appl
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Sequence 6568, Ap
Sequence 4264, Ap
Sequence 7, Appl
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Sequence 8, Appl
Sequence 8, Appl
Sequence 10186, A
Sequence 434, App
Sequence 7079, Ap
Sequence 5873, Ap
Sequence 1222, Ap

101	29	85.3	396	2	US-09-252-991A-31085	Sequence 31085, A	174	28	82.4	463	2	US-08-792-295-1	Sequence 1, Appli
102	29	85.3	420	1	US-09-248-796A-23880	Sequence 23880, A	175	28	82.4	463	2	US-09-076-432-1	Sequence 1, Appli
103	29	85.3	447	1	US-08-844-010-2	Sequence 2, Appli	176	28	82.4	464	2	US-08-914-375C-58	Sequence 58, Appli
104	29	85.3	447	2	US-09-012-873-2	Sequence 2, Appli	177	28	82.4	467	2	US-08-914-375C-57	Sequence 57, Appli
105	29	85.3	447	2	US-09-583-110-2928	Sequence 2928, Ap	178	28	82.4	467	2	US-09-134-001C-579	Sequence 3579, Ap
106	29	85.3	448	2	US-09-107-433-3371	Sequence 3371, Ap	179	28	82.4	470	2	US-09-710-279-1082	Sequence 1082, Ap
107	29	85.3	453	2	US-09-328-352-4181	Sequence 4181, Ap	180	28	82.4	471	2	US-09-583-110-3861	Sequence 3861, Ap
108	29	85.3	461	2	US-09-352-990-27	Sequence 27, Appli	181	28	82.4	471	2	US-09-107-433-4791	Sequence 4791, Ap
109	29	85.3	466	1	US-08-785-068-2	Sequence 2, Appli	182	28	82.4	472	2	US-09-303-518D-470	Sequence 470, App
110	29	85.3	466	2	US-09-007-355-2	Sequence 2, Appli	183	28	82.4	472	2	US-09-303-518D-472	Sequence 472, App
111	29	85.3	466	2	US-08-913-489-2	Sequence 2, Appli	184	28	82.4	472	2	US-09-303-518D-476	Sequence 476, App
112	29	85.3	467	1	US-08-704-744-81	Sequence 81, Appli	185	28	82.4	478	2	US-09-769-787-55	Sequence 55, Appli
113	29	85.3	469	2	US-09-543-681A-7068	Sequence 7068, Ap	186	28	82.4	480	2	US-09-489-039A-9157	Sequence 9157, Ap
114	29	85.3	478	2	US-09-107-532A-4922	Sequence 4922, Ap	187	28	82.4	484	2	US-09-634-238-216	Sequence 216, App
115	29	85.3	478	2	US-09-134-000C-4712	Sequence 4712, Ap	188	28	82.4	484	2	US-09-489-039A-11971	Sequence 11971, A
116	29	85.3	479	2	US-09-134-001C-4128	Sequence 4128, Ap	189	28	82.4	492	2	US-09-583-110-4046	Sequence 4046, Ap
117	29	85.3	479	2	US-09-489-039A-13436	Sequence 13436, A	190	28	82.4	495	2	US-09-107-532A-5715	Sequence 5715, Ap
118	29	85.3	480	1	US-07-882-293-2	Sequence 2, Appli	191	28	82.4	497	2	US-09-107-532A-5279	Sequence 5279, Ap
119	29	85.3	480	1	US-08-331-644-2	Sequence 2, Appli	192	28	82.4	503	2	US-09-107-532A-5013	Sequence 5013, Ap
120	29	85.3	480	4	PCT-US93-04102-2	Sequence 2, Appli	193	28	82.4	503	2	US-09-107-532A-5896	Sequence 5896, Ap
121	29	85.3	485	2	US-09-328-352-6791	Sequence 6791, Ap	194	28	82.4	510	2	US-09-107-433-3148	Sequence 3148, Ap
122	29	85.3	509	2	US-09-602-787A-12	Sequence 12, Appli	195	28	82.4	668	2	US-09-248-796A-19350	Sequence 19350, A
123	29	85.3	528	2	US-09-107-532A-4638	Sequence 4638, Ap	196	28	82.4	674	2	US-09-538-092-1125	Sequence 1125, Ap
124	29	85.3	579	2	US-08-851-567B-51	Sequence 51, Appli	197	28	82.4	685	2	US-09-489-039A-12981	Sequence 12981, A
125	29	85.3	580	2	US-09-902-540-16677	Sequence 16677, A	198	28	82.4	870	2	US-09-543-681A-4768	Sequence 4768, Ap
126	29	85.3	616	2	US-09-543-681A-5767	Sequence 5767, Ap	199	28	82.4	907	2	US-08-989-299-12	Sequence 12, Appli
127	29	85.3	617	1	US-08-361-920-29	Sequence 29, Appli	200	28	82.4	907	2	US-09-407-427-12	Sequence 12, Appli
128	29	85.3	617	1	US-08-479-939-29	Sequence 29, Appli	201	28	82.4	907	2	US-09-635-501-12	Sequence 12, Appli
129	29	85.3	617	1	US-08-483-432-29	Sequence 29, Appli	202	27	79.4	22	1	US-08-471-780C-75	Sequence 75, Appli
130	29	85.3	620	2	US-09-602-787A-10	Sequence 10, Appli	203	27	79.4	22	1	US-08-467-282B-75	Sequence 75, Appli
131	29	85.3	700	1	US-07-862-588B-2	Sequence 2, Appli	204	27	79.4	22	1	US-08-471-282A-75	Sequence 75, Appli
132	29	85.3	725	1	US-08-816-105A-1	Sequence 1, Appli	205	27	79.4	22	1	US-08-466-710C-75	Sequence 75, Appli
133	29	85.3	1832	2	US-09-335-409-4	Sequence 4, Appli	206	27	79.4	22	2	US-08-468-739C-75	Sequence 75, Appli
134	29	85.3	1832	2	US-09-568-102-4	Sequence 4, Appli	207	27	79.4	22	2	US-09-293-769A-75	Sequence 26, Appli
135	29	85.3	1832	2	US-09-567-969-4	Sequence 4, Appli	208	27	79.4	33	1	US-08-471-780C-26	Sequence 26, Appli
136	29	85.3	1832	2	US-09-568-480-4	Sequence 4, Appli	209	27	79.4	33	1	US-08-467-282B-26	Sequence 26, Appli
137	29	85.3	1832	2	US-09-568-486-4	Sequence 4, Appli	210	27	79.4	33	1	US-08-471-282A-26	Sequence 26, Appli
138	29	85.3	1832	2	US-09-568-472-4	Sequence 4, Appli	211	27	79.4	33	1	US-08-466-710C-26	Sequence 26, Appli
139	29	85.3	1832	2	US-09-567-899-4	Sequence 4, Appli	212	27	79.4	33	2	US-08-468-739C-26	Sequence 26, Appli
140	29	85.3	1832	2	US-10-014-717-4	Sequence 4, Appli	213	27	79.4	33	2	US-09-293-769A-26	Sequence 26, Appli
141	29	85.3	2516	2	US-08-851-567B-47	Sequence 47, Appli	214	27	79.4	66	2	US-09-640-211A-2360	Sequence 2360, Ap
142	29	85.3	2516	2	US-09-617-514A-2	Sequence 2, Appli	215	27	79.4	67	2	US-09-640-211A-2300	Sequence 2300, Ap
143	29	85.3	2522	2	US-09-251-645-13	Sequence 13, Appli	216	27	79.4	67	2	US-09-640-211A-2332	Sequence 2332, Ap
144	28	82.4	46	2	US-09-865-621A-38	Sequence 38, Appli	217	27	79.4	67	2	US-09-640-211A-2345	Sequence 2345, Ap
145	28	82.4	46	2	US-09-865-621A-39	Sequence 39, Appli	218	27	79.4	67	2	US-09-640-211A-2364	Sequence 2364, Ap
146	28	82.4	54	2	US-09-640-211A-2349	Sequence 2349, Ap	219	27	79.4	67	2	US-09-640-211A-2366	Sequence 2366, Ap
147	28	82.4	57	2	US-09-640-211A-2285	Sequence 2285, Ap	220	27	79.4	67	2	US-09-640-211A-2368	Sequence 2368, Ap
148	28	82.4	60	2	US-09-621-976-5306	Sequence 5306, Ap	221	27	79.4	67	2	US-09-640-211A-2111	Sequence 2111, Ap
149	28	82.4	73	2	US-09-134-001C-4351	Sequence 4351, Ap	222	27	79.4	99	2	US-09-640-211A-871	Sequence 871, App
150	28	82.4	78	2	US-09-248-796A-23929	Sequence 23929, A	223	27	79.4	104	2	US-09-640-211A-867	Sequence 867, App
151	28	82.4	99	2	US-09-248-796A-17758	Sequence 17758, A	224	27	79.4	113	2	US-09-640-211A-1099	Sequence 1099, Ap
152	28	82.4	130	2	US-09-640-211A-2109	Sequence 2109, Ap	225	27	79.4	113	2	US-09-640-211A-1082	Sequence 1082, Ap
153	28	82.4	135	1	US-07-857-224B-103	Sequence 103, App	226	27	79.4	119	2	US-09-640-211A-2219	Sequence 2219, Ap
154	28	82.4	146	2	US-09-370-767-33225	Sequence 33225, A	227	27	79.4	123	2	US-09-640-211A-2219	Sequence 2215, Ap
155	28	82.4	146	2	US-09-270-767-48442	Sequence 48442, A	228	27	79.4	124	2	US-09-640-211A-2222	Sequence 1093, Ap
156	28	82.4	149	2	US-09-270-767-33543	Sequence 33543, A	229	27	79.4	125	2	US-08-537-871A-27	Sequence 27, Appli
157	28	82.4	149	2	US-09-270-767-48760	Sequence 48760, A	230	27	79.4	128	2	US-09-640-211A-1083	Sequence 1083, Ap
158	28	82.4	167	2	US-09-248-796A-19320	Sequence 19320, A	231	27	79.4	139	2	US-09-640-211A-1085	Sequence 1085, Ap
159	28	82.4	208	2	US-09-640-211A-2250	Sequence 2250, Ap	232	27	79.4	144	2	US-09-640-211A-2260	Sequence 2260, Ap
160	28	82.4	234	2	US-09-640-211A-919	Sequence 919, App	233	27	79.4	146	2	US-09-640-211A-2210	Sequence 2210, Ap
161	28	82.4	268	2	US-09-248-796A-20224	Sequence 20224, A	234	27	79.4	146	2	US-09-640-211A-2215	Sequence 2215, Ap
162	28	82.4	273	2	US-09-533-029-40	Sequence 40, Appli	235	27	79.4	148	2	US-09-640-211A-1093	Sequence 1093, Ap
163	28	82.4	288	2	US-09-134-001C-3306	Sequence 3306, Ap	236	27	79.4	149	2	US-09-489-039A-9279	Sequence 9279, Ap
164	28	82.4	308	2	US-09-252-991A-29384	Sequence 29384, A	237	27	79.4	153	2	US-09-640-211A-910	Sequence 910, App
165	28	82.4	369	1	US-08-596-291-4	Sequence 4, Appli	238	27	79.4	168	2	US-09-640-211A-2245	Sequence 2245, Ap
166	28	82.4	369	2	US-09-100-804-4	Sequence 4, Appli	239	27	79.4	171	2	US-09-640-211A-2201	Sequence 2201, Ap
167	28	82.4	369	4	PCT-US94-09943-4	Sequence 4, Appli	240	27	79.4	176	2	US-09-640-211A-2238	Sequence 2238, Ap
168	28	82.4	370	2	US-09-879-312A-4	Sequence 2, Appli	241	27	79.4	180	2	US-09-393-634-33	Sequence 33, Appli
169	28	82.4	400	2	US-09-086-010-2	Sequence 2, Appli	242	27	79.4	185	2	US-09-543-681A-7906	Sequence 7906, Ap
170	28	82.4	400	2	US-09-879-312A-2	Sequence 2, Appli	243	27	79.4	187	2	US-09-640-211A-843	Sequence 843, App
171	28	82.4	408	2	US-09-107-532A-6992	Sequence 6992, Ap	244	27	79.4	205	2	US-09-640-211A-2248	Sequence 2248, Ap
172	28	82.4	448	2	US-09-328-352-4641	Sequence 4641, Ap	245	27	79.4	213	2	US-09-640-211A-729	Sequence 729, App
173	28	82.4	456	2	US-09-134-000C-5403	Sequence 5403, Ap	246	27	79.4	225	2	US-09-640-211A-2277	Sequence 2277, Ap

247	27	79.4	248	2	US-09-610-185C-2	Sequence 2, Appli	320	26	76.5	148	2	US-10-006-041A-340	Sequence 340, App
248	27	79.4	249	2	US-09-610-185C-4	Sequence 4, Appli	321	26	76.5	148	2	US-10-012-064A-340	Sequence 340, App
249	27	79.4	250	2	US-09-640-211A-2261	Sequence 2161, Ap	322	26	76.5	155	2	US-09-270-767-52222	Sequence 37005, A
250	27	79.4	251	2	US-09-270-767-60862	Sequence 60862, A	323	26	76.5	155	2	US-09-270-767-52222	Sequence 52222, A
251	27	79.4	252	2	US-09-533-029-94	Sequence 94, Appl	324	26	76.5	155	2	US-09-710-279-2704	Sequence 2704, Ap
252	27	79.4	253	2	US-09-453-387A-2	Sequence 2, Appli	325	26	76.5	172	2	US-08-107-532A-6560	Sequence 6560, Ap
253	27	79.4	254	2	US-09-453-387A-6	Sequence 6, Appli	326	26	76.5	172	2	US-09-543-681A-5295	Sequence 5295, Ap
254	27	79.4	255	2	US-09-533-029-58	Sequence 58, Appl	327	26	76.5	177	2	US-09-543-681A-7620	Sequence 7620, Ap
255	27	79.4	256	2	US-09-640-211A-2259	Sequence 2259, Ap	328	26	76.5	178	1	US-08-928-692-57	Sequence 57, Appl
256	27	79.4	257	2	US-09-640-211A-2258	Sequence 2258, Ap	329	26	76.5	178	2	US-09-339-972-57	Sequence 57, Appl
257	27	79.4	258	2	US-09-328-352-4779	Sequence 4779, Ap	330	26	76.5	185	2	US-09-107-532A-6934	Sequence 6934, Ap
258	27	79.4	259	2	US-09-270-767-45361	Sequence 45361, A	331	26	76.5	185	2	US-09-328-352-5156	Sequence 5156, Ap
259	27	79.4	260	2	US-09-248-796A-23363	Sequence 23363, A	332	26	76.5	199	2	US-09-489-039A-10609	Sequence 10609, A
260	27	79.4	261	2	US-09-489-039A-16950	Sequence 16950, A	333	26	76.5	201	2	US-09-919-039-311	Sequence 311, Appl
261	27	79.4	262	2	US-09-489-039A-13906	Sequence 13906, A	334	26	76.5	201	2	US-09-919-039-311	Sequence 99, Appl
262	27	79.4	263	2	US-08-997-251-2	Sequence 2, Appli	335	26	76.5	201	2	US-09-929-769-5	Sequence 5, Appli
263	27	79.4	264	2	US-08-997-251-4	Sequence 4, Appli	336	26	76.5	201	2	US-09-929-769-5	Sequence 99, Appl
264	27	79.4	265	2	US-09-815-923-14	Sequence 14, Appl	337	26	76.5	201	2	US-09-997-333-99	Sequence 99, Appl
265	27	79.4	266	2	US-09-590-991-6	Sequence 6, Appli	338	26	76.5	201	2	US-09-992-598-99	Sequence 99, Appl
266	27	79.4	267	2	US-09-585-858-31	Sequence 31, Appl	339	26	76.5	206	2	US-09-248-796A-23204	Sequence 23204, A
267	27	79.4	268	2	US-10-270-878-31	Sequence 31, Appl	340	26	76.5	212	2	US-09-352-991A-29648	Sequence 29648, A
268	27	79.4	269	2	US-09-198-452A-978	Sequence 978, App	341	26	76.5	212	2	US-09-583-110-4819	Sequence 4819, Ap
269	27	79.4	270	2	US-08-961-083-216	Sequence 907, App	342	26	76.5	221	2	US-09-599-360B-104	Sequence 104, App
270	27	79.4	271	2	US-09-536-784-216	Sequence 216, App	343	26	76.5	221	2	US-09-248-796A-16852	Sequence 16852, A
271	27	79.4	272	2	US-09-765-271-216	Sequence 216, App	344	26	76.5	226	2	US-09-949-016-9545	Sequence 9545, Ap
272	27	79.4	273	2	US-09-765-272A-216	Sequence 216, App	345	26	76.5	238	2	US-09-107-433-3918	Sequence 3918, Ap
273	27	79.4	274	2	US-08-463-092B-6	Sequence 6, Appli	346	26	76.5	244	2	US-09-270-767-42469	Sequence 42469, A
274	27	79.4	275	2	US-08-463-092B-4	Sequence 4, Appli	347	26	76.5	253	2	US-09-949-016-10695	Sequence 10695, A
275	27	79.4	276	2	US-08-462-109A-6	Sequence 6, Appli	348	26	76.5	254	2	US-09-978-758-2	Sequence 2, Appli
276	27	79.4	277	2	US-08-460-307B-6	Sequence 6, Appli	349	26	76.5	258	2	US-09-270-767-43579	Sequence 43579, A
277	27	79.4	278	2	US-08-463-179A-6	Sequence 6, Appli	350	26	76.5	261	2	US-10-012-231A-326	Sequence 326, App
278	27	79.4	279	2	US-08-461-384B-6	Sequence 6, Appli	351	26	76.5	261	2	US-10-015-389A-326	Sequence 326, App
279	27	79.4	280	2	US-08-141-893-2	Sequence 2, Appli	352	26	76.5	261	2	US-10-006-768A-326	Sequence 326, App
280	27	79.4	281	2	US-08-463-092B-2	Sequence 2, Appli	353	26	76.5	261	2	US-10-015-671A-326	Sequence 326, App
281	27	79.4	282	2	US-08-463-092B-4	Sequence 4, Appli	354	26	76.5	261	2	US-10-015-393A-326	Sequence 326, App
282	27	79.4	283	2	US-08-462-109A-2	Sequence 2, Appli	355	26	76.5	261	2	US-10-011-833A-326	Sequence 326, App
283	27	79.4	284	2	US-08-462-109A-4	Sequence 4, Appli	356	26	76.5	261	2	US-10-006-041A-326	Sequence 326, App
284	27	79.4	285	2	US-08-460-907B-2	Sequence 2, Appli	357	26	76.5	261	2	US-10-012-064A-326	Sequence 326, App
285	27	79.4	286	2	US-08-463-179A-2	Sequence 2, Appli	358	26	76.5	264	2	US-09-724-864A-64	Sequence 64, Appl
286	27	79.4	287	2	US-08-463-179A-4	Sequence 4, Appli	359	26	76.5	265	1	US-08-413-803-27	Sequence 27, Appl
287	27	79.4	288	2	US-08-461-384B-2	Sequence 2, Appli	360	26	76.5	265	2	US-09-248-796A-20812	Sequence 20812, A
288	27	79.4	289	2	US-08-461-384B-4	Sequence 4, Appli	361	26	76.5	265	4	PCT-US95-03776-29	Sequence 29, Appl
289	27	79.4	290	2	US-08-407-207A-2	Sequence 2, Appli	362	26	76.5	267	2	US-09-489-039A-13457	Sequence 13457, A
290	27	79.4	291	2	US-07-914-280-9	Sequence 19, Appl	363	26	76.5	273	2	US-09-107-433-4284	Sequence 3006, Ap
291	27	79.4	292	2	PCT-US93-05625-9	Sequence 9, Appli	364	26	76.5	275	2	US-09-583-110-3006	Sequence 1245, Ap
292	26	76.5	293	2	US-09-646-691B-82	Sequence 82, Appl	365	26	76.5	277	1	US-09-538-092-1245	Sequence 27, Appl
293	26	76.5	294	2	US-09-646-691B-54	Sequence 54, Appl	366	26	76.5	286	1	US-08-321-488A-27	Sequence 27, Appl
294	26	76.5	295	2	US-09-248-796A-27691	Sequence 27691, A	367	26	76.5	290	2	US-09-710-279-758	Sequence 758, App
295	26	76.5	296	2	US-09-489-039A-12905	Sequence 12905, A	368	26	76.5	290	2	US-09-949-016-9248	Sequence 9248, Ap
296	26	76.5	297	2	US-09-302-540-13369	Sequence 13369, A	369	26	76.5	292	2	US-09-248-796A-21070	Sequence 21070, A
297	26	76.5	298	2	US-09-107-532A-6823	Sequence 6823, Ap	370	26	76.5	294	1	US-08-142-439A-4	Sequence 4, Appli
298	26	76.5	299	2	US-09-134-001C-2855	Sequence 2855, Ap	371	26	76.5	294	1	US-08-869-477-4	Sequence 4, Appli
299	26	76.5	300	2	US-09-732-210-141	Sequence 141, App	372	26	76.5	297	2	US-09-270-767-34549	Sequence 34549, A
300	26	76.5	301	2	US-09-640-211A-1112	Sequence 1112, Ap	373	26	76.5	297	2	US-09-270-767-49766	Sequence 49766, A
301	26	76.5	302	2	US-08-414-926A-20	Sequence 20, Appl	374	26	76.5	302	2	US-09-252-991A-28202	Sequence 28202, A
302	26	76.5	303	2	US-08-926-922-20	Sequence 20, Appl	375	26	76.5	314	2	US-09-758-759-55	Sequence 55, Appl
303	26	76.5	304	2	US-09-253-682-20	Sequence 20, Appl	376	26	76.5	326	2	US-09-543-681A-6673	Sequence 6673, Ap
304	26	76.5	305	2	US-09-892-100-20	Sequence 20, Appl	377	26	76.5	330	2	US-09-489-039A-13171	Sequence 13171, A
305	26	76.5	306	2	US-09-513-999C-5038	Sequence 5038, Ap	378	26	76.5	333	2	US-09-540-236-2769	Sequence 2769, Ap
306	26	76.5	307	2	US-09-598-705-6	Sequence 6, Appli	379	26	76.5	354	2	US-09-198-452A-852	Sequence 852, App
307	26	76.5	308	2	US-09-328-352-5491	Sequence 5491, Ap	380	26	76.5	354	2	US-09-248-796A-17175	Sequence 17175, A
308	26	76.5	309	2	US-09-252-991A-24446	Sequence 24446, A	381	26	76.5	356	2	US-09-438-185A-801	Sequence 801, App
309	26	76.5	310	2	US-10-012-231A-340	Sequence 340, App	382	26	76.5	362	1	US-09-248-796A-14836	Sequence 14836, A
310	26	76.5	311	2	US-10-015-389A-340	Sequence 340, App	383	26	76.5	372	2	US-08-415-751-6	Sequence 6, Appli
311	26	76.5	312	2	US-10-006-768A-340	Sequence 340, App	384	26	76.5	376	2	US-09-248-796A-17994	Sequence 17994, A
312	26	76.5	313	2	US-10-015-671A-340	Sequence 340, App	385	26	76.5	398	2	US-09-091-725-15	Sequence 15, Appl
313	26	76.5	314	2	US-10-015-393A-340	Sequence 340, App	386	26	76.5	398	2	US-09-902-540-11740	Sequence 11740, A
314	26	76.5	315	2	US-10-015-393A-340	Sequence 340, App	387	26	76.5	411	2	US-09-134-000C-3961	Sequence 3961, Ap
315	26	76.5	316	2	US-10-015-671A-340	Sequence 340, App	388	26	76.5	412	2	US-09-248-796A-19140	Sequence 19140, A
316	26	76.5	317	2	US-10-015-671A-340	Sequence 340, App	389	26	76.5	422	2	US-09-248-796A-23935	Sequence 23935, A
317	26	76.5	318	2	US-10-015-671A-340	Sequence 340, App	390	26	76.5	424	2	US-09-303-518D-308	Sequence 308, App
318	26	76.5	319	2	US-10-015-393A-340	Sequence 340, App	391	26	76.5	428	2	US-09-052-778-12	Sequence 12, Appl
319	26	76.5		2	US-10-011-833A-340	Sequence 340, App	392	26	76.5	429	2	US-09-270-767-45937	Sequence 45937, A

393	26	76.5	431	2	US-09-107-532A-5796	Sequence 5796, Ap	466	25	73.5	6	2	US-09-209-676-10	Sequence 10, Appl
394	26	76.5	434	2	US-09-771-161A-92	Sequence 92, Appl	467	25	73.5	17	2	US-09-025-769B-239	Sequence 239, App
395	26	76.5	445	2	US-09-134-001C-3507	Sequence 3507, Ap	468	25	73.5	17	2	US-09-490-070A-239	Sequence 239, App
396	26	76.5	448	2	US-09-252-991A-23910	Sequence 23910, A	469	25	73.5	17	2	US-09-490-153-239	Sequence 239, App
397	26	76.5	448	2	US-09-134-000C-6746	Sequence 6746, Ap	470	25	73.5	17	2	US-09-490-324-239	Sequence 239, App
398	26	76.5	463	1	US-08-142-439A-2	Sequence 2, Appli	471	25	73.5	40	2	US-08-689-421-1	Sequence 1, Appli
399	26	76.5	463	1	US-08-869-477-2	Sequence 2, Appli	472	25	73.5	40	2	US-09-389-528-1	Sequence 1, Appli
400	26	76.5	463	1	US-09-631-603-16	Sequence 16, Appl	473	25	73.5	40	2	US-09-181-827A-1	Sequence 1, Appli
401	26	76.5	466	2	US-09-543-681A-8174	Sequence 8174, Ap	474	25	73.5	61	2	US-09-235-451-19	Sequence 19, Appl
402	26	76.5	466	2	US-09-698-705-11	Sequence 11, Appl	475	25	73.5	61	2	US-09-978-303-19	Sequence 19, Appl
403	26	76.5	474	2	US-09-315-444-116	Sequence 116, App	476	25	73.5	63	2	US-09-489-039A-11309	Sequence 11309, A
404	26	76.5	474	2	US-09-721-362-116	Sequence 116, App	477	25	73.5	63	2	US-09-621-976-5954	Sequence 5954, Ap
405	26	76.5	476	2	US-09-316-083-3	Sequence 3, Appli	478	25	73.5	63	2	US-09-621-976-5960	Sequence 5960, Ap
406	26	76.5	476	2	US-09-933-700-3	Sequence 3, Appli	479	25	73.5	70	2	US-09-270-767-31647	Sequence 31647, A
407	26	76.5	482	2	US-09-248-796A-20045	Sequence 20045, A	480	25	73.5	70	2	US-09-270-767-46864	Sequence 46864, A
408	26	76.5	492	2	US-09-248-796A-14755	Sequence 14755, A	481	25	73.5	74	2	US-09-583-110-3128	Sequence 3128, Ap
409	26	76.5	523	2	US-09-830-433A-6	Sequence 6, Appli	482	25	73.5	74	2	US-09-107-433-4569	Sequence 4569, Ap
410	26	76.5	524	2	US-09-830-433A-57	Sequence 57, Appl	483	25	73.5	77	2	US-09-134-001C-3822	Sequence 3822, Ap
411	26	76.5	524	2	US-09-303-518D-306	Sequence 306, App	484	25	73.5	79	2	US-09-270-767-60541	Sequence 60541, A
412	26	76.5	524	2	US-09-303-518D-310	Sequence 310, App	485	25	73.5	80	1	US-08-485-445D-55	Sequence 55, Appl
413	26	76.5	543	2	US-09-543-681A-6901	Sequence 6901, Ap	486	25	73.5	80	1	US-08-482-130C-55	Sequence 55, Appl
414	26	76.5	545	2	US-09-538-092-59	Sequence 59, Appl	487	25	73.5	80	2	US-08-484-211C-55	Sequence 55, Appl
415	26	76.5	561	1	US-08-756-317-14	Sequence 14, Appl	488	25	73.5	80	2	US-08-906-769-55	Sequence 55, Appl
416	26	76.5	572	2	US-09-662-254B-22	Sequence 22, Appl	489	25	73.5	80	2	US-08-906-616-55	Sequence 55, Appl
417	26	76.5	581	2	US-09-538-092-383	Sequence 383, App	490	25	73.5	80	2	US-08-817-795-55	Sequence 55, Appl
418	26	76.5	581	2	US-09-171-937C-55	Sequence 55, Appl	491	25	73.5	80	2	US-08-485-443B-55	Sequence 55, Appl
419	26	76.5	581	2	US-08-779-460B-10	Sequence 10, Appl	492	25	73.5	80	2	US-08-639-075A-55	Sequence 55, Appl
420	26	76.5	597	2	US-09-861-451A-40	Sequence 40, Appl	493	25	73.5	80	2	US-09-012-431-55	Sequence 55, Appl
421	26	76.5	598	2	US-09-540-236-3415	Sequence 3415, Ap	494	25	73.5	80	2	US-09-012-692-55	Sequence 55, Appl
422	26	76.5	622	1	US-08-664-646A-2	Sequence 2, Appli	495	25	73.5	80	2	US-08-906-613-55	Sequence 55, Appl
423	26	76.5	622	1	US-09-066-285-2	Sequence 2, Appli	496	25	73.5	82	4	PCT-US95-1442A-55	Sequence 55, Appl
424	26	76.5	622	1	US-09-261-006-2	Sequence 2, Appli	497	25	73.5	82	2	US-09-248-796A-24444	Sequence 24444, A
425	26	76.5	622	2	US-08-951-088-2	Sequence 2, Appli	498	25	73.5	87	2	US-09-248-796A-24444	Sequence 24444, A
426	26	76.5	622	2	US-09-609-566-2	Sequence 2, Appli	499	25	73.5	87	2	US-09-248-796A-28155	Sequence 28155, A
427	26	76.5	622	2	US-09-609-570-2	Sequence 2, Appli	500	25	73.5	89	2	US-09-107-532A-5527	Sequence 5527, Ap
428	26	76.5	622	2	US-09-427-372-2	Sequence 2, Appli	501	25	73.5	90	2	US-09-107-532A-5322	Sequence 5322, Ap
429	26	76.5	622	2	US-09-693-554-2	Sequence 2, Appli	502	25	73.5	92	2	US-09-270-767-62473	Sequence 62473, A
430	26	76.5	656	2	US-09-543-681A-6473	Sequence 6473, Ap	503	25	73.5	96	2	US-09-905-243-12	Sequence 12, Appl
431	26	76.5	693	2	US-09-336-910A-3	Sequence 3, Appli	504	25	73.5	96	2	US-09-905-243-13	Sequence 13, Appl
432	26	76.5	723	2	US-09-434-408-2	Sequence 2, Appli	505	25	73.5	98	1	US-07-942-245-37	Sequence 37, Appl
433	26	76.5	723	2	US-10-104-047-2572	Sequence 2572, Ap	506	25	73.5	98	1	US-08-428-197-17	Sequence 17, Appl
434	26	76.5	748	2	US-09-252-991A-32942	Sequence 32942, A	507	25	73.5	98	1	US-10-194-975-15	Sequence 15, Appl
435	26	76.5	786	2	US-09-252-991A-32117	Sequence 32117, A	508	25	73.5	98	2	US-09-534-717-664	Sequence 664, App
436	26	76.5	798	2	US-09-252-991A-25309	Sequence 25309, A	509	25	73.5	98	2	US-09-534-717-666	Sequence 666, App
437	26	76.5	825	2	US-09-543-681A-7287	Sequence 7287, Ap	510	25	73.5	98	4	PCT-US93-10555-17	Sequence 17, Appl
438	26	76.5	862	2	US-09-328-352-4421	Sequence 4421, Ap	511	25	73.5	99	1	US-08-244-626-10	Sequence 10, Appl
439	26	76.5	868	1	US-08-162-081B-33	Sequence 33, Appl	512	25	73.5	103	2	US-10-630-406-2	Sequence 2, Appli
440	26	76.5	868	1	US-08-780-872-33	Sequence 33, Appl	513	25	73.5	107	2	US-09-899-896-11	Sequence 11, Appl
441	26	76.5	868	1	US-09-085-957-33	Sequence 33, Appl	514	25	73.5	109	2	US-09-270-767-47233	Sequence 47233, A
442	26	76.5	870	2	US-09-543-681A-5184	Sequence 5184, Ap	515	25	73.5	111	2	US-09-726-219A-171	Sequence 171, App
443	26	76.5	878	2	US-09-489-039A-13174	Sequence 13174, A	516	25	73.5	111	2	US-09-196-522-171	Sequence 171, App
444	26	76.5	911	1	US-08-928-692-59	Sequence 59, Appl	517	25	73.5	117	2	US-08-545-809A-95	Sequence 95, Appl
445	26	76.5	911	1	US-09-339-972-59	Sequence 59, Appl	518	25	73.5	117	2	US-09-515-697-95	Sequence 95, Appl
446	26	76.5	916	1	US-08-928-692-58	Sequence 58, Appl	519	25	73.5	117	2	US-10-104-047-3312	Sequence 3312, Ap
447	26	76.5	916	1	US-09-339-972-58	Sequence 58, Appl	520	25	73.5	118	2	US-09-065-059-5	Sequence 5, Appli
448	26	76.5	977	2	US-09-771-161A-183	Sequence 183, App	521	25	73.5	118	2	US-09-583-110-4078	Sequence 4078, Ap
449	26	76.5	987	2	US-09-543-681A-7785	Sequence 7785, Ap	522	25	73.5	118	2	US-09-107-433-3519	Sequence 3519, Ap
450	26	76.5	1006	2	US-09-949-016-10730	Sequence 10730, A	523	25	73.5	118	2	US-08-913-555-5	Sequence 5, Appli
451	26	76.5	1189	2	US-09-489-039A-13776	Sequence 13776, A	524	25	73.5	119	2	US-09-254-180C-16	Sequence 16, Appl
452	26	76.5	1248	1	US-08-348-353-17	Sequence 17, Appl	525	25	73.5	119	2	US-09-254-180C-18	Sequence 18, Appl
453	26	76.5	1248	1	US-08-465-965-17	Sequence 17, Appl	526	25	73.5	119	2	US-09-254-180C-19	Sequence 19, Appl
454	26	76.5	1248	2	US-08-465-966-17	Sequence 17, Appl	527	25	73.5	119	2	US-09-254-180C-149	Sequence 23, Appl
455	26	76.5	1285	2	US-09-976-594-507	Sequence 507, App	528	25	73.5	128	1	US-08-913-555-23	Sequence 23, Appl
456	26	76.5	1285	2	US-09-949-016-6576	Sequence 6576, Ap	529	25	73.5	128	1	US-08-276-852-59	Sequence 59, Appl
457	26	76.5	1285	2	US-09-949-016-9990	Sequence 9990, Ap	530	25	73.5	128	1	US-08-276-852-60	Sequence 60, Appl
458	26	76.5	3852	2	US-10-025-225-4	Sequence 4, Appli	531	25	73.5	128	1	US-08-276-852-61	Sequence 61, Appl
459	26	76.5	4585	2	US-10-025-225-6	Sequence 6, Appli	532	25	73.5	128	1	US-08-276-852-62	Sequence 62, Appl
460	26	76.5	4588	2	US-10-025-225-8	Sequence 8, Appli	533	25	73.5	128	1	US-08-276-852-63	Sequence 63, Appl
461	26	76.5	4588	2	US-10-025-225-2	Sequence 2, Appli	534	25	73.5	128	1	US-08-276-852-64	Sequence 64, Appl
462	26	76.5	4630	2	US-09-091-609-2	Sequence 2, Appli	535	25	73.5	128	1	US-08-276-852-65	Sequence 65, Appl
463	26	76.5	5215	2	US-09-105-537-2	Sequence 2, Appli	536	25	73.5	128	1	US-08-276-852-78	Sequence 78, Appl
464	25	73.5	5	1	US-08-244-626-12	Sequence 12, Appl	537	25	73.5	128	1	US-08-276-852-79	Sequence 79, Appl
465	25	73.5	5	2	US-09-254-180C-1	Sequence 1, Appli	538	25	73.5	128	1	US-08-899-575-59	Sequence 59, Appl

685	25	73.5	400	1	US-07-989-991A-2	Sequence 2, Appli	758	25	73.5	493	2	US-09-333-077-2	Sequence 2, Appli
686	25	73.5	400	2	US-08-621-255-2	Sequence 2, Appli	759	25	73.5	493	2	US-10-018-386-2	Sequence 2, Appli
687	25	73.5	400	2	US-09-352-574-2	Sequence 2, Appli	760	25	73.5	494	2	US-09-198-956-2	Sequence 2, Appli
688	25	73.5	400	2	US-09-489-039A-12745	Sequence 12745, A	761	25	73.5	494	2	US-09-670-141-2	Sequence 2, Appli
689	25	73.5	400	2	US-09-270-767-31765	Sequence 31765, A	762	25	73.5	499	1	US-09-032-315-2	Sequence 2, Appli
690	25	73.5	400	2	US-09-270-767-46982	Sequence 46982, A	763	25	73.5	499	1	US-09-032-315-3	Sequence 3, Appli
691	25	73.5	401	2	US-09-489-847-202	Sequence 202, App	764	25	73.5	499	1	US-08-993-318A-2	Sequence 2, Appli
692	25	73.5	401	2	US-10-012-231A-100	Sequence 100, App	765	25	73.5	499	1	US-08-993-318A-3	Sequence 3, Appli
693	25	73.5	401	2	US-10-015-389A-100	Sequence 100, App	766	25	73.5	499	2	US-09-399-886-2	Sequence 2, Appli
694	25	73.5	401	2	US-10-015-389A-100	Sequence 100, App	767	25	73.5	499	2	US-09-399-886-3	Sequence 3, Appli
695	25	73.5	401	2	US-10-006-768A-100	Sequence 100, App	768	25	73.5	499	2	US-09-396-260-2	Sequence 2, Appli
696	25	73.5	401	2	US-10-272-490-38	Sequence 38, Appli	769	25	73.5	499	2	US-09-396-260-3	Sequence 3, Appli
697	25	73.5	401	2	US-10-015-671A-100	Sequence 100, App	770	25	73.5	499	2	US-09-576-281-2	Sequence 2, Appli
698	25	73.5	401	2	US-10-015-393A-100	Sequence 100, App	771	25	73.5	499	2	US-09-576-281-3	Sequence 3, Appli
699	25	73.5	401	2	US-10-011-833A-100	Sequence 100, App	772	25	73.5	499	2	US-09-881-165-2	Sequence 2, Appli
700	25	73.5	401	2	US-10-006-041A-100	Sequence 100, App	773	25	73.5	499	2	US-09-881-165-2	Sequence 2, Appli
701	25	73.5	401	2	US-10-012-064A-100	Sequence 100, App	774	25	73.5	512	1	US-09-786-960-2	Sequence 6, Appli
702	25	73.5	401	2	US-10-030-269A-8	Sequence 8, Appli	775	25	73.5	512	1	US-08-462-484-6	Sequence 6, Appli
703	25	73.5	402	2	US-09-134-000C-3699	Sequence 3699, Ap	776	25	73.5	512	4	US-08-441-147-6	Sequence 6, Appli
704	25	73.5	405	2	US-09-489-039A-11488	Sequence 11488, A	777	25	73.5	513	4	PCT-US95-07536-6	Sequence 6, Appli
705	25	73.5	408	2	US-09-248-796A-19029	Sequence 19029, A	778	25	73.5	513	2	US-09-862-631-4	Sequence 4, Appli
706	25	73.5	413	2	US-09-328-352-8239	Sequence 8239, Ap	779	25	73.5	516	2	US-08-689-421-29	Sequence 29, Appl
707	25	73.5	416	2	US-10-272-490-81	Sequence 81, Appl	780	25	73.5	516	2	US-09-181-827A-29	Sequence 29, Appl
708	25	73.5	416	2	US-10-272-490-87	Sequence 87, Appl	781	25	73.5	517	2	US-08-689-421-33	Sequence 33, Appl
709	25	73.5	419	2	US-09-248-796A-15135	Sequence 15135, A	782	25	73.5	517	2	US-09-389-528-33	Sequence 33, Appl
710	25	73.5	422	2	US-09-489-847-357	Sequence 357, App	783	25	73.5	517	1	US-09-181-827A-33	Sequence 33, Appl
711	25	73.5	422	2	US-10-272-490-88	Sequence 88, App	784	25	73.5	519	1	US-08-462-484-4	Sequence 4, Appli
712	25	73.5	429	2	US-09-949-016-10541	Sequence 10541, A	785	25	73.5	519	1	US-08-441-147-4	Sequence 4, Appli
713	25	73.5	432	2	US-09-393-245-2	Sequence 2, Appli	786	25	73.5	519	2	US-09-248-796A-20368	Sequence 20368, A
714	25	73.5	432	2	US-10-272-490-28	Sequence 28, Appl	787	25	73.5	519	4	PCT-US95-07536-4	Sequence 4, Appli
715	25	73.5	433	2	US-10-272-490-70	Sequence 70, Appl	788	25	73.5	520	1	US-08-462-484-2	Sequence 2, Appli
716	25	73.5	436	2	US-09-543-681A-5676	Sequence 5676, Ap	789	25	73.5	520	1	US-08-441-147-2	Sequence 2, Appli
717	25	73.5	439	2	US-09-107-532A-4168	Sequence 4168, Ap	790	25	73.5	520	4	PCT-US95-07536-2	Sequence 2, Appli
718	25	73.5	444	2	US-09-248-796A-18129	Sequence 18129, A	791	25	73.5	521	2	US-09-543-681A-5969	Sequence 5969, Ap
719	25	73.5	450	2	US-10-272-490-2	Sequence 2, Appli	792	25	73.5	524	2	US-09-230-944-11	Sequence 11, Appl
720	25	73.5	458	2	US-10-272-490-34	Sequence 34, Appl	793	25	73.5	524	2	US-09-873-233A-11	Sequence 11, Appl
721	25	73.5	459	2	US-09-352-990-26	Sequence 26, Appl	794	25	73.5	527	1	US-08-462-484-10	Sequence 10, Appl
722	25	73.5	460	2	US-10-630-406-5	Sequence 5, Appli	795	25	73.5	527	1	US-08-441-147-10	Sequence 10, Appl
723	25	73.5	460	2	US-10-272-490-40	Sequence 40, Appl	796	25	73.5	527	2	US-09-252-991A-17545	Sequence 17545, A
724	25	73.5	462	2	US-09-328-352-6483	Sequence 6483, Ap	797	25	73.5	527	4	PCT-US95-07536-10	Sequence 10, Appl
725	25	73.5	462	2	US-09-489-039A-12427	Sequence 12427, A	798	25	73.5	529	1	US-08-172-331B-14	Sequence 14, Appl
726	25	73.5	465	2	US-09-134-001C-4428	Sequence 4428, Ap	799	25	73.5	529	1	US-08-706-037-25	Sequence 25, Appl
727	25	73.5	466	2	US-08-914-375C-60	Sequence 60, Appl	800	25	73.5	529	1	US-09-005-397-25	Sequence 25, Appl
728	25	73.5	467	2	US-09-489-039A-12949	Sequence 12949, A	801	25	73.5	529	1	US-09-032-315-5	Sequence 5, Appli
729	25	73.5	470	2	US-09-489-039A-13061	Sequence 13061, A	802	25	73.5	529	1	US-08-993-318A-5	Sequence 5, Appli
730	25	73.5	471	2	US-09-583-110-2912	Sequence 2912, Ap	803	25	73.5	529	2	US-09-399-886-5	Sequence 5, Appli
731	25	73.5	472	2	US-09-252-991A-18544	Sequence 18544, A	804	25	73.5	529	2	US-09-396-260-5	Sequence 5, Appli
732	25	73.5	472	2	US-09-328-352-4537	Sequence 4537, Ap	805	25	73.5	529	2	US-09-576-281-5	Sequence 5, Appli
733	25	73.5	472	2	US-09-489-039A-13479	Sequence 13479, A	806	25	73.5	533	2	US-09-221-275-4	Sequence 4, Appli
734	25	73.5	472	2	US-09-602-777A-130	Sequence 130, App	807	25	73.5	539	1	US-09-032-315-1	Sequence 1, Appli
735	25	73.5	472	2	US-09-602-777A-132	Sequence 132, App	808	25	73.5	539	2	US-08-993-318A-1	Sequence 1, Appli
736	25	73.5	475	2	US-09-489-039A-10154	Sequence 10154, A	809	25	73.5	539	2	US-08-689-421-27	Sequence 27, Appl
737	25	73.5	475	2	US-09-107-433-5028	Sequence 5028, Ap	810	25	73.5	539	2	US-09-399-886-1	Sequence 1, Appli
738	25	73.5	476	2	US-09-328-352-5027	Sequence 5027, Ap	811	25	73.5	539	2	US-09-396-260-1	Sequence 1, Appli
739	25	73.5	478	2	US-09-328-352-7708	Sequence 7708, Ap	812	25	73.5	539	2	US-09-389-528-27	Sequence 27, Appl
740	25	73.5	478	2	US-09-134-000C-5543	Sequence 5543, Ap	813	25	73.5	539	2	US-09-181-827A-2	Sequence 27, Appl
741	25	73.5	482	2	US-09-328-352-6084	Sequence 6084, Ap	814	25	73.5	539	2	US-09-576-281-1	Sequence 1, Appli
742	25	73.5	484	2	US-09-328-352-6041	Sequence 6041, Ap	815	25	73.5	546	2	US-09-489-039A-14231	Sequence 14231, A
743	25	73.5	485	2	US-09-107-532A-4797	Sequence 4797, Ap	816	25	73.5	546	1	US-09-032-315-4	Sequence 4, Appli
744	25	73.5	487	2	US-09-252-991A-23912	Sequence 23912, A	817	25	73.5	548	1	US-08-993-318A-4	Sequence 4, Appli
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992 24 70.6 7 2 US-09-201-945-134 Sequence 134, App
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ALIGNMENTS

RESULT 1
US-09-155-106-1
; Sequence 1, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-1
Query Match 100.0%; Score 34; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 1 NYWMT 5

RESULT 2
US-09-155-106-18
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; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
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; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-18
Query Match 100.0%; Score 34; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 1 NYWMT 5
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; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
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; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-18
Query Match 100.0%; Score 34; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 31 NYWMT 35

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; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 31 NYWMT 35

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US-09-155-106-20
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; Patent No. 6730300
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

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; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-20

Query Match 100.0%; Score 34; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
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|
|
Db 31 NYWMT 35

RESULT 5

US-09-155-106-26
; Sequence 26, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-26

Query Match 100.0%; Score 34; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|
|
|
|
Db 31 NYWMT 35

RESULT 6

US-09-155-106-32

; Sequence 32, Application US/09155106

; Patent No. 6730300

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-32

Query Match 100.0%; Score 34; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|
|
|
|
Db 31 NYWMT 35

RESULT 7

US-09-564-329A-15

; Sequence 15, Application US/09564329A

; Patent No. 6541212

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/09/564,329A

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 8
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. 6756036
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435-54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 8
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. 6756036
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435-54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

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; ORGANISM: SCID Mice
US-09-963-620-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 9
US-09-855-632-15
; Sequence 15, Application US/09855632
; Patent No. 6790939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435-54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-632-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 10
US-09-934-773-15
; Sequence 15, Application US/09934773
; Patent No. 6825326
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.

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; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 11
US-09-855-153-15
; Sequence 15, Application US/09855153
; Patent No. 6881822
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
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; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54

RESULT 12
US-10-224-720-15
; Sequence 15, Application US/10224720
; Patent No. 6960443
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-15

Query Match      100.0%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      50 NYWMT 54
```

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RESULT 13
US-09-134-000C-5481
; Sequence 5481, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5481
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5481

Query Match      100.0%; Score 34; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy      1 NYWMT 5
Db      185 NYWMT 189

RESULT 14
US-09-248-796A-27215
; Sequence 27215, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27215
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27215

Query Match      91.2%; Score 31; DB 2; Length 79;
Best Local Similarity 80.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 NYWMT 5
Db      46 NYWMT 50

RESULT 15
US-09-540-236-2821
; Sequence 2821, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
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; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2821
; LENGTH: 241
; TYPE: PRT
; ORGANISM: M.cattarrhalis
US-09-540-236-2821

Query Match      91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 80.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 NYWMT 5
Db      130 NYWMT 134

RESULT 16
US-09-579-365-2
; Sequence 2, Application US/09579365
; Patent No. 6566585
; GENERAL INFORMATION:
; APPLICANT: Martin QUANZ
; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN
; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A
; TITLE OF INVENTION: BRANCHING ENZYME
; FILE REFERENCE: 0147-0200P
; CURRENT APPLICATION NUMBER: US/09/579,365
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Neisseria denitrificans
US-09-579-365-2

Query Match      91.2%; Score 31; DB 2; Length 762;
Best Local Similarity 80.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 NYWMT 5
Db      272 NYWMT 276

RESULT 17
US-09-807-063-2
; Sequence 2, Application US/09807063
; Patent No. 6699694
; GENERAL INFORMATION:
; APPLICANT: BUTTCHER, Volker et al.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A BRANCHING ENZYME FROM BACTERIA
; TITLE OF INVENTION: GENUS NEISSERIA AS WELL AS METHODS FOR THE PRODUCTION OF ALPHA-1
; TITLE OF INVENTION: ALPHA-1, 4-GLUCANS.
; FILE REFERENCE: 0147-0222P
; CURRENT APPLICATION NUMBER: US/09/807,063
; CURRENT FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Neisseria denitrificans
US-09-807-063-2

Query Match      91.2%; Score 31; DB 2; Length 762;
Best Local Similarity 80.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 NYWMT 5
Db      272 NYWMT 276
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RESULT 18
US-09-949-016-11001
; Sequence 11001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11001
; LENGTH: 861
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11001

Query Match 91.2%; Score 31; DB 2; Length 861;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||||
Db 455 NYWLT 459

RESULT 19
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36

Query Match 88.2%; Score 30; DB 2; Length 100;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 31 NYWMS 35
|||||
RESULT 20
US-09-497-625A-36
; Sequence 36, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-36

Query Match 88.2%; Score 30; DB 2; Length 100;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||||
Db 31 NYWMS 35

RESULT 21
US-08-845-381B-76
; Sequence 76, Application US/08845381E
; Patent No. 6602681
; GENERAL INFORMATION:
; APPLICANT: OHSUYE, Kazuhiro
; APPLICANT: KITANO, Katsuhiko
; APPLICANT: TANAKA, Shoji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: MIZUNO, Kensaku
; TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
ENZYME
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,381E
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62177184
FILING DATE: 17-JUL-1987

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62306867
; FILING DATE: 05-DEC-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/219,375
; FILING DATE: 15-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/509,583
; FILING DATE: 16-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 001560-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 209 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-381E-76

Query Match      88.2%; Score 30; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
DB      106 NYWMT 110

RESULT 22
US-08-845-381E-75
; Sequence 75, Application US/08845381E
; Patent No. 6602681
; GENERAL INFORMATION:
; APPLICANT: OHSUYE, Kazuhiro
; APPLICANT: KITANO, Katsuhiko
; APPLICANT: TANAKA, Shoji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: MIZUNO, Kenseku
; TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
; NUMBER OF SEQUENCES: 77
; NUMBER OF INVENTION: ENZYME
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,381E
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62177184
; FILING DATE: 17-JUL-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62306867
; FILING DATE: 05-DEC-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/219,375
; FILING DATE: 15-JUL-1988
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/509,583
; FILING DATE: 16-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 001560-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-381E-76

Query Match      88.2%; Score 30; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
DB      106 NYWMT 110

RESULT 23
US-09-270-767-36941
; Sequence 36941, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36941
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-36941

Query Match      88.2%; Score 30; DB 2; Length 247;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
DB      17 NYWMT 21

RESULT 24
US-09-270-767-52158
; Sequence 52158, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52158
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
```

OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52158

Query Match 88.2%; Score 30; DB 2; Length 247;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 17 NYWVT 21

RESULT 25

US-09-318-661-2
Sequence 2, Application US/09318661
Patent No. 6268488
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabat, Doron
APPLICANT: Rader, Christoph
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF00115
CURRENT APPLICATION NUMBER: US/09/318,661
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 298
TYPE: PRT
ORGANISM: Mus musculus
US-09-318-661-2

Query Match 88.2%; Score 30; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 186 NYWMS 190

RESULT 26

US-09-883-758-2
Sequence 2, Application US/09883758
Patent No. 6677435
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabat, Doron
APPLICANT: Rader, Christoph
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF00115
CURRENT APPLICATION NUMBER: US/09/883,758
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/09/318,661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 298
TYPE: PRT
ORGANISM: Mus musculus
US-09-883-758-2

Query Match 88.2%; Score 30; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 186 NYWMS 190

DB 186 NYWMS 190

RESULT 27

US-08-845-381B-74
Sequence 74, Application US/08845381E
Patent No. 6602681
GENERAL INFORMATION:
APPLICANT: OHSUYE, Kazuhiro
APPLICANT: KITANO, Katsuhiko
APPLICANT: TANAKA, Shoji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MIZUNO, Kensaku
TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,381E
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62177184
FILING DATE: 17-JUL-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62306867
FILING DATE: 05-DEC-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/219,375
FILING DATE: 15-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/509,583
FILING DATE: 16-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 001560-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-845-381B-74

Query Match 88.2%; Score 30; DB 2; Length 347;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 106 NYWVT 110

RESULT 28

US-09-949-016-6655
Sequence 6655, Application US/09949016
Patent No. 6812339

```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6655
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6655

```

```

Query Match      88.2%; Score 30; DB 2; Length 394;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |:|
Db      370 NFWMT 374

```

```

RESULT 29
US-09-949-016-7396
; Sequence 7396, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7396
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7396

```

```

Query Match      88.2%; Score 30; DB 2; Length 406;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |:|
Db      382 NFWMT 386

```

```

RESULT 30
US-08-845-381E-73
; Sequence 73, Application US/08845381E
; Patent No. 6602681
; GENERAL INFORMATION:
; APPLICANT: OHSUYE, Kazuhiro
; APPLICANT: KITANO, Katsuhiko
; APPLICANT: TANAKA, Shoji
; APPLICANT: MATSUO, Hisayuki

```

```

; APPLICANT: MIZUNO, Kensaku
; TITLE OF INVENTION: RECOMBINANT C-TERMINAL ALPHA-AMIDATING
; ENZYME
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,381E
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62177184
; FILING DATE: 17-JUL-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62306867
; FILING DATE: 05-DEC-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/219,375
; FILING DATE: 15-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/509,583
; FILING DATE: 16-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 001560-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-381E-73

Query Match      88.2%; Score 30; DB 2; Length 490;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |:|
Db      106 NYWMT 110

RESULT 31
US-09-722-129-2
; Sequence 2, Application US/09722129
; Patent No. 6582958
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: NO. 6582958el motor proteins and methods for
; their use
; FILE REFERENCE: 1054
; CURRENT APPLICATION NUMBER: US/09/722,129
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 492

```

```
; TYPE: PRT
; ORGANISM: Human
US-09-722-129-2

Query Match      88.2%; Score 30; DB 2; Length 492;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 33 NYWMT 37

RESULT 32
US-08-765-081-5
; Sequence 5, Application US/08765081
; Patent No. 5798260
; GENERAL INFORMATION:
; APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
; TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible/Pentium 3.1
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,081
; FILING DATE: March 26, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06994
; FILING DATE: June 7, 1995
; APPLICATION NUMBER: US 08/265,714
; FILING DATE: June 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: CHOR-1-10286
; TELEPHONE: 1-206-682-8100; 1-206-224-0779 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-081-5

Query Match      88.2%; Score 30; DB 1; Length 696;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 687 NYWMS 691

RESULT 34
PCT-US95-06994-5
; Sequence 5, Application PC/TUS9506994
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital & Medical Center
; APPLICANT: University of Washington
; APPLICANT: Washington State University Research Foundation
; APPLICANT: TARR, PHILLIP I
; APPLICANT: BILGE, SIMA S
; APPLICANT: BESSER, THOMAS E
; APPLICANT: VARY JR, JAMES C
; TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC
; STREET: SUITE 2800, 1420 FIFTH AVENUE
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06994
```

```
; FILING DATE: 07-JUN-95
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,714
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BRODERICK, THOMAS F
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: CHOR-18591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06994-5
```

```
Query Match 88.2%; Score 30; DB 4; Length 696;
Best Local Similarity 80.0%; Pred. NO. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYWMT 5
Db 687 NYWMS 691
```

```
RESULT 35
PCT-US95-06994-8
; Sequence 8, Application PC/TUS9506994
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital & Medical Center
; APPLICANT: University of Washington
; APPLICANT: Washington State University Research Foundation
; APPLICANT: TARR, PHILLIP I
; APPLICANT: BILGE, SIMA S
; APPLICANT: BESSER, THOMAS E
; APPLICANT: VARY JR, JAMES C
; TITLE OF INVENTION: ESCHERICHIA COLI O157:H7 EPITHELIAL ADHESIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC
; STREET: SUITE 2800, 1420 FIFTH AVENUE
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06994
; FILING DATE: 07-JUN-95
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,714
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BRODERICK, THOMAS F
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: CHOR-18591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; DESCRIPTION: E. coli O157:H7 adhesin amino acid sequence,
; DESCRIPTION: wherein "Xaa" residues represent gaps
; DESCRIPTION: introduced to facilitate best alignment with
; DESCRIPTION: SEQ ID NO:9.
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli O157:H7
; STRAIN: 86-24 NALR
PCT-US95-06994-8
```

```
Query Match 88.2%; Score 30; DB 4; Length 703;
Best Local Similarity 80.0%; Pred. NO. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYWMT 5
Db 694 NYWMS 698
```

```
RESULT 36
PCT-US95-06994-6
; Sequence 6, Application PC/TUS9506994
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital & Medical Center
; APPLICANT: University of Washington
; APPLICANT: Washington State University Research Foundation
; APPLICANT: TARR, PHILLIP I
; APPLICANT: BILGE, SIMA S
; APPLICANT: BESSER, THOMAS E
; APPLICANT: VARY JR, JAMES C
; TITLE OF INVENTION: ESCHERICHIA COLI O157:H7 EPITHELIAL ADHESIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC
; STREET: SUITE 2800, 1420 FIFTH AVENUE
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06994
; FILING DATE: 07-JUN-95
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/265,714
; FILING DATE: 24-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BRODERICK, THOMAS F
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: CHOR-18591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 718 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E. coli O157:H7 adhesin amino acid sequence,
; DESCRIPTION: wherein "Xaa" residues represent gaps
; DESCRIPTION: introduced to facilitate best alignment with
; DESCRIPTION: SEQ ID NO:7.
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli O157:H7
; STRAIN: 86-24 NALR
```

PCT-US95-06994-6

Query Match 88.2%; Score 30; DB 4; Length 718;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 709 NYWMS 713

RESULT 37

US-09-949-016-10552
; Sequence 10552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10552
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10552

Query Match 88.2%; Score 30; DB 2; Length 931;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 623 NYWMT 627

RESULT 38

US-07-707-367-2
; Sequence 2, Application US/07707367
; Patent No. 5196316
; GENERAL INFORMATION:
; APPLICANT: Iwasaki, Yasuno
; APPLICANT: Shimoi, Hiroko
; APPLICANT: Suzuki, Kenji
; APPLICANT: Ghsalaba, Oreste
; APPLICANT: Nishikawa, Yoshiaki
; APPLICANT: Kawahara, Takashi
; APPLICANT: Kangawa, Kenji
; TITLE OF INVENTION: No. 5196316el Enzyme and DNA Coding Therefor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/707,367

; FILING DATE: 19910530
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 141678/90
; FILING DATE: 01-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 210535/90
; FILING DATE: 10-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 329911/90
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Villamizar, JoAnn
; REGISTRATION NUMBER: 30,598
; REFERENCE/DOCKET NUMBER: 4-18110/A/CGJ 44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914)785-7120
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 935 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-707-367-2

Query Match 88.2%; Score 30; DB 1; Length 935;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 487 NYWMT 491

RESULT 39

US-08-070-301-14
; Sequence 14, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Orji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933

;
; FILING DATE: 31-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 989 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; US-08-070-301-14

Query Match 88.2%; Score 30; DB 1; Length 989;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 602 NYWMT 606

RESULT 40
US-08-070-301-16
; Sequence 16, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Ohji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687

;
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 989 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Frog
; US-08-070-301-16

Query Match 88.2%; Score 30; DB 1; Length 989;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 602 NYWMT 606

RESULT 41
US-08-070-301-17
; Sequence 17, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Ohji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-181933
FILING DATE: 31-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-76331
FILING DATE: 26-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-205475
FILING DATE: 02-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 989 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Rat
US-08-070-301-17

Query Match 88.2%; Score 30; DB 1; Length 989;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 603 NYWMT 607

RESULT 42
US-08-070-301-3
Sequence 3, Application US/08070301
Patent No. 5871995
GENERAL INFORMATION:
APPLICANT: IIDA, Toshio
APPLICANT: KAMINUMA, Toshihiko
APPLICANT: FUSE, Yuka
APPLICANT: TAJIMA, Masahiro
APPLICANT: YANAGI, Mitsuo
APPLICANT: OKAMOTO, Hiroshi
APPLICANT: KISHIMOTO, Jiro
APPLICANT: IFUKU, Ohji
APPLICANT: KATO, Ichiro
TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
STREET: 1233 20th Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
FILING DATE: 24-MAY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-181933
FILING DATE: 31-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-76331
FILING DATE: 26-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-205475
FILING DATE: 02-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-070-301-3

Query Match 88.2%; Score 30; DB 1; Length 1020;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
|||:|
Db 590 NYWMT 594

RESULT 43
US-08-318-970B-3
Sequence 3, Application US/08318970B
Patent No. 5589573
GENERAL INFORMATION:
APPLICANT: Hideaki HAGIWARA, et al.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Dell System 210; Intel 80 285 Microprocessor
OPERATING SYSTEM: MS DOS 3.3
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,970B
FILING DATE: October 6, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588

; REFERENCE/DOCKET NUMBER: S-2371
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 549-2282
 ; TELEFAX: (703) 836-0106
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: H-CDRI-3
 ; OTHER INFORMATION: hypervariable region
 US-08-318-970B-3

Query Match 85.3%; Score 29; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
 Db 1 NYWM 4

RESULT 44
 US-09-508-413A-2
 ; Sequence 2, Application US/09508413A
 ; Patent No. 6667035
 ; GENERAL INFORMATION:
 ; APPLICANT: von Eichel-Streiber, Christoph
 ; APPLICANT: Moos, Michael
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
 ; TITLE OF INVENTION: PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
 ; FILE OF INVENTION: DIFFICILE TOXINS
 ; FILE REFERENCE: 415142000200
 ; CURRENT APPLICATION NUMBER: US/09/508,413A
 ; CURRENT FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05759
 ; PRIOR FILING DATE: 1998-09-10
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-508-413A-2

Query Match 85.3%; Score 29; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
 Db 1 NYWM 4

RESULT 45
 US-08-482-228-39
 ; Sequence 39, Application US/08482228
 ; Patent No. 5968753
 ; GENERAL INFORMATION:
 ; APPLICANT: Tseng-Law, Janet
 ; APPLICANT: Kobori, Joan A.
 ; APPLICANT: Al-Abdaly, Fahad A.
 ; APPLICANT: Guillermo, Roy
 ; APPLICANT: Helgerson, Sam L.
 ; APPLICANT: Deans, Robert J.
 ; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
 ; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
 ; NUMBER OF SEQUENCES: 215
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Janice Guthrie, Ph.D.
 ; STREET: P.O. Box 15210

; CITY: Irvine
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92713-5210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,228
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Guthrie, Janice
 ; REGISTRATION NUMBER: 35,170
 ; REFERENCE/DOCKET NUMBER: IT-4630CIP3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (714) 440-5353
 ; TELEFAX: (714) 553-1952
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-482-228-39

Query Match 85.3%; Score 29; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
 Db 2 NYWM 5

RESULT 46
 US-08-482-528-39
 ; Sequence 39, Application US/08482528
 ; Patent No. 6017719
 ; GENERAL INFORMATION:
 ; APPLICANT: Tseng-Law, Janet
 ; APPLICANT: Kobori, Joan A.
 ; APPLICANT: Al-Abdaly, Fahad A.
 ; APPLICANT: Guillermo, Roy
 ; APPLICANT: Helgerson, Sam L.
 ; APPLICANT: Deans, Robert J.
 ; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
 ; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
 ; NUMBER OF SEQUENCES: 215
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Janice Guthrie, Ph.D.
 ; STREET: P.O. Box 15210
 ; CITY: Irvine
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92713-5210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,528
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Guthrie, Janice
 ; REGISTRATION NUMBER: 35,170
 ; REFERENCE/DOCKET NUMBER: IT-4630CIP4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (714) 440-5353

TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 39;
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-39

Query Match 85.3%; Score 29; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 2 NYWM 5

RESULT 47

US-08-482-228-45
Sequence 45, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-228-45

Query Match 85.3%; Score 29; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 2 NYWM 5

RESULT 48

US-08-482-528-45
Sequence 45, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-45

Query Match 85.3%; Score 29; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 2 NYWM 5

RESULT 49
US-08-816-105A-15
Sequence 15, Application US/08816105A
Patent No. 5989882
GENERAL INFORMATION:
APPLICANT: Crueger, Anneliese; Dellweg, Hans-Georg; Lenz,
APPLICANT: Jurgen; Schroder, Werner; Pape, Hermann;
APPLICANT: Goeke, Klaus; Schaper, Beate; Hemker, Michael;
APPLICANT: Piepersberg, Wolfgang; Distler, Jurgen;
APPLICANT: Stratmann, Ansgar
TITLE OF INVENTION: PROCESSES FOR PREPARING ACARVIOSYL
TITLE OF INVENTION: TRANSFERASE AND FOR USING IT IN THE
TITLE OF INVENTION: CONVERSION OF ACARBOSE HOMOLOGUES
TITLE OF INVENTION: INTO ACARBOSE, FOR THE PREPARATION
TITLE OF INVENTION: OF ACARBOSE HOMOLOGUES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
CITY: Tarrytown

; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10591-5144
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 ; COMPUTER: Apple Macintosh 6500
 ; OPERATING SYSTEM: System 7.5
 ; SOFTWARE: WordPerfect 3.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,105A
 ; FILING DATE: 14-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 19625269.5
 ; FILING DATE: 25-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 19611252.4
 ; FILING DATE: 22-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurt G. Briscoe
 ; REGISTRATION NUMBER: 33,141
 ; REFERENCE/DOCKET NUMBER: Bayer 9814-KGB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 332-1700
 ; TELEFAX: (914) 332-1844
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-816-105A-15

Query Match 85.3%; Score 29; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
 DB 4 NYWM 7

RESULT 50
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 ; Sequence 83, Application US/08208886C
 ; Patent No. 5597710
 ; GENERAL INFORMATION:
 ; APPLICANT: Dalie, Barbara
 ; APPLICANT: Miller, Kenneth
 ; APPLICANT: Murgolo, Nicholas
 ; APPLICANT: Tindall, Stephen
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering-Plough Corporation
 ; STREET: 2000 Galloping Hill Road
 ; CITY: Kenilworth
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07033-0530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.1
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 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/208,886C
 ; FILING DATE: March 10, 1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foulke, Cynthia L.

; REGISTRATION NUMBER: 32,364
 ; REFERENCE/DOCKET NUMBER: JB0429
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908 298 2987
 ; TELEFAX: 908 298 5388
 ; INFORMATION FOR SEQ ID NO: 83:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
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 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-208-886C-83
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 DB 6 SYWMT 10

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 Job time : 19.724 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:41 ; Search time 37.7049 Seconds
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Title: US-10-808-538-1

Perfect score: 34

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	34	100.0	122	3	US-09-155-106-20
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165	29	85.3	133	4	US-10-160-506-54	Sequence 54, Appl	238	29	85.3	400	4	US-10-650-112-24	Sequence 24, Appl
166	29	85.3	133	4	US-10-449-379-54	Sequence 54, Appl	239	29	85.3	402	4	US-10-087-080-32	Sequence 32, Appl
167	29	85.3	133	4	US-10-688-015-54	Sequence 54, Appl	240	29	85.3	402	4	US-10-229-345-18	Sequence 18, Appl
168	29	85.3	133	4	US-10-160-505-54	Sequence 54, Appl	241	29	85.3	402	4	US-10-274-177-18	Sequence 18, Appl
169	29	85.3	140	4	US-10-425-115-341289	Sequence 341289,	242	29	85.3	402	5	US-10-756-149-4687	Sequence 4687, Ap
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171	29	85.3	155	4	US-10-767-701-32467	Sequence 32467, A	244	29	85.3	403	4	US-10-650-112-22	Sequence 22, Appl
172	29	85.3	156	4	US-10-437-963-193007	Sequence 193007,	245	29	85.3	407	4	US-10-425-114-49353	Sequence 49353, A
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249	29	85.3	447	4	US-10-282-122A-73850	Sequence 73850, A	322	29	85.3	875	4	US-10-437-963-151604	Sequence 151604,
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251	29	85.3	447	5	US-10-472-928-1070	Sequence 1070, Ap	324	29	85.3	998	4	US-10-437-963-178627	Sequence 178627,
252	29	85.3	448	5	US-10-617-320-3371	Sequence 3371, Ap	325	29	85.3	1079	5	US-10-450-763-58915	Sequence 58915, A
253	29	85.3	449	4	US-10-767-701-43607	Sequence 43607, A	326	29	85.3	1098	5	US-10-450-763-60726	Sequence 60726, A
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255	29	85.3	458	6	US-11-097-143-26862	Sequence 26862, A	328	29	85.3	1142	4	US-10-425-115-258785	Sequence 258785,
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262	29	85.3	461	4	US-10-282-122A-75605	Sequence 75605, A	335	29	85.3	1832	4	US-10-014-717-4	Sequence 2, Appli
263	29	85.3	461	4	US-10-282-122A-78050	Sequence 78050, A	336	29	85.3	2516	3	US-09-817-514A-2	Sequence 2, Appli
264	29	85.3	461	4	US-10-796-667-27	Sequence 27, Appl	337	29	85.3	2516	4	US-10-262-794A-47	Sequence 47, Appl
265	29	85.3	461	5	US-10-953-901-95	Sequence 95, Appl	338	29	85.3	2516	4	US-10-706-424-2	Sequence 2, Appli
266	29	85.3	461	5	US-10-953-901-97	Sequence 97, Appl	339	29	85.3	2516	5	US-10-703-280-4	Sequence 4, Appli
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272	29	85.3	467	4	US-10-282-122A-44513	Sequence 44513, A	345	28	82.4	14	4	US-10-462-262-318	Sequence 318, App
273	29	85.3	467	6	US-11-097-143-33438	Sequence 33438, A	346	28	82.4	34	4	US-10-218-102-10	Sequence 10, Appl
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281	29	85.3	479	4	US-10-724-972A-5427	Sequence 5427, Ap	354	28	82.4	34	4	US-10-218-102-51	Sequence 51, Appl
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283	29	85.3	489	5	US-10-193-860-2741	Sequence 2741, Ap	356	28	82.4	34	4	US-10-218-102-71	Sequence 71, Appl
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286	29	85.3	503	4	US-10-239-656-77	Sequence 77, Appl	359	28	82.4	34	4	US-10-218-102-82	Sequence 82, Appl
287	29	85.3	507	4	US-10-074-596-11	Sequence 11, Appl	360	28	82.4	34	4	US-10-218-102-84	Sequence 84, Appl
288	29	85.3	509	4	US-10-627-476-12	Sequence 12, Appl	361	28	82.4	34	4	US-10-218-102-85	Sequence 85, Appl
289	29	85.3	513	5	US-10-926-731A-12	Sequence 12, Appl	362	28	82.4	34	4	US-10-218-102-86	Sequence 86, Appl
290	29	85.3	517	4	US-10-369-493-10053	Sequence 10053, A	363	28	82.4	34	4	US-10-218-102-87	Sequence 87, Appl
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292	29	85.3	551	4	US-10-425-114-68596	Sequence 68596, A	365	28	82.4	34	4	US-10-218-102-90	Sequence 90, Appl
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294	29	85.3	579	4	US-10-262-794A-51	Sequence 51, Appl	367	28	82.4	46	3	US-09-865-621A-39	Sequence 39, Appl
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297	29	85.3	604	4	US-10-369-493-17651	Sequence 17651, A	370	28	82.4	46	4	US-10-387-388-39	Sequence 39, Appl
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299	29	85.3	608	4	US-10-282-122A-44213	Sequence 44213, A	372	28	82.4	57	4	US-10-424-599-189767	Sequence 189767,
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305	29	85.3	626	4	US-10-369-493-363	Sequence 363, App	378	28	82.4	75	4	US-10-425-115-241221	Sequence 241221,
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313	29	85.3	673	4	US-10-437-963-143752	Sequence 143752, A	386	28	82.4	106	5	US-10-424-599-163564	Sequence 163564,
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319	29	85.3	804	4	US-10-156-761-8615	Sequence 8615, Ap	392	28	82.4	120	4		

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411	28	82.4	154	4	US-10-767-701-59217	Sequence 59217, A	484	28	82.4	238	4	US-10-374-780A-2568	Sequence 2568, Ap
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436	28	82.4	196	4	US-10-659-869-44	Sequence 44, Appl	509	28	82.4	262	4	US-10-425-114-54675	Sequence 54675, A
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444	28	82.4	206	4	US-10-021-811-36	Sequence 36, Appl	517	28	82.4	273	4	US-10-412-699B-162	Sequence 162, App
445	28	82.4	206	4	US-10-659-869-36	Sequence 36, Appl	518	28	82.4	276	4	US-10-424-599-162352	Sequence 162352, A
446	28	82.4	207	4	US-10-425-115-219294	Sequence 219294, A	519	28	82.4	276	4	US-10-302-267-164	Sequence 164, App
447	28	82.4	208	4	US-10-021-811-30	Sequence 30, Appl	520	28	82.4	276	4	US-10-412-699B-664	Sequence 664, App
448	28	82.4	208	4	US-10-659-869-30	Sequence 30, Appl	521	28	82.4	280	4	US-10-437-963-194997	Sequence 194997, A
449	28	82.4	208	5	US-10-856-499-2250	Sequence 2250, Ap	522	28	82.4	283	4	US-10-225-066A-100	Sequence 100, App
450	28	82.4	210	4	US-10-437-963-106342	Sequence 106342, A	523	28	82.4	283	4	US-10-374-780A-2906	Sequence 2906, Ap
451	28	82.4	211	4	US-10-425-114-36865	Sequence 36865, A	524	28	82.4	283	5	US-10-225-066A-100	Sequence 100, App
452	28	82.4	216	4	US-10-225-066A-196	Sequence 196, App	525	28	82.4	285	4	US-10-437-963-107627	Sequence 107627, A
453	28	82.4	216	4	US-10-374-780A-2900	Sequence 2900, Ap	526	28	82.4	285	4	US-10-425-115-318282	Sequence 318282, A
454	28	82.4	216	5	US-10-225-066A-196	Sequence 196, App	527	28	82.4	286	4	US-10-302-267-152	Sequence 152, App
455	28	82.4	217	3	US-09-443-704-14	Sequence 14, Appl	528	28	82.4	286	4	US-10-412-699B-846	Sequence 846, App
456	28	82.4	217	4	US-10-008-118A-14	Sequence 14, Appl	529	28	82.4	289	4	US-10-374-780A-1572	Sequence 1572, Ap
457	28	82.4	221	4	US-10-021-811-14	Sequence 14, Appl	530	28	82.4	289	4	US-10-437-963-179146	Sequence 179146, A
458	28	82.4	221	4	US-10-425-114-40019	Sequence 40019, A	531	28	82.4	293	4	US-10-374-780A-1565	Sequence 1565, Ap
459	28	82.4	221	4	US-10-659-869-14	Sequence 14, Appl	532	28	82.4	293	4	US-10-437-963-151143	Sequence 151143, A
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461	28	82.4	224	5	US-10-856-499-919	Sequence 919, App	534	28	82.4	298	4	US-10-374-780A-1563	Sequence 1563, Ap
462	28	82.4	227	4	US-10-425-114-66242	Sequence 66242, A	535	28	82.4	298	4	US-10-282-122A-43945	Sequence 43945, A
463	28	82.4	228	4	US-10-374-780A-1541	Sequence 1541, Ap	536	28	82.4	298	4	US-10-437-963-110857	Sequence 110857, A
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465	28	82.4	228	4	US-10-437-963-149962	Sequence 149962, A	538	28	82.4	300	4	US-10-424-599-272400	Sequence 272400, A

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541	28	82.4	303	5	US-10-650-274-168	Sequence 168, App	614	28	82.4	468	4	US-10-282-122A-74751	Sequence 74751, A
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543	28	82.4	307	4	US-10-225-068-156	Sequence 156, App	616	28	82.4	470	3	US-09-815-242-5637	Sequence 5637, Ap
544	28	82.4	307	4	US-10-225-066A-282	Sequence 282, App	617	28	82.4	470	3	US-09-815-242-1248	Sequence 12248, A
545	28	82.4	307	4	US-10-374-780A-262	Sequence 262, App	618	28	82.4	470	4	US-10-282-122A-43887	Sequence 43887, A
546	28	82.4	307	5	US-10-225-068-156	Sequence 156, App	619	28	82.4	470	4	US-10-282-122A-71148	Sequence 71148, A
547	28	82.4	307	5	US-10-225-066A-282	Sequence 282, App	620	28	82.4	471	3	US-09-815-242-13377	Sequence 13377, A
548	28	82.4	308	4	US-10-424-599-178293	Sequence 178293,	621	28	82.4	471	5	US-10-472-928-23368	Sequence 23368, Ap
549	28	82.4	310	4	US-10-437-963-136286	Sequence 136286,	622	28	82.4	471	5	US-10-617-320-4791	Sequence 4791, Ap
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553	28	82.4	312	4	US-10-424-599-175657	Sequence 175657,	626	28	82.4	475	4	US-10-724-972A-6450	Sequence 6450, Ap
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557	28	82.4	323	3	US-09-934-455-484	Sequence 484, App	630	28	82.4	477	4	US-10-369-493-17133	Sequence 17133, A
558	28	82.4	323	4	US-10-374-780A-2178	Sequence 2178, Ap	631	28	82.4	477	4	US-10-282-122A-53951	Sequence 53951, A
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562	28	82.4	329	4	US-10-424-599-201446	Sequence 201446,	635	28	82.4	477	4	US-10-282-122A-74898	Sequence 74898, A
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572	28	82.4	336	4	US-10-425-114-40013	Sequence 40013, A	645	28	82.4	478	5	US-10-472-928-438	Sequence 438, App
573	28	82.4	336	4	US-10-425-114-54136	Sequence 54136, A	646	28	82.4	478	5	US-10-650-274-88	Sequence 88, Appl
574	28	82.4	340	4	US-10-425-115-251806	Sequence 251806,	647	28	82.4	479	3	US-09-815-242-10288	Sequence 10288, A
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584	28	82.4	358	4	US-10-437-963-127818	Sequence 127818,	657	28	82.4	523	6	US-11-097-143-10614	Sequence 10614, A
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586	28	82.4	363	4	US-10-425-115-253807	Sequence 253807,	659	28	82.4	582	4	US-10-425-115-192825	Sequence 192825, A
587	28	82.4	371	4	US-10-425-114-38797	Sequence 38797, A	660	28	82.4	599	4	US-10-210-130-14	Sequence 14, Appl
588	28	82.4	373	4	US-10-755-889-376	Sequence 376, App	661	28	82.4	608	4	US-10-108-260A-4385	Sequence 4385, Ap
589	28	82.4	379	6	US-11-097-143-29823	Sequence 29823, A	662	28	82.4	627	4	US-10-090-455-8	Sequence 8, Appli
590	28	82.4	380	4	US-10-425-115-212382	Sequence 212382,	663	28	82.4	637	4	US-10-267-502-310	Sequence 310, App
591	28	82.4	383	4	US-10-425-114-60446	Sequence 60446, A	664	28	82.4	637	4	US-10-437-963-170248	Sequence 170248, A
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593	28	82.4	400	3	US-09-888-370-2	Sequence 2, Appli	666	28	82.4	642	4	US-10-437-963-183447	Sequence 183447, A
594	28	82.4	400	3	US-09-879-312-2	Sequence 2, Appli	667	28	82.4	646	4	US-10-072-621-9	Sequence 9, Appli
595	28	82.4	400	5	US-10-923-520-2	Sequence 2, Appli	668	28	82.4	646	4	US-10-154-452-4	Sequence 4, Appli
596	28	82.4	402	5	US-10-450-763-35033	Sequence 35033, A	669	28	82.4	646	4	US-10-154-452-8	Sequence 8, Appli
597	28	82.4	407	6	US-11-097-143-23277	Sequence 23277, A	670	28	82.4	646	4	US-10-090-455-2	Sequence 2, Appli
598	28	82.4	411	4	US-10-282-122A-61381	Sequence 61381, A	671	28	82.4	646	4	US-10-090-455-13	Sequence 13, Appl
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600	28	82.4	449	3	US-09-768-781-7	Sequence 7, Appli	673	28	82.4	649	4	US-10-267-502-308	Sequence 308, App
601	28	82.4	460	6	US-11-097-143-9444	Sequence 9444, Ap	674	28	82.4	649	4	US-10-369-493-22078	Sequence 22078, A
602	28	82.4	462	3	US-09-815-242-5562	Sequence 5562, Ap	675	28	82.4	662	5	US-10-732-923-8630	Sequence 8630, Ap
603	28	82.4	462	3	US-09-768-781-4	Sequence 4, Appli	676	28	82.4	666	4	US-10-267-502-309	Sequence 309, App
604	28	82.4	462	5	US-10-875-518-17	Sequence 17, Appl	677	28	82.4	671	4	US-10-320-797-3275	Sequence 3275, Ap
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606	28	82.4	463	3	US-09-815-242-12572	Sequence 12572, A	679	28	82.4	674	4	US-10-429-160-10	Sequence 10, Appl
607	28	82.4	463	3	US-09-815-242-12754	Sequence 12754, A	680	28	82.4	674	4	US-10-267-502-307	Sequence 307, App
608	28	82.4	463	4	US-10-282-122A-44091	Sequence 44091, A	681	28	82.4	674	4	US-10-648-593-214	Sequence 214, App
609	28	82.4	463	4	US-10-282-122A-70764	Sequence 70764, A	682	28	82.4	674	5	US-10-756-149-5634	Sequence 5634, Ap
610	28	82.4	463	4	US-10-282-122A-77164	Sequence 77164, A	683	28	82.4	674	5	US-10-287-436A-518	Sequence 518, App
611	28	82.4	463	5	US-10-857-625-805	Sequence 805, App	684	28	82.4	674	5	US-10-287-436A-1209	Sequence 1209, App

685	28	82.4	699	4	US-10-437-963-125390	Sequence 125390,	758	28	82.4	2144	5	US-10-723-860-2303	Sequence 2303, Ap
686	28	82.4	713	4	US-10-437-963-104568	Sequence 104568,	759	28	82.4	2551	4	US-10-144-194A-80	Sequence 80, Appl
687	28	82.4	725	4	US-10-437-963-183497	Sequence 183497,	760	28	82.4	2551	5	US-10-491-566-80	Sequence 80, Appl
688	28	82.4	726	4	US-10-437-963-202368	Sequence 202368,	761	28	82.4	2633	4	US-10-144-194A-82	Sequence 82, Appl
689	28	82.4	730	4	US-10-042-865-51	Sequence 51, Appl	762	28	82.4	2633	5	US-10-491-566-82	Sequence 82, Appl
690	28	82.4	730	4	US-10-029-020-50	Sequence 50, Appl	763	28	82.4	2724	3	US-09-808-602-13	Sequence 13, Appl
691	28	82.4	730	4	US-10-408-765A-2505	Sequence 2505, Ap	764	28	82.4	2724	3	US-09-800-198-13	Sequence 13, Appl
692	28	82.4	739	4	US-10-437-963-183547	Sequence 183547,	765	28	82.4	2725	4	US-10-295-027-928	Sequence 928, App
693	28	82.4	750	4	US-10-425-115-239486	Sequence 239486,	766	28	82.4	2725	4	US-10-023-020-52	Sequence 52, Appl
694	28	82.4	754	4	US-10-425-563-18	Sequence 18, Appl	767	28	82.4	2725	4	US-10-408-765A-1687	Sequence 1687, Ap
695	28	82.4	754	5	US-10-972-789A-18	Sequence 18, Appl	768	28	82.4	2725	5	US-10-723-860-4102	Sequence 4102, Ap
696	28	82.4	775	4	US-10-437-963-183388	Sequence 183388,	769	28	82.4	2733	3	US-09-808-602-8	Sequence 8, Appl
697	28	82.4	775	4	US-10-726-148A-15	Sequence 15, Appl	770	28	82.4	2733	3	US-09-800-198-8	Sequence 8, Appl
698	28	82.4	775	6	US-11-088-999-15	Sequence 15, Appl	771	28	82.4	2758	4	US-10-467-535-10	Sequence 10, Appl
699	28	82.4	777	6	US-11-097-143-23379	Sequence 23379, A	772	28	82.4	2758	4	US-10-072-012-144	Sequence 144, App
700	28	82.4	779	4	US-10-437-963-200727	Sequence 200727,	773	28	82.4	2764	3	US-09-808-602-80	Sequence 80, Appl
701	28	82.4	784	4	US-10-425-115-192823	Sequence 192823,	774	28	82.4	2764	3	US-09-800-198-68	Sequence 68, Appl
702	28	82.4	804	4	US-10-437-963-183488	Sequence 183488,	775	28	82.4	2764	4	US-10-072-012-487	Sequence 487, App
703	28	82.4	827	4	US-10-437-963-177840	Sequence 177840,	776	28	82.4	2764	5	US-10-631-467-1514	Sequence 1514, Ap
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705	28	82.4	852	4	US-10-437-963-189221	Sequence 189221,	778	28	82.4	2765	3	US-09-800-198-72	Sequence 72, Appl
706	28	82.4	867	4	US-10-282-122A-69006	Sequence 69006, A	779	28	82.4	2765	4	US-10-072-012-488	Sequence 488, App
707	28	82.4	883	4	US-10-437-963-125386	Sequence 125386	780	28	82.4	2769	4	US-10-383-201-44	Sequence 44, Appl
708	28	82.4	907	6	US-10-369-493-6777	Sequence 6777, Ap	781	28	82.4	2769	4	US-10-029-020-14	Sequence 14, Appl
709	28	82.4	907	6	US-11-059-218-12	Sequence 12, Appl	782	28	82.4	2771	3	US-09-808-602-82	Sequence 82, Appl
710	28	82.4	910	4	US-10-437-963-183401	Sequence 183401,	783	28	82.4	2771	3	US-09-800-198-70	Sequence 70, Appl
711	28	82.4	921	4	US-10-467-685-14	Sequence 14, Appl	784	28	82.4	2775	4	US-10-383-201-56	Sequence 56, Appl
712	28	82.4	927	4	US-10-408-765A-2938	Sequence 2938, Ap	785	28	82.4	2794	4	US-10-042-865-2	Sequence 2, Appl
713	28	82.4	948	4	US-10-437-963-183451	Sequence 183451,	786	28	82.4	2802	3	US-09-808-602-81	Sequence 81, Appl
714	28	82.4	959	4	US-10-437-963-183639	Sequence 183639,	787	28	82.4	2802	3	US-09-800-198-69	Sequence 69, Appl
715	28	82.4	987	4	US-10-437-963-183653	Sequence 183653,	788	28	82.4	2802	4	US-10-072-012-489	Sequence 489, App
716	28	82.4	1006	6	US-11-097-143-9360	Sequence 9360, Ap	789	27	79.4	22	5	US-10-751-826-75	Sequence 75, Appl
717	28	82.4	1081	4	US-10-369-493-3989	Sequence 3989, Ap	790	27	79.4	33	5	US-10-751-826-26	Sequence 26, Appl
718	28	82.4	1086	5	US-10-723-860-3170	Sequence 3170, Ap	791	27	79.4	33	5	US-10-424-599-158120	Sequence 158120,
719	28	82.4	1086	5	US-10-756-149-5574	Sequence 5574, Ap	792	27	79.4	62	4	US-10-437-963-143663	Sequence 143663,
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721	28	82.4	1150	4	US-10-369-493-5940	Sequence 5940, Ap	794	27	79.4	67	5	US-10-856-499-2300	Sequence 2300, Ap
722	28	82.4	1162	4	US-10-437-963-183436	Sequence 183436,	795	27	79.4	67	5	US-10-856-499-2332	Sequence 2332, Ap
723	28	82.4	1162	5	US-10-450-763-33411	Sequence 33411, A	796	27	79.4	67	5	US-10-856-499-2345	Sequence 2345, Ap
724	28	82.4	1169	4	US-10-369-493-22308	Sequence 22308, A	797	27	79.4	67	5	US-10-856-499-2362	Sequence 2362, Ap
725	28	82.4	1169	5	US-10-732-923-8631	Sequence 8631, Ap	798	27	79.4	67	5	US-10-856-499-2364	Sequence 2364, Ap
726	28	82.4	1179	4	US-10-437-963-137323	Sequence 137323,	799	27	79.4	67	5	US-10-856-499-2366	Sequence 2366, Ap
727	28	82.4	1248	4	US-10-437-963-162465	Sequence 162465,	800	27	79.4	67	5	US-10-856-499-2368	Sequence 2368, Ap
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ALIGNMENTS

RESULT 1
US-09-155-106-1
; Sequence 1, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNOMEDICS, INC.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 19-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: peptide
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-155-106-1
100.0%; Score 34; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
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RESULT 2
US-10-808-538-1
; Sequence 1, Application US/10808538
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; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
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RESULT 3
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; Sequence 29, Application US/10769308
; Publication No. US20050003465A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Ava
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,308
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
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; PRIOR FILING DATE: 1998-02-13
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; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/124,658
; PRIOR FILING DATE: 1999-03-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PSCA mAb 2H9
; OTHER INFORMATION: CDR1
US-10-769-308-29

Query Match      100.0%; Score 34; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      6 NYWMT 10
      |||||

RESULT 4
US-10-769-074-29
; Sequence 29, Application US/10769074
; Publication No. US2005005909A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10769,074
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US/10769,308
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PSCA mAb 2H9
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; OTHER INFORMATION: CDR1
US-10-769-074-29

Query Match      100.0%; Score 34; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      6 NYWMT 10
      |||||

RESULT 5
US-09-155-106-18
; Sequence 18, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-18

Query Match      100.0%; Score 34; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      31 NYWMT 35
      |||||

RESULT 6
US-09-155-106-19
; Sequence 19, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
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; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19

Query Match 100.0%; Score 34; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 7

US-09-155-106-20
; Sequence 20, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-20

Query Match 100.0%; Score 34; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 8

US-09-155-106-26
; Sequence 26, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-26

Query Match 100.0%; Score 34; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 9

US-09-155-106-32
; Sequence 32, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-32

Query Match 100.0%; Score 34; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 10

US-10-808-538-18
; Sequence 18, Application US/10808538
; Publication No. US20050048053A1


```
;
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-808-538-18

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 11
US-10-808-538-19
; Sequence 19, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-808-538-20

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 12
US-10-808-538-20
; Sequence 20, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-808-538-20

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 13
US-10-808-538-26
; Sequence 26, Application US/10808538
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;
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-808-538-19

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 12
US-10-808-538-20
; Sequence 20, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-808-538-20

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 31 NYWMT 35

RESULT 13
US-10-808-538-26
; Sequence 26, Application US/10808538
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; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
;
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-808-538-26

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 31 NYWMT 35

RESULT 14
US-10-808-538-32
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
;
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997

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; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-808-538-32

Query Match 100.0%; Score 34; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 31 NYWMT 35

RESULT 15
US-09-564-329A-15
; Sequence 15, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 50 NYWMT 54

RESULT 16
US-09-855-153-15

```

; Sequence 15, Application US/09855153
; Patent No. US20020102866A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 50 NYWMT 54

RESULT 17
US-09-854-811-15
; Sequence 15, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US/09/854,811
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/359,326
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice

US-09-854-811-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 50 NYWMT 54

RESULT 18
US-09-934-773-15
; Sequence 15, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
DB 50 NYWMT 54

RESULT 19
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/963,620
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
TYPE: PRT
ORGANISM: SCID Mice
US-09-963-620-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 50 NYWMT 54

RESULT 20
US-09-855-632-15
Sequence 15, Application US/09855632
Publication No. US20030113818A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/855,632
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 151
TYPE: PRT
ORGANISM: SCID Mice
US-09-855-632-15

Query Match 100.0%; Score 34; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 50 NYWMT 54

RESULT 21
US-10-225-784-15
Sequence 15, Application US/10225784
Publication No. US20030113820A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/10/225,784
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US/09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 151
TYPE: PRT
ORGANISM: SCID Mice
US-10-225-784-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 50 NYWMT 54

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RESULT 22
US-10-224-720-15
; Sequence 15, Application US/10224720
; Publication No. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 50 NYWMT 54

US-10-224-720-15
; Sequence 15, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13

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; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-779-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 50 NYWMT 54

RESULT 24
US-10-374-381-15
; Sequence 15, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-374-381-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 50 NYWMT 54

US-10-374-381-15
; Sequence 15, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-374-381-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 50 NYWMT 54

US-10-224-720-15
; Sequence 15, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13

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QY 1 NYWMT 5
Db 50 NYWMT 54

RESULT 25
US-10-446-542-15
; Sequence 15, Application US/10446542
; Publication No. US20040018571A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/446,542
; PRIOR FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-446-542-15

Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 50 NYWMT 54

RESULT 26
US-10-769-308-27
; Sequence 27, Application US/10769308
; Publication No. US2005003465A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert B.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,308
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816

; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/124,658
; PRIOR FILING DATE: 1999-03-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody
; OTHER INFORMATION: 2H9
US-10-769-308-27

Query Match 100.0%; Score 34; DB 5; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
Db 50 NYWMT 54

RESULT 27
US-10-769-074-27
; Sequence 27, Application US/10769074
; Publication No. US20050059099A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,074
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US/10/769,308
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536

; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody
; OTHER INFORMATION: 2H9
US-10-769-074-27

Query Match 100.0%; Score 34; DB 5; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||
Db 50 NYWMT 54

RESULT 28
US-10-997-735-15
; Publication 15, Application US/10997735
; Publication No. US20050152909A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/997,735
; CURRENT FILING DATE: 2004-11-23
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15
LENGTH: 151
TYPE: PRT
ORGANISM: SCID Mice

US-10-997-735-15

Query Match 100.0%; Score 34; DB 5; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||
Db 50 NYWMT 54

RESULT 29
US-11-021-950-15
; Sequence 15, Application US/11021950
; Publication No. US20050169930A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/11/021,950
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/225,784
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-11-021-950-15

Query Match 100.0%; Score 34; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
|||
Db 50 NYWMT 54

RESULT 30
US-09-880-748-974
; Sequence 974, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 974

```
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-974

Query Match      100.0%; Score 34; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      31 NYWMT 35

RESULT 31
US-10-293-418-974
; Sequence 974, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 974
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-974

Query Match      100.0%; Score 34; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      31 NYWMT 35

RESULT 32
US-10-424-599-247693
; Sequence 247693, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247693
; LENGTH: 67
```

```
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65697C.1.pep
US-10-424-599-247693

Query Match      91.2%; Score 31; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      5 NYWMT 9

RESULT 33
US-10-282-122A-63299
; Sequence 63299, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63299
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-282-122A-63299

Query Match      91.2%; Score 31; DB 4; Length 233;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      122 NYWMT 126
```

```
RESULT 34
US-10-425-115-353384
; Sequence 353384, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353384
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(255)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85460C.1.pep
US-10-425-115-353384

Query Match          91.2%; Score 31; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      55 NYWLT 59

RESULT 35
US-10-032-585-7816
; Sequence 7816, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7816
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7816

Query Match          91.2%; Score 31; DB 4; Length 454;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      136 NYWLT 140

RESULT 36
US-10-282-122A-67258
; Sequence 67258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
```

```
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67258
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-67258

Query Match          91.2%; Score 31; DB 4; Length 489;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      163 NYWLT 167

RESULT 37
US-10-282-122A-58409
; Sequence 58409, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
```



```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58409
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-282-122A-58409

Query Match          91.2%; Score 31; DB 4; Length 511;
Best Local Similarity 80.0%; Pred.No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
    |||:|
Db 185 NYWLT 189

RESULT 38
US-11-097-143-42837
; Sequence 42837, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42837
; LENGTH: 539
; TYPE: PRT
```

```
; ORGANISM: DROSOPHILA
US-11-097-143-42837

Query Match          91.2%; Score 31; DB 6; Length 539;
Best Local Similarity 80.0%; Pred.No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
    |||:|
Db 531 NYWLT 535

RESULT 39
US-10-705-195-2
; Sequence 2, Application US/10705195
; Publication No. US20040110254A1
; GENERAL INFORMATION:
; APPLICANT: BUTTCHER, Volker et al.
; TITLE OF INVENTION: Method for producing alpha-1, 6-branched alpha-1, 4-glucans from
; FILE REFERENCE: 0147-0253P
; CURRENT APPLICATION NUMBER: US/10/705,195
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/807,063
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Neisseria denitrificans
US-10-705-195-2

Query Match          91.2%; Score 31; DB 4; Length 762;
Best Local Similarity 80.0%; Pred.No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
    |||:|
Db 272 NYWLT 276

RESULT 40
US-10-094-749-2636
; Sequence 2636, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2636

; LENGTH: 781

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-094-749-2636

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 781;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 372 NYWLT 376

RESULT 41

US-10-622-377-14

; Sequence 14, Application US/10622377

; Publication No. US20040265837A1

; GENERAL INFORMATION:

; APPLICANT: JENTISCH, THOMAS J.

; TITLE OF INVENTION: TEST SYSTEM FOR THE DEVELOPMENT OF THERAPEUTIC AGENTS,

; TITLE OF INVENTION: IN PARTICULAR ACTIVE COMPOUNDS FOR THE TREATMENT OF

; FILE REFERENCE: 59572(46865)

; CURRENT APPLICATION NUMBER: US/10/622,377

; PRIOR FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: PCT/DK02/00038

; PRIOR FILING DATE: 2002-01-17

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 14

; LENGTH: 789

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-622-377-14

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 789;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 380 NYWLT 384

RESULT 42

US-10-349-670-4

; Sequence 4, Application US/10349670

; Publication No. US20030215787A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: Modulators of the CLC-7 Chloride Channel and Methods for Their

; TITLE OF INVENTION: Identification and Use in the Treatment and Prevention of

; TITLE OF INVENTION: Osteoporosis and Related Disease States

; FILE REFERENCE: D0172

; CURRENT APPLICATION NUMBER: US/10/349,670

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: 60/351,187

; PRIOR FILING DATE: 2002-01-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 803

; TYPE: PRT

; ORGANISM: Rat

US-10-349-670-4

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 803;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 394 NYWLT 398

RESULT 43

US-10-349-670-6

; Sequence 6, Application US/10349670

; Publication No. US20030215787A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: Modulators of the CLC-7 Chloride Channel and Methods for Their

; TITLE OF INVENTION: Identification and Use in the Treatment and Prevention of

; TITLE OF INVENTION: Osteoporosis and Related Disease States

; FILE REFERENCE: D0172

; CURRENT APPLICATION NUMBER: US/10/349,670

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: 60/351,187

; PRIOR FILING DATE: 2002-01-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 803

; TYPE: PRT

; ORGANISM: Mouse

US-10-349-670-6

Query Match

Best Local Similarity 91.2%; Score 31; DB 4; Length 803;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 394 NYWLT 398

RESULT 44

US-10-622-377-12

; Sequence 12, Application US/10622377

; Publication No. US20040265837A1

; GENERAL INFORMATION:

; APPLICANT: JENTISCH, THOMAS J.

; TITLE OF INVENTION: TEST SYSTEM FOR THE DEVELOPMENT OF THERAPEUTIC AGENTS,

; TITLE OF INVENTION: IN PARTICULAR ACTIVE COMPOUNDS FOR THE TREATMENT OF

; TITLE OF INVENTION: OSTEOPOROSIS

; FILE REFERENCE: 59572(46865)

; CURRENT APPLICATION NUMBER: US/10/622,377

; PRIOR FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: PCT/DK02/00038

; PRIOR FILING DATE: 2002-01-17

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 12

; LENGTH: 803

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-622-377-12

Query Match

Best Local Similarity 91.2%; Score 31; DB 5; Length 803;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5

Db 394 NYWLT 398

RESULT 45

US-10-349-670-2

; Sequence 2, Application US/10349670

; Publication No. US20030215787A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: Modulators of the CLC-7 Chloride Channel and Methods for Their
 ; TITLE OF INVENTION: Identification and Use in the Treatment and Prevention of
 ; FILE REFERENCE: D0172
 ; CURRENT APPLICATION NUMBER: US/10/349,670
 ; CURRENT FILING DATE: 2003-01-23
 ; PRIOR APPLICATION NUMBER: 60/351,187
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 805
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-349-670-2

Query Match 91.2%; Score 31; DB 4; Length 805;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 DB 396 NYWLT 400

RESULT 46
 US-10-408-765A-1815
 ; Sequence 1815, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Roin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows version 4.0
 ; SEQ ID NO 1815
 ; LENGTH: 805
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1815

Query Match 91.2%; Score 31; DB 4; Length 805;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 DB 396 NYWLT 400

RESULT 47
 US-10-723-860-1059
 ; Sequence 1059, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginzburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10/723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1059
 ; LENGTH: 805
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-860-1059

Query Match 91.2%; Score 31; DB 5; Length 805;
 Best Local Similarity 80.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
 DB 396 NYWLT 400

RESULT 48
 US-10-450-763-49833
 ; Sequence 49833, Application US/10450763
 ; Publication No. US20050196754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 790CIP3/US
 ; CURRENT APPLICATION NUMBER: US/10/450,763
 ; CURRENT FILING DATE: 2003-06-11
 ; PRIOR APPLICATION NUMBER: PCT/US01/08631
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 09/649,167
 ; PRIOR FILING DATE: 2000-08-23
 ; NUMBER OF SEQ ID NOS: 60736
 ; SOFTWARE: Custom
 ; SEQ ID NO 49833
 ; LENGTH: 816
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
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 ; LOCATION: (305)..(325)
 ; OTHER INFORMATION: CHLORIDE CHANNEL SIGNATURE domain identified by eMATRIX,
 ; OTHER INFORMATION: accession number PR00762C, p-value=4.682e-21, raw score of 9.29
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (195)..(611)
 ; OTHER INFORMATION: Voltage gated chloride channels domain identified by PFam,
 ; OTHER INFORMATION: accession name voltage_CLC, E-value=2.2e-185, PFam score of 629.1

Query Match 91.2%; Score 31; DB 5; Length 816;
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 DB 407 NYWLT 411

RESULT 49
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 ; Sequence 2203, Application US/10276774
 ; Publication No. US20040053245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; APPLICANT: Tang, Y, Tom et al
 ; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-030
 ; CURRENT APPLICATION NUMBER: US/10/276,774
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 09/560,875

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2203
; LENGTH: 1097
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2203

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Best Local Similarity 80.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 460 NYWLT 464

RESULT 50
US-10-873-467-150
; Sequence 150, Application US/10873467
; Publication No US20050123941A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Alterman, Eric
; TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: FRUCTO-OLIGOSACCHARIDE UTILIZATION COMPOUNDS AND USES THEREOF
; FILE REFERENCE: 5051.691
; CURRENT APPLICATION NUMBER: US/10/873,467
; CURRENT FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/480,764
; PRIOR FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 150
; LENGTH: 1217
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-10-873-467-150

Query Match 91.2%; Score 31; DB 5; Length 1217;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWT 5
| | | | |
Db 499 NYWLT 503

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OM protein - protein search, using sw model

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37.693 Million cell updates/sec

Title: US-10-808-538-1

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Sequence: 1 NYNMT 5

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	30	88.2	247	11	US-11-054-515-2103
6	30	88.2	247	11	US-11-266-444-2103
7	30	88.2	558	11	US-11-096-568A-23953
8	30	88.2	593	11	US-11-096-568A-23952
9	30	88.2	606	11	US-11-096-568A-23951
10	30	88.2	1684	11	US-11-188-298-16493
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13	29	85.3	10	9	US-10-880-238-51
14	29	85.3	10	9	US-10-880-238-54
15	29	85.3	10	9	US-10-880-238-57
16	29	85.3	10	11	US-11-219-563-29
17	29	85.3	10	11	US-11-218-813-29
18	29	85.3	116	10	US-11-219-563-49
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25	85.3	116	11	US-11-218-813-59	Sequence 59, Appl
26	85.3	116	11	US-11-218-813-60	Sequence 60, Appl
27	85.3	116	11	US-11-218-813-61	Sequence 61, Appl
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29	85.3	123	10	US-11-219-563-69	Sequence 69, Appl
30	85.3	123	10	US-11-219-563-70	Sequence 70, Appl
31	85.3	123	11	US-11-218-813-69	Sequence 69, Appl
32	85.3	123	11	US-11-218-813-70	Sequence 70, Appl
33	85.3	125	11	US-11-116-144-157	Sequence 157, Appl
34	85.3	125	11	US-11-220-372-157	Sequence 157, Appl
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38	85.3	167	11	US-11-210-316-18	Sequence 18, Appl
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57	85.3	286	11	US-11-096-568A-22666	Sequence 22666, A
58	85.3	288	9	US-10-467-657-2234	Sequence 2234, Ap
59	85.3	290	11	US-11-096-568A-19698	Sequence 19698, A
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84	82.4	148	11	US-11-096-568A-14957	Sequence 14957, A
85	82.4	151	11	US-11-087-099-10723	Sequence 10723, A
86	82.4	151	11	US-11-188-298-12015	Sequence 12015, A
87	82.4	158	11	US-11-087-099-5996	Sequence 5996, Ap
88	82.4	168	11	US-11-087-099-9205	Sequence 9205, Ap
89	82.4	173	11	US-11-096-568A-28161	Sequence 28161, A
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91	82.4	182	11	US-11-172-740-828	Sequence 21444, A
92	82.4	204	11	US-11-172-740-828	Sequence 828, App
93	82.4	210	11	US-11-172-740-830	Sequence 830, App
94	82.4	210	7	US-09-995-493-116	Sequence 116, App

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98	28	82.4	256	11	US-11-087-099-9614	Sequence 9614, Ap	171	27	79.4	222	11	US-11-096-568A-21404	Sequence 21404, A
99	28	82.4	264	11	US-11-096-568A-6027	Sequence 6027, Ap	172	27	79.4	223	11	US-11-087-099-11386	Sequence 11386, A
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109	28	82.4	319	11	US-11-087-099-2986	Sequence 2986, Ap	182	27	79.4	247	11	US-11-188-298-395	Sequence 395, App
110	28	82.4	319	11	US-11-096-568A-6065	Sequence 6065, Ap	183	27	79.4	247	11	US-11-188-298-2093	Sequence 2093, Ap
111	28	82.4	322	11	US-11-096-568A-7836	Sequence 7836, Ap	184	27	79.4	247	11	US-11-188-298-7734	Sequence 7734, Ap
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115	28	82.4	334	11	US-11-096-568A-16328	Sequence 16328, A	188	27	79.4	250	11	US-11-188-298-4406	Sequence 4406, Ap
116	28	82.4	334	11	US-11-096-568A-20427	Sequence 20427, A	189	27	79.4	251	11	US-11-087-099-1955	Sequence 1955, Ap
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119	28	82.4	340	11	US-11-010-239-54	Sequence 54, Appl	192	27	79.4	252	11	US-11-188-298-2634	Sequence 2634, Ap
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121	28	82.4	341	11	US-11-096-568A-6064	Sequence 6064, Ap	194	27	79.4	255	11	US-11-087-099-11594	Sequence 11594, A
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128	28	82.4	477	9	US-11-045-004-2528	Sequence 2528, Ap	201	27	79.4	259	11	US-11-172-740-947	Sequence 947, App
129	28	82.4	478	9	US-10-873-528-55	Sequence 55, Appl	202	27	79.4	260	11	US-11-188-298-11487	Sequence 11487, A
130	28	82.4	503	11	US-11-079-463-6790	Sequence 6790, Ap	203	27	79.4	263	11	US-11-188-298-11742	Sequence 11742, A
131	28	82.4	532	11	US-11-079-463-9519	Sequence 9519, Ap	204	27	79.4	263	11	US-11-188-298-18802	Sequence 18802, A
132	28	82.4	536	11	US-11-079-463-8209	Sequence 8209, Ap	205	27	79.4	263	11	US-11-188-298-20544	Sequence 20544, A
133	28	82.4	674	11	US-11-072-175-214	Sequence 214, App	206	27	79.4	264	11	US-11-188-298-11993	Sequence 11993, A
134	28	82.4	730	11	US-11-113-424-50	Sequence 50, Appl	207	27	79.4	264	11	US-11-188-298-13762	Sequence 13762, A
135	28	82.4	754	11	US-11-197-133A-18	Sequence 18, Appl	208	27	79.4	265	11	US-11-188-298-3734	Sequence 3734, Ap
136	28	82.4	787	11	US-11-079-463-9004	Sequence 9004, Ap	209	27	79.4	265	11	US-11-087-099-4256	Sequence 4256, Ap
137	28	82.4	1342	9	US-11-188-298-10811	Sequence 10811, A	210	27	79.4	267	11	US-11-096-568A-34068	Sequence 34068, A
138	28	82.4	2333	9	US-10-453-372-170	Sequence 170, App	211	27	79.4	267	11	US-11-188-298-14954	Sequence 14954, A
139	28	82.4	2662	9	US-10-453-372-114	Sequence 114, App	212	27	79.4	268	11	US-11-188-298-17657	Sequence 17657, A
140	28	82.4	2724	9	US-10-453-372-148	Sequence 148, App	213	27	79.4	269	11	US-11-188-298-16857	Sequence 16857, A
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142	28	82.4	2725	11	US-11-100-640-10	Sequence 10, Appl	215	27	79.4	270	11	US-11-188-298-21957	Sequence 21957, A
143	28	82.4	2725	11	US-11-100-640-16	Sequence 16, Appl	216	27	79.4	273	11	US-11-087-099-11050	Sequence 11050, A
144	28	82.4	2733	9	US-10-453-372-136	Sequence 136, App	217	27	79.4	273	11	US-11-188-298-21219	Sequence 21219, A
145	28	82.4	2733	9	US-10-453-372-142	Sequence 142, App	218	27	79.4	274	11	US-11-188-298-17507	Sequence 17507, A
146	28	82.4	2733	9	US-10-453-372-146	Sequence 146, App	219	27	79.4	274	11	US-11-188-298-19272	Sequence 19272, A
147	28	82.4	2733	9	US-10-453-372-150	Sequence 150, App	220	27	79.4	282	11	US-11-096-568A-25745	Sequence 25745, A
148	28	82.4	2733	9	US-10-453-372-154	Sequence 154, App	221	27	79.4	282	11	US-11-188-298-6452	Sequence 6452, Ap
149	28	82.4	2759	9	US-10-453-372-168	Sequence 168, App	222	27	79.4	282	11	US-11-188-298-12037	Sequence 12037, A
150	28	82.4	2765	9	US-10-453-372-116	Sequence 116, App	223	27	79.4	299	11	US-11-096-568A-24511	Sequence 24511, A
151	28	82.4	2769	11	US-11-113-424-14	Sequence 14, Appl	224	27	79.4	309	11	US-11-172-740-2022	Sequence 2022, Ap
152	27	79.4	110	11	US-11-087-099-2500	Sequence 2500, Ap	225	27	79.4	310	11	US-11-172-740-2021	Sequence 2021, Ap
153	27	79.4	110	11	US-11-188-298-2387	Sequence 2387, Ap	226	27	79.4	320	11	US-11-188-298-22463	Sequence 22463, A
154	27	79.4	115	11	US-11-188-298-16510	Sequence 16510, A	227	27	79.4	321	11	US-11-172-740-2023	Sequence 2023, Ap
155	27	79.4	120	11	US-11-087-099-9736	Sequence 9736, Ap	228	27	79.4	328	11	US-11-096-568A-25744	Sequence 25744, A
156	27	79.4	120	11	US-11-188-298-16111	Sequence 16111, A	229	27	79.4	331	11	US-11-096-568A-25820	Sequence 25820, A
157	27	79.4	121	11	US-11-188-298-1016	Sequence 1016, Ap	230	27	79.4	340	11	US-11-087-099-4414	Sequence 4414, Ap
158	27	79.4	129	11	US-11-087-099-6558	Sequence 6558, Ap	231	27	79.4	340	11	US-11-188-298-15084	Sequence 15084, Ap
159	27	79.4	129	11	US-11-087-099-10178	Sequence 10178, A	232	27	79.4	367	11	US-11-087-099-10327	Sequence 10327, A
160	27	79.4	129	11	US-11-188-298-8079	Sequence 8079, Ap	233	27	79.4	375	11	US-11-087-099-1201	Sequence 1201, Ap
161	27	79.4	176	11	US-11-087-099-9107	Sequence 9107, Ap	234	27	79.4	375	11	US-11-188-298-12157	Sequence 12157, A
162	27	79.4	176	11	US-11-188-298-19433	Sequence 19433, A	235	27	79.4	376	11	US-11-079-463-5341	Sequence 5341, Ap
163	27	79.4	188	11	US-11-087-099-8568	Sequence 8568, Ap	236	27	79.4	388	11	US-11-087-099-7526	Sequence 7526, Ap
164	27	79.4	188	11	US-11-188-298-17509	Sequence 17509, A	237	27	79.4	388	11	US-11-188-298-6899	Sequence 6899, Ap
165	27	79.4	192	11	US-11-188-298-19928	Sequence 19928, A	238	27	79.4	402	11	US-11-079-463-6274	Sequence 6274, Ap
166	27	79.4	193	11	US-11-087-099-9617	Sequence 9617, Ap	239	27	79.4	421	11	US-11-087-099-6078	Sequence 6078, Ap
167	27	79.4	216	11	US-11-087-099-12240	Sequence 12240, A	240	27	79.4	421	11	US-11-188-298-5534	Sequence 5534, Ap

241	27	79.4	422	9	US-10-336-263A-4	Sequence 4, Appli	314	26	76.5	390	11	US-11-096-568A-23573	Sequence 23573, A
242	27	79.4	423	9	US-10-336-263A-12	Sequence 12, Appli	315	26	76.5	406	11	US-11-079-463-7078	Sequence 7078, Ap
243	27	79.4	424	9	US-10-336-263A-10	Sequence 10, Appli	316	26	76.5	426	11	US-11-024-959-449	Sequence 449, App
244	27	79.4	425	9	US-10-336-263A-2	Sequence 2, Appli	317	26	76.5	450	11	US-11-079-463-8782	Sequence 8782, A
245	27	79.4	480	9	US-10-336-263A-8	Sequence 8, Appli	318	26	76.5	455	11	US-11-098-686-11372	Sequence 11372, A
246	27	79.4	546	11	US-11-087-099-7160	Sequence 7160, Ap	319	26	76.5	457	11	US-11-087-099-2507	Sequence 2507, Ap
247	27	79.4	548	11	US-11-087-099-1751	Sequence 1750, Ap	320	26	76.5	463	9	US-10-501-411A-341	Sequence 341, Appl
248	27	79.4	553	11	US-11-087-099-6208	Sequence 6208, Ap	321	26	76.5	463	11	US-11-199-821-9	Sequence 9, Appli
249	27	79.4	560	11	US-11-087-099-3291	Sequence 3291, Ap	322	26	76.5	473	11	US-11-096-568A-28409	Sequence 28409, A
250	27	79.4	560	11	US-11-188-298-14097	Sequence 14097, A	323	26	76.5	475	9	US-10-878-556A-115	Sequence 115, App
251	27	79.4	1531	8	US-10-505-928-853	Sequence 853, App	324	26	76.5	477	11	US-11-087-099-2355	Sequence 2355, Ap
252	27	79.4	2358	11	US-11-188-298-18189	Sequence 18189, A	325	26	76.5	480	11	US-11-096-568A-28408	Sequence 28408, A
253	27	79.4	2371	11	US-11-188-298-7516	Sequence 7516, Ap	326	26	76.5	489	9	US-10-467-657-7846	Sequence 7846, Ap
254	27	79.4	3343	11	US-11-122-396-7	Sequence 7, Appli	327	26	76.5	500	11	US-11-188-298-15240	Sequence 15240, A
255	26	76.5	9	9	US-10-530-061-1030	Sequence 1030, Ap	328	26	76.5	505	11	US-11-087-099-11380	Sequence 11380, A
256	26	76.5	13	9	US-10-537-002-116	Sequence 116, App	329	26	76.5	506	11	US-11-087-099-1513	Sequence 1513, Ap
257	26	76.5	24	11	US-11-004-399-1186	Sequence 1186, Ap	330	26	76.5	510	11	US-11-096-568A-28407	Sequence 28407, A
258	26	76.5	32	9	US-10-537-002-137	Sequence 137, App	331	26	76.5	570	11	US-11-143-984A-10	Sequence 10, Appl
259	26	76.5	84	11	US-11-079-463-7680	Sequence 7680, Ap	332	26	76.5	642	11	US-11-073-463-10008	Sequence 10008, A
260	26	76.5	98	11	US-11-079-463-6194	Sequence 6194, Ap	333	26	76.5	703	11	US-11-078-189-13	Sequence 13, Appl
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262	26	76.5	122	11	US-11-177-509-2	Sequence 2, Appli	335	26	76.5	810	11	US-11-188-298-11900	Sequence 11900, A
263	26	76.5	122	11	US-11-177-509-3	Sequence 3, Appli	336	26	76.5	821	11	US-11-045-004-1235	Sequence 1235, Ap
264	26	76.5	122	11	US-11-177-509-4	Sequence 4, Appli	337	26	76.5	841	11	US-11-052-554A-102	Sequence 102, App
265	26	76.5	122	11	US-11-177-509-5	Sequence 5, Appli	338	26	76.5	858	9	US-10-330-773-195	Sequence 195, App
266	26	76.5	122	11	US-11-177-509-6	Sequence 6, Appli	339	26	76.5	870	11	US-11-188-298-3186	Sequence 3186, Ap
267	26	76.5	122	11	US-11-177-509-7	Sequence 7, Appli	340	26	76.5	1147	9	US-10-330-773-190	Sequence 190, App
268	26	76.5	122	11	US-11-177-509-8	Sequence 8, Appli	341	26	76.5	1202	9	US-10-330-773-193	Sequence 193, App
269	26	76.5	148	8	US-10-196-749-362	Sequence 362, App	342	26	76.5	1448	11	US-11-188-298-1954	Sequence 1954, Ap
270	26	76.5	148	9	US-10-512-109-19	Sequence 19, Appl	343	26	76.5	3377	11	US-11-124-367A-271	Sequence 271, App
271	26	76.5	148	9	US-10-194-487-362	Sequence 362, App	344	26	76.5	3488	11	US-11-087-099-9005	Sequence 9005, Ap
272	26	76.5	148	9	US-10-195-883-362	Sequence 362, App	345	26	76.5	3841	11	US-11-124-367A-272	Sequence 272, App
273	26	76.5	148	9	US-10-195-888-362	Sequence 362, App	346	26	76.5	4590	8	US-10-505-928-569	Sequence 569, App
274	26	76.5	148	9	US-10-195-889-362	Sequence 362, App	347	25	73.5	5	11	US-10-850-635-54	Sequence 54, Appl
275	26	76.5	155	9	US-10-793-626-2704	Sequence 2704, Ap	348	25	73.5	5	11	US-11-108-135-1	Sequence 1, Appli
276	26	76.5	181	11	US-11-000-463-409	Sequence 409, App	349	25	73.5	5	11	US-11-126-978-1	Sequence 1, Appli
277	26	76.5	219	11	US-11-188-298-16448	Sequence 16448, A	350	25	73.5	5	11	US-11-157-494-3	Sequence 3, Appli
278	26	76.5	221	7	US-09-978-360A-436	Sequence 436, App	351	25	73.5	14	11	US-11-167-872-61	Sequence 61, Appl
279	26	76.5	222	11	US-11-188-298-20436	Sequence 20436, A	352	25	73.5	15	11	US-11-157-494-4	Sequence 4, Appli
280	26	76.5	234	11	US-11-096-568A-22183	Sequence 22183, A	353	25	73.5	16	9	US-10-895-064-2650	Sequence 2650, Ap
281	26	76.5	236	11	US-11-156-084-284	Sequence 284, App	354	25	73.5	16	11	US-11-129-741-2650	Sequence 2650, Ap
282	26	76.5	261	8	US-10-196-749-356	Sequence 356, App	355	25	73.5	17	9	US-10-834-397-239	Sequence 239, App
283	26	76.5	261	9	US-10-663-703-118	Sequence 118, App	356	25	73.5	50	11	US-11-096-568A-8249	Sequence 8249, Ap
284	26	76.5	261	9	US-10-537-002-16	Sequence 16, Appl	357	25	73.5	59	11	US-11-264-096-303	Sequence 303, App
285	26	76.5	261	9	US-10-537-002-118	Sequence 118, App	358	25	73.5	92	11	US-11-079-463-7313	Sequence 7313, Ap
286	26	76.5	261	9	US-10-194-487-356	Sequence 356, App	359	25	73.5	97	11	US-11-093-274-35	Sequence 35, Appl
287	26	76.5	261	9	US-10-195-883-356	Sequence 356, App	360	25	73.5	98	11	US-11-054-669-15	Sequence 15, Appl
288	26	76.5	261	9	US-10-195-888-356	Sequence 356, App	361	25	73.5	98	11	US-11-084-554-44	Sequence 44, Appl
289	26	76.5	261	9	US-10-195-889-356	Sequence 356, App	362	25	73.5	98	11	US-11-004-590-14	Sequence 14, Appl
290	26	76.5	261	11	US-11-102-240-118	Sequence 118, App	363	25	73.5	98	11	US-11-136-250-44	Sequence 44, Appl
291	26	76.5	261	11	US-11-103-195-118	Sequence 118, App	364	25	73.5	110	11	US-11-096-568A-30894	Sequence 30894, A
292	26	76.5	261	11	US-11-264-096-1827	Sequence 1827, Ap	365	25	73.5	111	11	US-11-096-568A-2062	Sequence 2062, Ap
293	26	76.5	261	11	US-11-264-096-1828	Sequence 1828, Ap	366	25	73.5	114	11	US-11-096-568A-26324	Sequence 26324, A
294	26	76.5	264	9	US-10-467-657-6940	Sequence 6940, Ap	367	25	73.5	117	11	US-11-072-532-3312	Sequence 3312, Ap
295	26	76.5	275	11	US-11-045-004-11750	Sequence 1750, Ap	368	25	73.5	117	11	US-11-157-494-27	Sequence 27, Appl
296	26	76.5	275	9	US-10-469-469-118	Sequence 118, App	369	25	73.5	117	11	US-11-157-494-28	Sequence 28, Appl
297	26	76.5	286	9	US-10-467-657-4140	Sequence 4140, Ap	370	25	73.5	119	9	US-10-507-662-27	Sequence 27, Appl
298	26	76.5	286	9	US-10-467-657-7784	Sequence 7784, Ap	371	25	73.5	119	9	US-10-507-662-28	Sequence 28, Appl
299	26	76.5	290	9	US-10-793-626-758	Sequence 758, App	372	25	73.5	119	11	US-11-112-481C-9	Sequence 9, Appli
300	26	76.5	293	11	US-11-096-568A-5733	Sequence 5733, Ap	373	25	73.5	120	9	US-10-956-008-62	Sequence 62, Appl
301	26	76.5	313	11	US-11-096-568A-22182	Sequence 22182, A	374	25	73.5	120	9	US-10-956-008-78	Sequence 78, Appl
302	26	76.5	322	11	US-11-087-099-6568	Sequence 6568, Ap	375	25	73.5	121	11	US-11-108-135-24	Sequence 24, Appl
303	26	76.5	327	11	US-11-152-811-5	Sequence 5, Appli	376	25	73.5	121	11	US-11-108-135-28	Sequence 28, Appl
304	26	76.5	330	11	US-11-098-686-10903	Sequence 10903, A	377	25	73.5	121	11	US-11-126-978-24	Sequence 24, Appl
305	26	76.5	333	11	US-11-087-099-1308	Sequence 1308, Ap	378	25	73.5	121	11	US-11-126-978-28	Sequence 28, Appl
306	26	76.5	333	11	US-11-087-099-4388	Sequence 4388, Ap	379	25	73.5	129	8	US-10-542-038-18	Sequence 18, Appl
307	26	76.5	333	11	US-11-087-099-8052	Sequence 8052, A	380	25	73.5	129	9	US-10-850-635-12	Sequence 12, Appl
308	26	76.5	333	11	US-11-087-099-10608	Sequence 10608, A	381	25	73.5	132	11	US-11-045-004-570	Sequence 570, App
309	26	76.5	335	11	US-11-087-099-429	Sequence 429, App	382	25	73.5	146	9	US-10-793-626-34	Sequence 34, Appl
310	26	76.5	338	11	US-11-096-568A-16519	Sequence 16519, A	383	25	73.5	148	8	US-10-542-038-6	Sequence 6, Appli
311	26	76.5	342	11	US-11-087-099-6256	Sequence 6256, Ap	384	25	73.5	148	11	US-11-220-372-307	Sequence 307, App
312	26	76.5	343	11	US-11-087-099-10578	Sequence 10578, A	385	25	73.5	156	9	US-10-504-879-38	Sequence 38, Appl
313	26	76.5	352	11	US-11-087-099-8255	Sequence 8255, Ap	386	25	73.5	161	11	US-11-096-568A-4949	Sequence 4949, Ap

387	25	73.5	171	11	US-11-096-568A-1481	Sequence 1481, Ap	460	25	73.5	381	11	US-11-072-512-3313	Sequence 3313, Ap
388	25	73.5	200	11	US-11-096-568A-30893	Sequence 30893, A	461	25	73.5	399	11	US-11-079-463-8800	Sequence 8800, Ap
389	25	73.5	201	11	US-11-096-568A-4948	Sequence 4948, Ap	462	25	73.5	401	9	US-10-131-826A-486	Sequence 486, App
390	25	73.5	202	9	US-10-714-887-244	Sequence 244, App	463	25	73.5	401	9	US-10-973-115B-486	Sequence 486, App
391	25	73.5	208	11	US-11-096-568A-4947	Sequence 4947, Ap	464	25	73.5	401	9	US-10-137-873A-486	Sequence 486, App
392	25	73.5	208	11	US-11-096-568A-33688	Sequence 33688, A	465	25	73.5	401	9	US-10-152-370-486	Sequence 486, App
393	25	73.5	214	11	US-11-087-099-9374	Sequence 9374, Ap	466	25	73.5	401	9	US-10-152-370-486	Sequence 486, App
394	25	73.5	225	11	US-11-096-568A-1480	Sequence 1480, Ap	467	25	73.5	401	11	US-11-290-153-486	Sequence 486, App
395	25	73.5	235	11	US-11-096-568A-1479	Sequence 1479, Ap	468	25	73.5	401	11	US-11-290-153-486	Sequence 486, App
396	25	73.5	239	11	US-11-096-568A-4422	Sequence 4422, Ap	469	25	73.5	405	9	US-10-793-626-2962	Sequence 2962, Ap
397	25	73.5	241	11	US-11-054-515-1889	Sequence 1889, Ap	470	25	73.5	422	11	US-11-229-769-357	Sequence 357, App
398	25	73.5	241	11	US-11-266-444-1889	Sequence 1889, Ap	471	25	73.5	425	11	US-11-198-886-17	Sequence 17, Appl
399	25	73.5	243	11	US-11-096-568A-4421	Sequence 4421, Ap	472	25	73.5	432	11	US-11-103-957-5	Sequence 5, Appl
400	25	73.5	247	11	US-11-054-515-1470	Sequence 1470, Ap	473	25	73.5	432	11	US-11-018-868-34	Sequence 34, Appl
401	25	73.5	247	11	US-11-266-444-1470	Sequence 1470, Ap	474	25	73.5	443	11	US-11-079-463-5307	Sequence 5307, Ap
402	25	73.5	248	11	US-11-054-515-1963	Sequence 1963, Ap	475	25	73.5	452	11	US-11-198-886-21	Sequence 21, Appl
403	25	73.5	248	11	US-11-054-515-1976	Sequence 1976, Ap	476	25	73.5	453	11	US-11-087-099-6300	Sequence 6300, Ap
404	25	73.5	248	11	US-11-054-515-1995	Sequence 1995, Ap	477	25	73.5	453	11	US-11-188-298-16793	Sequence 16793, A
405	25	73.5	248	11	US-11-054-515-2000	Sequence 2000, Ap	478	25	73.5	456	11	US-11-087-099-3798	Sequence 3798, Ap
406	25	73.5	248	11	US-11-054-515-2070	Sequence 2070, Ap	479	25	73.5	456	11	US-11-087-099-6259	Sequence 6259, Ap
407	25	73.5	248	11	US-11-266-444-1963	Sequence 1963, Ap	480	25	73.5	456	11	US-11-087-099-9642	Sequence 9642, Ap
408	25	73.5	248	11	US-11-266-444-1976	Sequence 1976, Ap	481	25	73.5	456	11	US-11-188-298-14550	Sequence 14550, A
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410	25	73.5	248	11	US-11-266-444-2000	Sequence 2000, Ap	483	25	73.5	457	11	US-11-087-099-5321	Sequence 5321, Ap
411	25	73.5	248	11	US-11-266-444-2070	Sequence 2070, Ap	484	25	73.5	457	11	US-11-087-099-5761	Sequence 5761, Ap
412	25	73.5	251	11	US-11-054-515-943	Sequence 943, App	485	25	73.5	457	11	US-11-087-099-9118	Sequence 9118, Ap
413	25	73.5	251	11	US-11-054-515-949	Sequence 949, App	486	25	73.5	457	11	US-11-087-099-10468	Sequence 10468, A
414	25	73.5	251	11	US-11-054-515-1594	Sequence 1594, Ap	487	25	73.5	457	11	US-11-087-099-11070	Sequence 11070, A
415	25	73.5	251	11	US-11-054-515-3245	Sequence 3245, Ap	488	25	73.5	457	11	US-11-188-298-4860	Sequence 4860, Ap
416	25	73.5	251	11	US-11-266-444-943	Sequence 943, App	489	25	73.5	457	11	US-11-188-298-8450	Sequence 8450, Ap
417	25	73.5	251	11	US-11-266-444-949	Sequence 949, App	490	25	73.5	457	11	US-11-188-298-10221	Sequence 10221, A
418	25	73.5	251	11	US-11-266-444-1594	Sequence 1594, Ap	491	25	73.5	457	11	US-11-188-298-16296	Sequence 16296, A
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421	25	73.5	260	11	US-11-079-463-9790	Sequence 9790, Ap	494	25	73.5	458	11	US-11-087-099-6929	Sequence 6929, Ap
422	25	73.5	269	9	US-10-506-454-1211	Sequence 1211, Ap	495	25	73.5	458	11	US-11-087-099-10120	Sequence 10120, A
423	25	73.5	283	9	US-10-218-784-44	Sequence 44, Appl	496	25	73.5	458	11	US-11-188-298-3061	Sequence 3061, A
424	25	73.5	283	9	US-10-219-061-44	Sequence 44, Appl	497	25	73.5	458	11	US-11-188-298-9326	Sequence 9326, Ap
425	25	73.5	283	9	US-10-219-062-44	Sequence 44, Appl	498	25	73.5	458	11	US-11-188-298-9366	Sequence 9366, A
426	25	73.5	283	9	US-10-219-064-44	Sequence 44, Appl	499	25	73.5	459	11	US-11-087-099-8941	Sequence 8941, Ap
427	25	73.5	283	9	US-10-233-134-44	Sequence 44, Appl	500	25	73.5	459	11	US-11-087-099-8941	Sequence 8941, Ap
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429	25	73.5	294	11	US-11-096-568A-33687	Sequence 33687, A	502	25	73.5	460	11	US-11-087-099-3691	Sequence 3691, A
430	25	73.5	295	11	US-11-079-463-6257	Sequence 6257, Ap	503	25	73.5	461	11	US-11-188-298-14458	Sequence 14458, A
431	25	73.5	312	11	US-11-245-053-10	Sequence 10, Appl	504	25	73.5	462	11	US-11-087-099-7509	Sequence 7509, Ap
432	25	73.5	312	11	US-11-297-327-10	Sequence 10, Appl	505	25	73.5	462	11	US-11-188-298-17974	Sequence 17974, A
433	25	73.5	312	11	US-11-297-328-10	Sequence 10, Appl	506	25	73.5	464	9	US-10-506-454-442	Sequence 442, App
434	25	73.5	328	11	US-11-098-686-10582	Sequence 10582, A	507	25	73.5	464	11	US-11-087-099-10721	Sequence 10721, A
435	25	73.5	333	11	US-11-229-371-72	Sequence 72, Appl	508	25	73.5	464	11	US-11-087-099-11033	Sequence 11033, A
436	25	73.5	333	11	US-11-228-923-72	Sequence 72, Appl	509	25	73.5	464	11	US-11-188-298-1979	Sequence 1979, Ap
437	25	73.5	333	11	US-11-228-875-72	Sequence 72, Appl	510	25	73.5	464	11	US-11-198-886-2	Sequence 2, Appl
438	25	73.5	333	11	US-11-087-099-4452	Sequence 4452, Ap	511	25	73.5	465	11	US-11-087-099-1964	Sequence 1964, Ap
439	25	73.5	346	11	US-11-229-371-76	Sequence 76, Appl	512	25	73.5	465	11	US-11-087-099-8665	Sequence 8665, Ap
440	25	73.5	346	11	US-11-228-923-76	Sequence 76, Appl	513	25	73.5	465	11	US-11-188-298-1940	Sequence 1940, Ap
441	25	73.5	346	11	US-11-228-875-76	Sequence 76, Appl	514	25	73.5	465	11	US-11-188-298-19056	Sequence 19056, A
442	25	73.5	346	11	US-11-087-099-11847	Sequence 11847, A	515	25	73.5	466	11	US-11-087-099-8259	Sequence 8259, Ap
443	25	73.5	347	11	US-11-229-371-39	Sequence 39, Appl	516	25	73.5	466	11	US-11-188-298-18632	Sequence 18632, A
444	25	73.5	347	11	US-11-228-923-39	Sequence 39, Appl	517	25	73.5	467	11	US-11-087-099-585	Sequence 585, App
445	25	73.5	347	11	US-11-228-875-39	Sequence 39, Appl	518	25	73.5	467	11	US-11-188-298-9406	Sequence 9406, Ap
446	25	73.5	356	11	US-11-045-004-2735	Sequence 2735, Ap	519	25	73.5	469	11	US-11-087-099-10242	Sequence 10242, A
447	25	73.5	356	11	US-11-188-298-6735	Sequence 6735, Ap	520	25	73.5	469	11	US-11-188-298-2971	Sequence 2971, Ap
448	25	73.5	357	11	US-11-188-298-19416	Sequence 19416, A	521	25	73.5	469	11	US-11-188-298-9435	Sequence 9435, Ap
449	25	73.5	358	11	US-11-229-371-77	Sequence 77, Appl	522	25	73.5	470	11	US-11-087-099-3614	Sequence 3614, Ap
450	25	73.5	358	11	US-11-228-923-77	Sequence 77, Appl	523	25	73.5	470	11	US-11-087-099-3723	Sequence 3723, Ap
451	25	73.5	358	11	US-11-228-875-77	Sequence 77, Appl	524	25	73.5	470	11	US-11-087-099-7603	Sequence 7603, Ap
452	25	73.5	358	11	US-11-079-463-7399	Sequence 7399, Ap	525	25	73.5	470	11	US-11-188-298-6972	Sequence 6972, Ap
453	25	73.5	358	11	US-11-079-463-9439	Sequence 9439, A	526	25	73.5	470	11	US-11-188-298-14390	Sequence 14390, A
454	25	73.5	361	11	US-11-087-099-11472	Sequence 11472, A	527	25	73.5	470	11	US-11-188-298-14487	Sequence 14487, A
455	25	73.5	362	11	US-11-087-099-9198	Sequence 9198, Ap	528	25	73.5	471	11	US-11-045-004-1047	Sequence 1047, Ap
456	25	73.5	368	11	US-11-053-185-12	Sequence 12, Appl	529	25	73.5	472	9	US-10-454-437-130	Sequence 130, App
457	25	73.5	376	8	US-10-505-928-77	Sequence 77, Appl	530	25	73.5	472	9	US-10-454-437-132	Sequence 132, App
458	25	73.5	376	9	US-10-517-939-102	Sequence 102, App	531	25	73.5	472	11	US-11-087-099-8780	Sequence 8780, Ap
459	25	73.5	379	11	US-11-096-568A-33686	Sequence 33686, A	532	25	73.5	472	11	US-11-188-298-8153	Sequence 8153, Ap

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534	25	73.5	473	11	US-11-198-886-4	Sequence 4, Appl	607	25	73.5	574	9	US-10-527-771-14	Sequence 14, Appl
535	25	73.5	473	11	US-11-198-886-19	Sequence 19, Appl	608	25	73.5	582	11	US-11-188-298-16519	Sequence 16519, A
536	25	73.5	475	11	US-11-087-099-6187	Sequence 1267, Ap	609	25	73.5	584	11	US-11-188-298-20486	Sequence 20486, A
537	25	73.5	475	11	US-11-188-298-1267	Sequence 1267, Ap	610	25	73.5	588	9	US-10-469-469-95	Sequence 95, Appl
538	25	73.5	478	11	US-11-087-099-8625	Sequence 8625, Ap	611	25	73.5	591	11	US-11-079-463-9402	Sequence 9402, Ap
539	25	73.5	478	11	US-11-188-298-19025	Sequence 19025, A	612	25	73.5	594	9	US-10-504-879-24	Sequence 24, Appl
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541	25	73.5	479	11	US-11-188-298-17131	Sequence 17131, A	614	25	73.5	599	11	US-11-079-463-7000	Sequence 7000, Ap
542	25	73.5	483	11	US-11-037-243-79	Sequence 79, Appl	615	25	73.5	601	11	US-11-188-298-13213	Sequence 13213, A
543	25	73.5	485	11	US-11-079-463-9299	Sequence 9299, Ap	616	25	73.5	608	11	US-11-079-463-7066	Sequence 7066, Ap
544	25	73.5	486	11	US-11-045-004-686	Sequence 686, App	617	25	73.5	610	11	US-11-188-298-19318	Sequence 19318, A
545	25	73.5	490	9	US-10-506-454-1010	Sequence 1010, Ap	618	25	73.5	611	9	US-10-504-879-4	Sequence 4, Appl
546	25	73.5	490	11	US-11-087-099-9461	Sequence 9461, Ap	619	25	73.5	618	9	US-10-504-879-22	Sequence 22, Appl
547	25	73.5	490	11	US-11-188-298-16824	Sequence 16824, A	620	25	73.5	619	9	US-10-537-002-102	Sequence 102, App
548	25	73.5	491	8	US-10-511-937-2973	Sequence 2973, Ap	621	25	73.5	620	8	US-10-511-937-2959	Sequence 2959, Ap
549	25	73.5	491	11	US-11-053-185-22	Sequence 22, Appl	622	25	73.5	630	9	US-10-504-879-26	Sequence 26, Appl
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552	25	73.5	491	11	US-11-087-099-11329	Sequence 11329, A	625	25	73.5	679	11	US-11-202-507A-5	Sequence 5, Appl
553	25	73.5	493	9	US-10-131-826A-268	Sequence 268, App	626	25	73.5	680	9	US-10-467-657-7612	Sequence 7612, Ap
554	25	73.5	493	9	US-10-973-1158-268	Sequence 268, App	627	25	73.5	693	11	US-11-167-856-2	Sequence 2, Appl
555	25	73.5	493	9	US-10-137-873A-268	Sequence 268, App	628	25	73.5	708	11	US-11-078-189-10	Sequence 10, Appl
556	25	73.5	493	9	US-10-152-370-268	Sequence 268, App	629	25	73.5	716	9	US-10-467-657-8370	Sequence 8370, Appl
557	25	73.5	493	11	US-11-067-121-10	Sequence 10, Appl	630	25	73.5	724	11	US-11-103-156-19	Sequence 19, Appl
558	25	73.5	493	11	US-11-067-121-20	Sequence 20, Appl	631	25	73.5	736	11	US-11-079-463-7425	Sequence 7425, Ap
559	25	73.5	493	11	US-11-087-099-2821	Sequence 2821, Ap	632	25	73.5	752	9	US-10-469-469-93	Sequence 93, Appl
560	25	73.5	493	11	US-11-087-099-9453	Sequence 9453, Ap	633	25	73.5	754	11	US-11-188-298-4080	Sequence 4080, Ap
561	25	73.5	493	11	US-11-188-298-13708	Sequence 13708, A	634	25	73.5	754	11	US-11-188-298-9686	Sequence 9686, Ap
562	25	73.5	493	11	US-11-290-153-268	Sequence 268, App	635	25	73.5	754	11	US-11-188-298-17425	Sequence 17425, A
563	25	73.5	495	11	US-11-087-099-11237	Sequence 11237, A	636	25	73.5	754	11	US-11-188-298-19237	Sequence 19237, A
564	25	73.5	495	11	US-11-188-298-21368	Sequence 21368, A	637	25	73.5	755	11	US-11-188-298-8373	Sequence 8373, Ap
565	25	73.5	509	9	US-10-506-454-1303	Sequence 1303, Ap	638	25	73.5	766	11	US-11-188-298-14671	Sequence 14671, A
566	25	73.5	513	9	US-10-131-826A-192	Sequence 192, App	639	25	73.5	801	11	US-11-264-096-2229	Sequence 2229, Ap
567	25	73.5	513	9	US-10-995-561-566	Sequence 566, App	640	25	73.5	801	11	US-11-079-463-5791	Sequence 5791, Ap
568	25	73.5	513	9	US-10-973-1158-192	Sequence 192, App	641	25	73.5	809	11	US-11-072-532-3367	Sequence 3367, Ap
569	25	73.5	513	9	US-10-137-873A-192	Sequence 192, App	642	25	73.5	826	9	US-10-878-556A-68	Sequence 68, Appl
570	25	73.5	513	9	US-10-152-370-192	Sequence 192, App	643	25	73.5	827	9	US-10-534-894-2	Sequence 2, Appl
571	25	73.5	513	11	US-11-290-153-192	Sequence 192, App	644	25	73.5	843	11	US-11-188-298-14395	Sequence 14395, A
572	25	73.5	515	11	US-11-087-099-10971	Sequence 10971, A	645	25	73.5	845	11	US-11-188-298-14852	Sequence 14852, A
573	25	73.5	515	11	US-11-188-298-10142	Sequence 10142, A	646	25	73.5	915	11	US-11-156-084-119	Sequence 119, App
574	25	73.5	518	11	US-11-096-568A-30180	Sequence 30180, A	647	25	73.5	921	9	US-10-880-144-2	Sequence 2, Appl
575	25	73.5	519	11	US-11-079-463-6278	Sequence 6278, Ap	648	25	73.5	961	11	US-11-079-463-7024	Sequence 7024, Ap
576	25	73.5	521	11	US-11-087-099-5589	Sequence 5589, Ap	649	25	73.5	989	11	US-11-096-568A-29282	Sequence 29282, A
577	25	73.5	521	11	US-11-188-298-5101	Sequence 5101, Ap	650	25	73.5	1011	11	US-11-188-298-8943	Sequence 8943, Ap
578	25	73.5	523	11	US-11-087-099-11192	Sequence 1192, Ap	651	25	73.5	1022	11	US-11-156-084-118	Sequence 118, App
579	25	73.5	523	11	US-11-087-099-8662	Sequence 8662, Ap	652	25	73.5	1063	11	US-11-096-568A-29281	Sequence 29281, A
580	25	73.5	523	11	US-11-188-298-8049	Sequence 8049, Ap	653	25	73.5	1065	11	US-11-188-298-8767	Sequence 8767, Ap
581	25	73.5	524	11	US-11-188-298-12140	Sequence 12140, A	654	25	73.5	1070	9	US-10-537-002-14	Sequence 14, Appl
582	25	73.5	524	11	US-11-087-099-9289	Sequence 9289, Ap	655	25	73.5	1073	9	US-10-537-002-11	Sequence 11, Appl
583	25	73.5	524	11	US-11-188-298-8620	Sequence 8620, Ap	656	25	73.5	1155	9	US-10-793-626-1780	Sequence 1780, Ap
584	25	73.5	524	11	US-11-188-298-19642	Sequence 19642, A	657	25	73.5	1184	11	US-11-096-568A-29280	Sequence 29280, A
585	25	73.5	527	9	US-10-886-504-7	Sequence 7, Appl	658	25	73.5	1210	11	US-11-108-172-692	Sequence 692, App
586	25	73.5	527	9	US-10-886-504-8	Sequence 8, Appl	659	25	73.5	1440	11	US-11-096-568A-28130	Sequence 28130, A
587	25	73.5	527	9	US-10-886-504-9	Sequence 9, Appl	660	25	73.5	1441	11	US-11-096-568A-28129	Sequence 28129, A
588	25	73.5	527	9	US-10-886-504-10	Sequence 10, Appl	661	25	73.5	1490	11	US-11-096-568A-28128	Sequence 28128, A
589	25	73.5	527	9	US-10-886-505-7	Sequence 7, Appl	662	25	73.5	1548	11	US-11-108-172-1095	Sequence 1095, Ap
590	25	73.5	527	9	US-10-886-505-8	Sequence 8, Appl	663	25	73.5	2204	11	US-11-052-554A-174	Sequence 174, App
591	25	73.5	527	9	US-10-886-505-9	Sequence 9, Appl	664	25	73.5	4868	11	US-11-044-111-24	Sequence 24, Appl
592	25	73.5	527	9	US-10-886-505-10	Sequence 10, Appl	665	25	73.5	7102	11	US-11-143-980-48	Sequence 48, Appl
593	25	73.5	527	9	US-10-886-527-7	Sequence 7, Appl	666	24	70.6	5	9	US-10-932-334-1	Sequence 1, Appl
594	25	73.5	527	9	US-10-886-527-8	Sequence 8, Appl	667	24	70.6	5	9	US-10-982-357-15	Sequence 15, Appl
595	25	73.5	527	9	US-10-886-527-9	Sequence 9, Appl	668	24	70.6	5	9	US-10-982-357-21	Sequence 21, Appl
596	25	73.5	527	9	US-10-886-527-10	Sequence 10, Appl	669	24	70.6	5	9	US-10-982-357-30	Sequence 30, Appl
597	25	73.5	527	9	US-10-947-612-7	Sequence 7, Appl	670	24	70.6	5	11	US-11-173-071-5	Sequence 5, Appl
598	25	73.5	527	9	US-10-947-612-8	Sequence 8, Appl	671	24	70.6	5	11	US-11-069-834-4	Sequence 4, Appl
599	25	73.5	527	9	US-10-947-612-9	Sequence 9, Appl	672	24	70.6	5	11	US-11-177-648-1	Sequence 1, Appl
600	25	73.5	527	9	US-10-947-612-10	Sequence 10, Appl	673	24	70.6	8	11	US-11-152-747-43	Sequence 43, Appl
601	25	73.5	548	9	US-10-886-504-11	Sequence 11, Appl	674	24	70.6	10	9	US-10-932-334-53	Sequence 53, Appl
602	25	73.5	548	9	US-10-886-505-11	Sequence 11, Appl	675	24	70.6	10	9	US-10-982-357-17	Sequence 17, Appl
603	25	73.5	548	9	US-10-886-527-11	Sequence 11, Appl	676	24	70.6	10	9	US-10-982-357-32	Sequence 32, Appl
604	25	73.5	548	9	US-10-947-612-11	Sequence 11, Appl	677	24	70.6	10	10	US-11-219-121-4	Sequence 4, Appl
605	25	73.5	554	11	US-11-087-099-8925	Sequence 8925, Ap	678	24	70.6	10	11	US-11-171-567-147	Sequence 147, App

679	24	70.6	13	9	US-10-929-988-459	Sequence 459, App	752	24	70.6	113	11	US-11-087-099-9784	Sequence 9784, Ap
680	24	70.6	13	11	US-11-005-726-100	Sequence 100, App	753	24	70.6	113	11	US-11-087-099-11100	Sequence 11100, A
681	24	70.6	13	11	US-11-005-726-101	Sequence 101, App	754	24	70.6	113	11	US-11-087-099-11748	Sequence 11748, A
682	24	70.6	13	11	US-11-005-726-102	Sequence 102, App	755	24	70.6	113	11	US-11-188-298-4321	Sequence 4321, Ap
683	24	70.6	13	11	US-11-005-726-103	Sequence 103, App	756	24	70.6	113	11	US-11-188-298-6727	Sequence 6727, Ap
684	24	70.6	14	11	US-11-167-872-49	Sequence 49, Appl	757	24	70.6	113	11	US-11-188-298-12649	Sequence 12649, A
685	24	70.6	16	9	US-10-895-064-2405	Sequence 2405, Ap	758	24	70.6	114	9	US-10-763-712A-51	Sequence 51, Appl
686	24	70.6	16	11	US-11-054-515-2166	Sequence 2166, Ap	759	24	70.6	114	11	US-11-079-463-6516	Sequence 6516, Ap
687	24	70.6	16	11	US-11-054-515-2746	Sequence 2746, Ap	760	24	70.6	116	11	US-11-055-163-17	Sequence 17, Appl
688	24	70.6	16	11	US-11-054-515-2950	Sequence 2950, Ap	761	24	70.6	116	11	US-11-051-453-3	Sequence 3, Appli
689	24	70.6	16	11	US-11-129-741-2405	Sequence 2405, Ap	762	24	70.6	116	11	US-11-120-308-4	Sequence 4, Appli
690	24	70.6	16	11	US-11-152-974A-231	Sequence 231, App	763	24	70.6	116	11	US-11-188-298-22357	Sequence 22357, A
691	24	70.6	16	11	US-11-153-143A-231	Sequence 231, App	764	24	70.6	117	10	US-11-219-121-11	Sequence 11, Appl
692	24	70.6	16	11	US-11-266-444-2166	Sequence 2166, Ap	765	24	70.6	117	10	US-11-219-121-26	Sequence 26, Appl
693	24	70.6	16	11	US-11-266-444-2746	Sequence 2746, Ap	766	24	70.6	117	11	US-11-097-812-23	Sequence 23, Appl
694	24	70.6	16	11	US-11-266-444-2950	Sequence 2950, Ap	767	24	70.6	117	11	US-11-097-812-29	Sequence 29, Appl
695	24	70.6	20	9	US-10-939-890-167	Sequence 167, App	768	24	70.6	117	11	US-11-057-812-33	Sequence 33, Appl
696	24	70.6	29	9	US-10-895-064-232	Sequence 232, App	769	24	70.6	117	11	US-11-149-943-61	Sequence 61, Appl
697	24	70.6	29	11	US-11-129-741-232	Sequence 232, App	770	24	70.6	117	11	US-11-004-590-119	Sequence 119, App
698	24	70.6	29	11	US-11-129-741-3164	Sequence 3164, Ap	771	24	70.6	117	11	US-11-004-590-121	Sequence 121, App
699	24	70.6	53	11	US-11-144-630-39	Sequence 39, Appl	772	24	70.6	117	11	US-11-004-590-161	Sequence 161, App
700	24	70.6	53	11	US-11-235-009-10	Sequence 10, Appl	773	24	70.6	117	11	US-11-004-590-162	Sequence 162, App
701	24	70.6	55	9	US-10-517-696-109	Sequence 109, App	774	24	70.6	117	11	US-11-004-590-163	Sequence 163, App
702	24	70.6	57	11	US-10-074-176-292	Sequence 292, App	775	24	70.6	117	11	US-11-004-590-164	Sequence 164, App
703	24	70.6	60	9	US-10-475-075-793	Sequence 793, App	776	24	70.6	117	11	US-11-004-590-165	Sequence 165, App
704	24	70.6	62	11	US-11-096-568A-1387	Sequence 1387, Ap	777	24	70.6	117	11	US-11-004-590-166	Sequence 166, App
705	24	70.6	64	11	US-11-079-463-7910	Sequence 7910, Ap	778	24	70.6	117	11	US-11-004-590-167	Sequence 167, App
706	24	70.6	65	11	US-11-124-368A-334	Sequence 334, App	779	24	70.6	117	11	US-11-004-590-168	Sequence 168, App
707	24	70.6	65	11	US-11-096-568A-552	Sequence 552, App	780	24	70.6	117	11	US-11-004-590-169	Sequence 169, App
708	24	70.6	69	11	US-11-096-568A-4369	Sequence 4369, Ap	781	24	70.6	117	11	US-11-004-590-170	Sequence 170, App
709	24	70.6	72	11	US-11-116-881A-532	Sequence 532, App	782	24	70.6	117	11	US-11-004-590-171	Sequence 171, App
710	24	70.6	76	11	US-11-079-463-9470	Sequence 9470, Ap	783	24	70.6	117	11	US-11-004-590-172	Sequence 172, App
711	24	70.6	78	11	US-11-120-308-50	Sequence 50, Appl	784	24	70.6	117	11	US-11-004-590-173	Sequence 173, App
712	24	70.6	81	11	US-11-079-463-9412	Sequence 9412, Ap	785	24	70.6	117	11	US-11-004-590-174	Sequence 174, App
713	24	70.6	85	9	US-10-201-060-32	Sequence 32, Appl	786	24	70.6	117	11	US-11-004-590-175	Sequence 175, App
714	24	70.6	93	11	US-11-096-568A-551	Sequence 551, App	787	24	70.6	117	11	US-11-004-590-176	Sequence 176, App
715	24	70.6	98	9	US-10-932-334-57	Sequence 57, Appl	788	24	70.6	117	11	US-11-004-590-177	Sequence 177, App
716	24	70.6	98	11	US-11-054-669-33	Sequence 33, Appl	789	24	70.6	117	11	US-11-004-590-178	Sequence 178, App
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722	24	70.6	106	11	US-11-087-099-8467	Sequence 8467, Ap	795	24	70.6	117	11	US-11-004-590-184	Sequence 184, App
723	24	70.6	107	11	US-11-072-512-2000	Sequence 2000, Ap	796	24	70.6	117	11	US-11-004-590-185	Sequence 185, App
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725	24	70.6	111	11	US-11-097-812-20	Sequence 20, Appl	798	24	70.6	117	11	US-11-004-590-187	Sequence 187, App
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732	24	70.6	111	11	US-11-097-812-205	Sequence 205, App	805	24	70.6	117	11	US-11-004-590-194	Sequence 194, App
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826	24	70.6	117	11	US-11-004-590-215	Sequence 215, App	899	24	70.6	134	11	US-11-120-308-20	Sequence 20, Appl
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828	24	70.6	117	11	US-11-004-590-217	Sequence 217, App	901	24	70.6	135	11	US-11-172-740-1489	Sequence 1489, Ap
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838	24	70.6	119	9	US-10-982-357-5	Sequence 5, Appl	911	24	70.6	139	11	US-11-172-740-1487	Sequence 1487, Ap
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893	24	70.6	131	9	US-10-201-060-27	Sequence 27, Appl	967	24	70.6	176	9	US-10-195-883-392	Sequence 392, App
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971 24 70.6 176 11 US-11-102-240-146 Sequence 146, App
972 24 70.6 176 11 US-11-103-195-146 Sequence 146, App
973 24 70.6 178 9 US-10-467-657-2108 Sequence 2108, Ap
974 24 70.6 181 11 US-11-087-099-10479 Sequence 10479, A
975 24 70.6 181 11 US-11-096-568A-14659 Sequence 14659, A
976 24 70.6 182 9 US-10-793-626-2414 Sequence 2414, Ap
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979 24 70.6 187 11 US-11-087-099-6173 Sequence 6173, Ap
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989 24 70.6 194 8 US-10-542-038-8 Sequence 8, Appli
990 24 70.6 194 11 US-11-220-372-304 Sequence 304, App
991 24 70.6 194 11 US-11-220-372-305 Sequence 305, App
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993 24 70.6 195 11 US-11-087-099-7718 Sequence 7718, Ap
994 24 70.6 198 11 US-11-087-099-6365 Sequence 6365, Ap
995 24 70.6 198 11 US-11-096-568A-20312 Sequence 20312, A
996 24 70.6 201 9 US-10-454-437-438 Sequence 438, App
997 24 70.6 203 11 US-11-096-568A-20311 Sequence 20311, A
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999 24 70.6 204 11 US-11-045-004-2093 Sequence 2093, Ap
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ALIGNMENTS

RESULT 1

US-11-054-515-974
; Sequence 974, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 974

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-974

Query Match 100.0%; Score 34; DB 11; Length 249;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 NYWMT 35

RESULT 2

US-11-266-444-974

; Sequence 974, Application US/11266444

; Publication No. US20060062789A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators

; FILE REFERENCE: PF523P1D1

; CURRENT APPLICATION NUMBER: US/11/266,444

; CURRENT FILING DATE: 2005-11-04

; PRIOR APPLICATION NUMBER: 09/880,746

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 974

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-266-444-974

Query Match 100.0%; Score 34; DB 11; Length 249;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
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Db 31 NYWMT 35

RESULT 3

US-11-074-176-252

; Sequence 252, Application US/11074176

; Publication No. US20050250135A1

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAuliffe, Olivia

; APPLICANT: Perill, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

; FILE REFERENCE: 5051-694

; CURRENT APPLICATION NUMBER: US/11/074,176

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/551,161

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 252

; LENGTH: 1217

; TYPE: PRT

; ORGANISM: Lactobacillus acidophilus

US-11-074-176-252

```

Query Match      91.2%; Score 31; DB 11; Length 1217;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      499 NYWLT 503

RESULT 4
US-10-880-238-60
; Sequence 60, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheng, Wing-Tai
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
; FILE REFERENCE: 17329-033001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-60

Query Match      88.2%; Score 30; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      6 NYWMS 10

RESULT 5
US-11-054-515-2103
; Sequence 2103, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2103

```

```

; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2103

Query Match      88.2%; Score 30; DB 11; Length 247;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      31 NYWIT 35

RESULT 6
US-11-266-444-2103
; Sequence 2103, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523PID1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2103
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2103

Query Match      88.2%; Score 30; DB 11; Length 247;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
      |||:|
Db      31 NYWIT 35

RESULT 7
US-11-096-568A-23953
; Sequence 23953, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23953
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(558)
; OTHER INFORMATION: Ceres Seq. ID no. 12417055

```

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (239)..(239)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (241)..(241)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (395)..(395)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (398)..(398)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (399)..(399)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (539)..(539)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-23953
```

```
Query Match      88.2%; Score 30; DB 11; Length 558;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYWMT 5
         ||||:
Db      41 NYWMS 45
```

```
RESULT 8
US-11-096-568A-23952
; Sequence 23952, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23952
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(593)
; OTHER INFORMATION: Ceres Seq. ID no. 12417054
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (274)..(274)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (430)..(430)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (433)..(433)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (434)..(434)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (574)..(574)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-23952

Query Match      88.2%; Score 30; DB 11; Length 593;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYWMT 5
         ||||:
Db      76 NYWMS 80
```

```
RESULT 9
US-11-096-568A-23951
; Sequence 23951, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23951
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(606)
; OTHER INFORMATION: Ceres Seq. ID no. 12417053
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (289)..(289)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (446)..(446)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (447)..(447)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (574)..(574)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (587)..(587)
; OTHER INFORMATION: Xaa is any aa, unknown or other
```



```
US-11-096-568A-23951
Query Match      88.2%; Score 30; DB 11; Length 606;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 89 NYWMS 93

RESULT 10
US-11-188-298-16493
; Sequence 16493, Application US/11188298
; Publication No. US2006007552A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16493
; LENGTH: 1684
; TYPE: PRT
; ORGANISM: alkaliphilic eubacterium 163-26
US-11-188-298-16493
Query Match      88.2%; Score 30; DB 11; Length 1684;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWMT 5
Db 375 NFWMT 379

RESULT 11
US-10-880-238-45
; Sequence 45, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Man
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-45
Query Match      85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 6 NYWM 9

RESULT 12
US-10-880-238-48
; Sequence 48, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Man
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-48
Query Match      85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 6 NYWM 9

RESULT 13
US-10-880-238-51
; Sequence 51, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Man
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-51
Query Match      85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 6 NYWM 9

RESULT 14
US-10-880-238-54
; Sequence 54, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Man
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-54
Query Match      85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYWM 4
Db 6 NYWM 9
```


; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-54

Query Match 85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
6 NYWM 9

RESULT 15
US-10-880-238-57
; Sequence 57, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
; APPLICANT: Cheung, Wing-Tai
; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
; TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
; FILE REFERENCE: 17329-003001
; CURRENT APPLICATION NUMBER: US/10/880,238
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-57

Query Match 85.3%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
6 NYWM 9

RESULT 16
US-11-219-563-29
; Sequence 29, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-29

Query Match 85.3%; Score 29; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
6 NYWM 9

RESULT 17
US-11-218-813-29
; Sequence 29, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-218-813-29

Query Match 85.3%; Score 29; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
6 NYWM 9

RESULT 18
US-11-219-563-47
; Sequence 47, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-47

Query Match 85.3%; Score 29; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
Db ||||
31 NYWM 34

RESULT 19
US-11-219-563-49
; Sequence 49, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
US-11-219-563-49

Query Match 85.3%; Score 29; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
DB 31 NYWM 34

RESULT 20
US-11-219-563-59
; Sequence 59, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-2
US-11-219-563-59

Query Match 85.3%; Score 29; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
DB 31 NYWM 34

RESULT 21
US-11-219-563-60
; Sequence 60, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-3
US-11-219-563-60

Query Match 85.3%; Score 29; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
DB 31 NYWM 34

RESULT 22
US-11-219-563-61
; Sequence 61, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-61

Query Match 85.3%; Score 29; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||||
DB 31 NYWM 34

RESULT 23

```
US-11-218-813-47
; Sequence 47, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-218-813-47

Query Match      85.3%; Score 29; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 24
US-11-218-813-49
; Sequence 49, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
US-11-218-813-49

Query Match      85.3%; Score 29; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 25
US-11-218-813-59
; Sequence 59, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-5
US-11-218-813-59

Query Match      85.3%; Score 29; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 26
US-11-218-813-60
; Sequence 60, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-3
US-11-218-813-60

Query Match      85.3%; Score 29; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 27
US-11-218-813-61
; Sequence 61, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
```

```
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-218-813-61

Query Match      85.3%; Score 29; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 28
US-10-507-662-29
; Sequence 29, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: AI36PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-29

Query Match      85.3%; Score 29; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 29
US-11-219-563-69
; Sequence 69, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-69

Query Match      85.3%; Score 29; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 30
US-11-219-563-70
; Sequence 70, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-70

Query Match      85.3%; Score 29; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34

RESULT 31
US-11-218-813-69
; Sequence 69, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-218-813-69

Query Match      85.3%; Score 29; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
Db      31 NYWM 34
```

```
Db          31 NYWM 34

RESULT 32
US-11-218-813-70
; Sequence 70, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-218-813-70

Query Match      85.3%; Score 29; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
      :||||
Db      31 NYWM 34

RESULT 33
US-11-116-144-157
; Sequence 157, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; FILE REFERENCE: INL-084
; CURRENT APPLICATION NUMBER: US/11/116,144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 157
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-116-144-157

Query Match      85.3%; Score 29; DB 11; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 5
      :||||
Db      116 SYWM 120

RESULT 34
US-11-116-144-157
; Sequence 157, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; FILE REFERENCE: INL-084
; CURRENT APPLICATION NUMBER: US/11/116,144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 157
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-116-144-157

Query Match      85.3%; Score 29; DB 11; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 5
      :||||
Db      116 SYWM 120

RESULT 35
US-11-219-563-54
; Sequence 54, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651-001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-1
US-11-219-563-54

Query Match      85.3%; Score 29; DB 10; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 4
      :||||
Db      48 NYWM 51

US-11-220-372-157
; Sequence 157, Application US/11220372
; Publication No. US20060063149A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN INFECTION
; FILE REFERENCE: INL-084CP
; CURRENT APPLICATION NUMBER: US/11/220,372
; CURRENT FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: PCT/ES05/00355
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US 11/116,144
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03 380 307.3
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 157
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-220-372-157

Query Match      85.3%; Score 29; DB 11; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWM 5
      :||||
Db      116 SYWM 120
```

RESULT 36
US-11-218-813-54
; Sequence 54, Application US/11218813
; Publication No. US20060062793A1
; GENERAL INFORMATION:
; APPLICANT: Webb, Iain J.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163005
; CURRENT APPLICATION NUMBER: US/11/218,813
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US2004/006543
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: delimmunized heavy chain J415-1
US-11-218-813-54

Query Match 85.3%; Score 29; DB 11; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
DB 48 NYWM 51

RESULT 37
US-10-506-454-919
; Sequence 919, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozvavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 919
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-919

Query Match 85.3%; Score 29; DB 9; Length 151;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
DB 132 NYWM 135

RESULT 38
US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; FEATURE:
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match 85.3%; Score 29; DB 11; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWM 4
|||
DB 119 NYWM 122

RESULT 39
US-11-096-568A-22667
; Sequence 22667, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22667
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(225)
; OTHER INFORMATION: Ceres Seq. ID no. 12409624

US-11-096-568A-22667

Query Match 85.3%; Score 29; DB 11; Length 225;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:||||
Db 15 SYWMT 19

RESULT 40

US-11-194-890-7
; Sequence 7, Application US/11194890
; Publication No. US20050287579A1
; GENERAL INFORMATION:
; APPLICANT: Wolfner, Mariana
; APPLICANT: Lung, Oliver
; APPLICANT: Tram, Khanh-Uyen
; TITLE OF INVENTION: GENES FOR MALE ACCESSORY GLAND PROTEINS IN DROSOPHILA
; TITLE OF INVENTION: MELANOCASTER

; FILE REFERENCE: 19603/1791
; CURRENT APPLICATION NUMBER: US/11/194,890
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/114,774
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/219,983
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-11-194-890-7

Query Match 85.3%; Score 29; DB 11; Length 234;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NYWMT 5
:||||
Db 50 NWMT 54

RESULT 41

US-11-054-515-1932
; Sequence 1932, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1932
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1932

Query Match 85.3%; Score 29; DB 11; Length 241;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:||||
Db 31 HYWMT 35

RESULT 42

US-11-054-515-2054
; Sequence 2054, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2054

Query Match 85.3%; Score 29; DB 11; Length 241;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:||||
Db 31 HYWMT 35

RESULT 43

US-11-266-444-1932
; Sequence 1932, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat

; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1932
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1932

Query Match 85.3%; Score 29; DB 11; Length 241;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:|||||
Db 31 HYWMT 35

RESULT 44
US-11-266-444-2054
; Sequence 2054, Application US/11266444
; Publication No. US20060082789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-2054

Query Match 85.3%; Score 29; DB 11; Length 241;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:|||||
Db 31 HYWMT 35

RESULT 45
US-11-054-515-1909

; Sequence 1909, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1909
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1909

Query Match 85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYWMT 5
:|||||
Db 31 HYWMT 35

RESULT 46
US-11-054-515-1916
; Sequence 1916, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16


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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1916
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1916
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Query Match      85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYWMT 5
       :||||
Db      31 HYWMT 35
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RESULT 47
US-11-054-515-2051
; Sequence 2051, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2051
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2051
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Query Match      85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYWMT 5
       :||||
Db      31 HYWMT 35
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RESULT 48
US-11-266-444-1909
; Sequence 1909, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
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; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1909
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1909
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Query Match      85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYWMT 5
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Db      31 HYWMT 35
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RESULT 49
US-11-266-444-1916
; Sequence 1916, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1916
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1916
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Query Match      85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYWMT 5
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Db      31 HYWMT 35
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RESULT 50
US-11-266-444-2051
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; Sequence 2051, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2051
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-266-444-2051

Query Match      85.3%; Score 29; DB 11; Length 243;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYWMT 5
Db      31 HYWMT 35

Search completed: May 11, 2006, 16:50:41
Job time : 12.2295 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:15:30 ; Search time 147.934 Seconds
(without alignments)
47.521 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82

Sequence: 1 SITSTGGTYHAEVKG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

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5: Geneseq2002s.*

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7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	16	2	Aaw23430 CDR-2 of
2	71.5	87.2	122	2	Aaw23432 rW12 heav
3	71.5	87.2	122	2	Aaw23437 Modified
4	71.5	87.2	122	2	Aaw23441 hW12 heav
5	71.5	87.2	122	2	Aaw23438 Modified
6	58	70.7	16	7	Adm07764 Canine im
7	57	69.5	16	8	Adu86658 Peptide d
8	56	68.3	117	9	Aeb46921 Human var
9	56	68.3	119	8	Aeb46921 Human IGF
10	56	68.3	119	8	Adt88872 Human IGF
11	56	68.3	119	8	Adt88866 Human IGF
12	56	68.3	119	8	Adt88862 Human IGF
13	56	68.3	119	8	Adt88873 Human IGF
14	56	68.3	139	2	AAR327053 Anti-CEA
15	56	68.3	139	2	AAR30480 hCEA spec
16	56	68.3	240	9	Aeb46939 Human Cbl
17	56	68.3	447	9	Aeb46964 CD1a spec
18	55.5	67.7	125	8	ADO25822 Camelidae
19	55.5	67.7	133	8	ADO25845 Camelidae
20	55.5	67.7	247	5	ABP45942 Human Bly
21	55.5	67.7	247	7	ADG96769 Single ch
22	55.5	67.7	251	8	ADO04876 Anti-mous
23	55.5	67.7	252	8	ADO04874 Anti-mous
24	55.5	67.7	252	8	ADO04875 Anti-mous

25	55	67.1	16	5	Aau82610 Liama CDR
26	55	67.1	115	8	Adp22214 Human ant
27	55	67.1	217	8	Adri6818 Human bre
28	54.5	66.5	17	8	Adu86691 Peptide d
29	54.5	66.5	117	5	Abb07238 Anti-IL-4
30	54.5	66.5	117	9	Aea08943 Antibody
31	54.5	66.5	118	9	Adz41229 Anti-HAS
32	54.5	66.5	125	8	Adp09930 Anti-huma
33	54	65.9	116	7	Adf11393 2283 anti-
34	54	65.9	116	7	Adf11413 9H7 anti-
35	54	65.9	116	8	Adw39293 Melanin c
36	54	65.9	446	7	Adf11437 9H7 anti-
37	54	65.9	446	7	Adf11417 2283 anti-
38	53	64.6	567	6	Abp96588 Pig Igs h
39	53	64.6	16	5	ABG70430 CDR2 regi
40	53	64.6	16	5	Aau82466 Liama CDR
41	53	64.6	17	9	Aea45760 Apolipop
42	53	64.6	95	4	Aam33349 Peptide #
43	53	64.6	95	4	Aam73134 Human bon
44	53	64.6	95	4	ABG54850 Human liv
45	53	64.6	95	5	ABG42982 Human pep
46	53	64.6	97	3	Aab40091 Anti-hiLi
47	53	64.6	97	3	Aab40092 Anti-hiLi
48	53	64.6	97	5	Abg78195 Human Fv
49	53	64.6	97	5	Abg78196 Human Fv
50	53	64.6	97	5	ABG91886 Human ant
51	53	64.6	97	5	ABG91887 Human ant
52	53	64.6	97	6	ABO27115 Human ger
53	53	64.6	97	9	Ady93868 Anti-SARS
54	53	64.6	101	4	Aam18809 Peptide #
55	53	64.6	101	4	Abb37915 Peptide #
56	53	64.6	101	4	Aam31325 Peptide #
57	53	64.6	101	4	Abb23170 Protein #
58	53	64.6	101	4	Aam71048 Human bon
59	53	64.6	101	4	Aam58547 Human bra
60	53	64.6	101	4	ABG52763 Human liv
61	53	64.6	101	5	ABG40841 Human pep
62	53	64.6	105	2	Aaw41018 Anti-glut
63	53	64.6	116	4	Aau02631 Anti-adip
64	53	64.6	116	8	AdS88105 Human CD2
65	53	64.6	117	9	Aeb46919 Human var
66	53	64.6	118	9	Aea79525 Integrin
67	53	64.6	118	9	Aea79527 Integrin
68	53	64.6	118	9	Aea79526 Integrin
69	53	64.6	118	9	Aea79531 Integrin
70	53	64.6	118	9	Aea79530 Integrin
71	53	64.6	118	9	Aea79528 Integrin
72	53	64.6	118	9	Aea79529 Integrin
73	53	64.6	121	7	ADP03960 Murine-ex
74	53	64.6	122	8	ADL15640 Murine an
75	53	64.6	122	8	ADL15666 Partial m
76	53	64.6	123	5	Abb07236 Anti-IL-4
77	53	64.6	123	5	Aea08941 Antibody
78	53	64.6	239	5	Aau90905 Insulin/i
79	53	64.6	240	5	Aeb46937 Human Cbl
80	53	64.6	242	5	Aau90904 Insulin/i
81	53	64.6	442	8	ADL15724 Murine an
82	53	64.6	447	9	Aeb46962 CD1a spec
83	53	64.6	850	4	ABG04634 Novel hum
84	53	64.6	869	4	ABG19658 Novel hum
85	52.5	64.0	105	9	ADY93867 Anti-SARS
86	52.5	64.0	116	2	ADY93863 Anti-SARS
87	52.5	64.0	118	2	Aay43251 VH domain
88	52.5	64.0	118	2	Aay43252 VH domain
89	52.5	64.0	144	8	AdS88061 Human CD2
90	52.5	64.0	240	4	AAB46040 Human TF
91	52	63.4	116	7	ADf11409 16E1 anti
92	52	63.4	116	7	ADf11401 anti-
93	52	63.4	121	8	ADO25812 Camelidae
94	52	63.4	157	1	ADP81250 Sequence
95	52	63.4	446	7	ADf11425 2D8 anti-
96	52	63.4	446	7	ADf11433 16E1 anti
97	51.5	62.8	17	9	ADw77386 Human pla

98	51.5	62.8	17	9	ABA45716	Aea45716 Apolipop	171	50.5	61.6	467	6	ABP71365	Abp71365 Anti-OPGL
99	51.5	62.8	249	5	ABP44952	Abp44952 Human Bly	172	50.5	61.6	524	9	ABE48609	Abe48609 Human IgG
100	51.5	62.8	249	7	ADG95779	Adg95779 Single ch	173	50	61.0	17	5	AU82546	Au82546 Llana CDR
101	51	62.2	16	8	ADE25798	Adi-25798 Anti-alpha	174	50	61.0	17	8	ADU86622	Adu86622 Peptide d
102	51	62.2	88	4	AAE06988	Aae06988 Mouse ger	175	50	61.0	17	8	ADU86646	Adu86646 Peptide d
103	51	62.2	88	8	ADQ89273	Adq89273 Mouse imm	176	50	61.0	17	8	ADU86676	Adu86676 Peptide d
104	51	62.2	88	9	ABE09546	Abe09546 Murine ge	177	50	61.0	17	8	ADU86661	Adu86661 Peptide d
105	51	62.2	116	9	AEA16578	Aea16578 Protein o	178	50	61.0	101	9	ADW97151	Adw97151 Human IL-
106	51	62.2	116	9	AEA16576	Aea16576 Protein o	179	50	61.0	102	2	AAE80088	Aae80088 Human der
107	51	62.2	120	8	ADE25816	Adi-25816 Anti-alpha	180	50	61.0	102	2	AAW95486	Aaw95486 Human-der
108	51	62.2	122	8	ADO25836	Ado25836 Camelidae	181	50	61.0	117	7	ADM09084	Adm09084 Canine im
109	51	62.2	122	8	ADR30760	Adr30760 Mouse B2G	182	50	61.0	129	8	ADP09942	Adp09942 Anti-mous
110	51	62.2	125	8	ADO25821	Ado25821 Camelidae	183	50	61.0	129	8	ADO25692	Ado25692 Anti-TNF-
111	51	62.2	125	8	ADW39241	Adw39241 Pgp-resis	184	50	61.0	129	8	ADO25711	Ado25711 Anti-TNF-
112	51	62.2	131	2	AAE54048	Aae54048 Sequence	185	50	61.0	129	8	ADO25709	Ado25709 Anti-TNF-
113	51	62.2	131	2	AAW01524	Aaw01524 Monoclon	186	50	61.0	129	8	ADO25712	Ado25712 Anti-TNF-
114	51	62.2	131	2	AAW24985	Aaw24985 Monoclon	187	50	61.0	129	8	ADO25713	Ado25713 Anti-TNF-
115	51	62.2	208	2	AAW41168	Aay41168 Llana Vhh	188	50	61.0	129	8	ADO25805	Ado25805 Anti-TNF-
116	51	62.2	254	5	ABP44960	Abp44960 Human Bly	189	50	61.0	129	8	ADO25710	Ado25710 Anti-TNF-
117	51	62.2	254	7	ADG95787	Adg95787 Peptide d	190	50	61.0	134	5	ABG30618	Abg30618 Immunoglo
118	50.5	61.6	17	2	AAW90330	Aaw90330 Human ant	191	50	61.0	151	8	ADO25823	Ado25823 Camelidae
119	50.5	61.6	17	5	AAU82550	Aau82550 Llana CDR	192	50	61.0	219	2	AA41176	Aay41176 Llana Vhh
120	50.5	61.6	17	8	ADU81112	Adu81112 MAB G15B4	193	50	61.0	255	8	ADO04865	Ado04865 Anti-mous
121	50.5	61.6	17	8	ADU81127	Adu81127 MAB G15-V	194	50	61.0	255	8	ADO04860	Ado04860 Anti-mous
122	50.5	61.6	17	8	ADU86631	Adu86631 Peptide d	195	50	61.0	255	8	ADO04859	Ado04859 Anti-mous
123	50.5	61.6	17	8	ADU86637	Adu86637 Peptide d	196	50	61.0	255	8	ADO25720	Ado25720 Anti-TNF-
124	50.5	61.6	17	9	AEA45781	Aea45781 Apolipop	197	50	61.0	255	8	ADO25721	Ado25721 Anti-TNF-
125	50.5	61.6	17	9	AEA46034	Aea46034 Apolipop	198	50	61.0	255	8	ADO25726	Ado25726 Anti-TNF-
126	50.5	61.6	40	6	ABJ25307	Abj25307 SAC isola	199	50	61.0	256	8	ADO04857	Ado04857 Anti-mous
127	50.5	61.6	96	8	ADU04241	Adu04241 Human imm	200	50	61.0	256	8	ADO04858	Ado04858 Anti-mous
128	50.5	61.6	98	3	ABAB40108	Abab40108 Anti-hiL1	201	50	61.0	256	8	ADO25718	Ado25718 Anti-TNF-
129	50.5	61.6	98	3	ABAB40107	Abab40107 Anti-hiL1	202	50	61.0	256	8	ADO25719	Ado25719 Anti-TNF-
130	50.5	61.6	98	3	ABAB40094	Abab40094 Anti-hiL1	203	50	61.0	312	4	AAU14227	Aau14227 Human nov
131	50.5	61.6	98	3	ABAB40095	Abab40095 Anti-hiL1	204	50	61.0	383	8	ADO04861	Ado04861 Anti-mous
132	50.5	61.6	98	5	ABG78197	Abg78197 Human Fv	205	50	61.0	383	8	ADO25722	Ado25722 Anti-TNF-
133	50.5	61.6	98	5	ABG91888	Abg91888 Human ant	206	50	61.0	411	8	ADO25762	Ado25762 Anti-IFN
134	50.5	61.6	98	7	ADD28086	Add28086 Lymphoma	207	50	61.0	472	9	ADW44415	Adw44415 Dog immun
135	50.5	61.6	116	9	ABE27735	Abe27735 Prostate	208	50	61.0	492	8	ADR10164	Adr10164 Human pro
136	50.5	61.6	118	2	AAE19877	Aae19877 CEA-speci	209	50	61.0	552	8	ADO25763	Ado25763 Anti-IFN
137	50.5	61.6	120	2	AAE88510	Aae88510 Vhmu for	210	49.5	60.4	17	8	ADL93626	Adl93626 Human CD4
138	50.5	61.6	120	2	AAE88510	Aae88510 Human c-M	211	49.5	60.4	17	9	AEA45718	Aea45718 Apolipop
139	50.5	61.6	120	5	ABG09378	Abg09378 Anti-IGF-	212	49.5	60.4	116	8	ADL93566	Adl93566 Human CD4
140	50.5	61.6	122	5	ABG71367	Abp71367 Anti-OPGL	213	49.5	60.4	124	7	ADM41876	Adm41876 Human ant
141	50.5	61.6	122	8	ABP71367	Abp71367 Human ant	214	49.5	60.4	462	8	ADL93660	Adl93660 Human CD4
142	50.5	61.6	122	8	ADP28558	Adp28558 Human int	215	49	59.8	16	7	ADJ32098	Adj32098 Human int
143	50.5	61.6	123	9	ADX011773	Adx011773 SARS coro	216	49	59.8	16	7	ADJ32098	Adj32098 Human int
144	50.5	61.6	126	2	AAE54273	Aae54273 Anti-HIV	217	49	59.8	16	9	ADW77380	Adw77380 Human pla
145	50.5	61.6	126	2	AAW01318	Aaw01318 VH of Fab	218	49	59.8	16	9	ADW77398	Adw77398 Human pla
146	50.5	61.6	126	3	AAV95168	Aay95168 Anti-gp41	219	49	59.8	17	8	ADU86628	Adu86628 Peptide d
147	50.5	61.6	126	5	ABG69155	Abg69155 Human mon	220	49	59.8	95	2	AAW35098	Aaw35098 Product o
148	50.5	61.6	126	5	ABG69155	Abg69155 Human mon	221	49	59.8	96	7	ADK18854	Adk18854 Anti-huma
149	50.5	61.6	132	4	AAU00583	Aau00583 Modified	222	49	59.8	97	3	AAE40090	Aae40090 Anti-hiL1
150	50.5	61.6	132	4	AAU00580	Aau00580 Modified	223	49	59.8	97	5	ABG78193	Abg78193 Human Fv
151	50.5	61.6	132	4	AAU00576	Aau00576 VH ligand	224	49	59.8	97	5	ABG78193	Abg78193 Human Fv
152	50.5	61.6	132	4	AAU00581	Aau00581 Modified	225	49	59.8	97	5	ABG91885	Abg91885 Human ant
153	50.5	61.6	132	4	AAU00582	Aau00582 Modified	226	49	59.8	97	5	ABG91884	Abg91884 Human ant
154	50.5	61.6	132	4	AAU00584	Aau00584 Modified	227	49	59.8	97	6	ABO27096	AbO27096 Human ger
155	50.5	61.6	132	5	ABG69149	Abg69149 Human mon	228	49	59.8	97	6	ABO27098	AbO27098 Human ger
156	50.5	61.6	132	5	ABG69152	Abg69152 Human mon	229	49	59.8	97	7	ADD28084	Add28084 Lymphoma
157	50.5	61.6	132	5	ABG69150	Abg69150 Human mon	230	49	59.8	97	7	ADP10138	Adp10138 Antibody
158	50.5	61.6	132	5	ABG69151	Abg69151 Human mon	231	49	59.8	97	7	ADP09928	Adp09928 Antibody
159	50.5	61.6	132	5	ABG69153	Abg69153 Human mon	232	49	59.8	97	7	ADP10038	Adp10038 VEGF anti
160	50.5	61.6	185	8	ABG69154	Abg69154 Human mon	233	49	59.8	97	7	ADP10038	Adp10038 VEGF anti
161	50.5	61.6	239	9	ABE27755	Abe27755 Anti-pros	234	49	59.8	97	7	ADP10036	Adp10036 VEGF anti
162	50.5	61.6	240	5	ABP45919	Abp45919 Human Bly	235	49	59.8	97	7	ADF10140	Adf10140 Antibody
163	50.5	61.6	240	7	ADG96746	Adg96746 Single ch	236	49	59.8	97	7	ADK18853	Adk18853 Anti-huma
164	50.5	61.6	243	5	ABP45934	Abp45934 Human Bly	237	49	59.8	97	7	ADK18851	Adk18851 Anti-huma
165	50.5	61.6	243	7	ADG96761	Adg96761 Single ch	238	49	59.8	97	7	ADJ80312	Adj80312 VH gene 1
166	50.5	61.6	248	9	ADW90310	Adw90310 Phage scF	239	49	59.8	97	7	ADJ80310	Adj80310 VH gene 1
167	50.5	61.6	248	9	ADX01805	Adx01805 SARS coro	240	49	59.8	97	9	ADY54704	Ady54704 Human VH
168	50.5	61.6	262	7	ADH44200	Adh44200 sFv antib	241	49	59.8	97	9	ADY54703	Ady54703 Human VH
169	50.5	61.6	268	5	AAU97197	Aau97197 Human ant	242	49	59.8	97	9	ADY75315	Ady75315 Protein e
170	50.5	61.6	451	9	ADX01865	Adx01865 SARS coro	243	49	59.8	97	9	ADY75317	Ady75317 Protein e

244	49	59.8	97	9	AEb13594	Human var	317	48	58.5	16	9	AEa51635	Human ant
245	49	59.8	98	4	AAm73652	Human bron	318	48	58.5	17	4	AAg65316	Anti-IL-1
246	49	59.8	98	4	AAm60959	Human bron	319	48	58.5	17	5	ABG70429	CDR2 regi
247	49	59.8	98	4	ABG55387	Human liv	320	48	58.5	17	5	ABG70451	CDR2 regi
248	49	59.8	98	5	ABG43524	Human pep	321	48	58.5	17	5	AAU82487	Llama CDR
249	49	59.8	108	8	ADP22380	Human ant	322	48	58.5	17	5	AAU82465	Llama CDR
250	49	59.8	108	8	ADP22362	Human ant	323	48	58.5	17	7	ADRS0941	Antibody
251	49	59.8	108	8	ADP22391	Human ant	324	48	58.5	17	9	ADY72622	Human ant
252	49	59.8	108	8	ADP22376	Human ant	325	48	58.5	17	9	ADY77471	Human fib
253	49	59.8	108	8	ADP22394	Human ant	326	48	58.5	17	9	ADz59456	L19 scFv
254	49	59.8	108	9	ADx45253	Anti-inte	327	48	58.5	17	9	AEa46292	Apolipoppr
255	49	59.8	111	8	ADH50831	Human hea	328	48	58.5	19	5	AAU70371	Human hea
256	49	59.8	114	9	ADV86722	Anti-FLJ3	329	48	58.5	115	5	ADFL1397	2811 anti
257	49	59.8	114	9	ADV86723	Anti-FLJ3	330	48	58.5	116	3	AAy53772	VH compon
258	49	59.8	115	8	ADP22276	Human ant	331	48	58.5	116	4	AAE08817	Human scF
259	49	59.8	115	8	ADP22230	Human ant	332	48	58.5	116	7	ADH69261	Human L19
260	49	59.8	115	8	ADP22246	Human ant	333	48	58.5	117	5	ABH05053	Fibronect
261	49	59.8	115	8	ADP22280	Human ant	334	48	58.5	118	2	AAy05237	Testoster
262	49	59.8	116	2	AAK66341	Human imm	335	48	58.5	118	2	AAy05238	Testoster
263	49	59.8	116	9	AEb12763	Antibody	336	48	58.5	118	2	AAy05240	Testoster
264	49	59.8	119	4	AAb67779	Amino aci	337	48	58.5	118	2	AAy05235	Testoster
265	49	59.8	120	7	ADK18852	Anti-huma	338	48	58.5	118	2	AAy05236	Testoster
266	49	59.8	120	7	ADK18591	Anti-huma	339	48	58.5	118	8	ADP09900	Anti-huma
267	49	59.8	120	7	ADK18788	Anti-huma	340	48	58.5	118	8	ADO25735	Anti-IPN
268	49	59.8	120	8	ADL25400	Human mAb	341	48	58.5	118	8	ADO25859	Camelidae
269	49	59.8	125	8	ADO36383	Intracell	342	48	58.5	119	4	AAE51642	Human ant
270	49	59.8	126	8	ADO04888	Anti-mous	343	48	58.5	119	4	AAE67778	Amino aci
271	49	59.8	126	8	ADP09966	Anti-huma	344	48	58.5	119	8	ADO36392	Intracell
272	49	59.8	126	8	ADO25781	Anti-TNP-	345	48	58.5	120	9	ADx02115	SARS coro
273	49	59.8	126	8	ADO25891	Camelidae	346	48	58.5	120	9	ADx02119	SARS coro
274	49	59.8	126	8	ADQ81984	Camelidae	347	48	58.5	122	8	ADO25840	Camelidae
275	49	59.8	128	5	ABP43136	Human ova	348	48	58.5	124	8	ADO25828	Camelidae
276	49	59.8	139	1	AAp90480	Chimeric	349	48	58.5	124	8	ADO25830	Camelidae
277	49	59.8	160	6	ABr55916	Human mAb	350	48	58.5	124	8	ADO25827	Camelidae
278	49	59.8	220	7	ADJ32124	Human int	351	48	58.5	126	7	ADW41869	Human ant
279	49	59.8	243	5	ABP44984	Human Bly	352	48	58.5	127	4	AAE07024	Human hea
280	49	59.8	243	7	ADG30420	Human GMB	353	48	58.5	127	8	ADO25851	Camelidae
281	49	59.8	243	7	ADG95811	Single ch	354	48	58.5	127	8	ADQ89309	Human imm
282	49	59.8	247	5	ABP45166	Human Bly	355	48	58.5	127	9	AEb09582	Human hea
283	49	59.8	247	5	ADG95953	Single ch	356	48	58.5	129	8	ADO25837	Camelidae
284	49	59.8	247	8	ADH34573	scFv SC02	357	48	58.5	130	2	AAW71045	Peptide 8
285	49	59.8	249	5	ABP45324	Human Bly	358	48	58.5	131	4	AAE10555	HPL inhib
286	49	59.8	249	5	ADG96151	Single ch	359	48	58.5	137	8	ADH17895	Human 15H
287	49	59.8	252	5	ABP45300	Human Bly	360	48	58.5	137	8	ADH17936	Human 15H
288	49	59.8	252	7	ADG96127	Single ch	361	48	58.5	137	8	ADH18003	Human mod
289	49	59.8	253	5	ABP45438	Human Bly	362	48	58.5	137	9	AEa16302	Human 15H
290	49	59.8	253	5	ABP45803	Human Bly	363	48	58.5	137	9	AEa16298	Human 15H
291	49	59.8	253	7	ADG96285	Single ch	364	48	58.5	137	9	AEa51630	Human ant
292	49	59.8	253	7	ADG96630	Single ch	365	48	58.5	137	9	AEa51640	Human ant
293	49	59.8	255	5	ABP45126	Human Bly	366	48	58.5	236	8	ADO19051	Murine an
294	49	59.8	255	7	ADG95953	Single ch	367	48	58.5	236	8	ADO19053	Murine an
295	49	59.8	405	8	ADU23606	Phage dis	368	48	58.5	238	3	AAy53775	An antibo
296	49	59.8	474	9	ADV86668	FLJ32028	369	48	58.5	238	6	AAE37734	Antibody
297	49	59.8	474	9	ADW44419	Dog immun	370	48	58.5	238	6	ADZ59451	L19 scFv
298	48.5	59.1	16	8	ADH88077	Human CD2	371	48	58.5	240	6	AAE37745	Re combina
299	48.5	59.1	17	8	ADU86670	Peptide d	372	48	58.5	240	6	AAE37743	Re combina
300	48.5	59.1	98	3	AAb40096	Anti-hi11	373	48	58.5	241	6	AAE37744	Re combina
301	48.5	59.1	98	3	ADF10139	Antibody	374	48	58.5	241	6	AAE37746	Re combina
302	48.5	59.1	98	7	ADP09929	Antibody	375	48	58.5	241	8	ADJ38418	AP39 prot
303	48.5	59.1	98	7	ADFL0037	VEGF anti	376	48	58.5	242	9	ADZ59468	L19 antib
304	48.5	59.1	98	7	ADJ80311	VH gene 1	377	48	58.5	242	9	ADZ59466	L19 antib
305	48.5	59.1	98	9	ADY75316	Protein e	378	48	58.5	243	9	ADZ59473	L19 antib
306	48.5	59.1	98	9	ABE13593	Human var	379	48	58.5	243	9	ADZ59467	L19 antib
307	48.5	59.1	118	2	AAr66351	Human imm	380	48	58.5	243	9	ADZ59469	L19 antib
308	48.5	59.1	126	8	ADO25818	Camelidae	381	48	58.5	244	9	ADZ59472	Tagged pr
309	48.5	59.1	227	9	ADX18552	VEGF-spec	382	48	58.5	247	6	AAE37742	Re combina
310	48.5	59.1	227	9	ADX18556	VEGF-spec	383	48	58.5	248	9	ADX01992	SARS coro
311	48.5	59.1	227	9	ADX18558	VEGF-spec	384	48	58.5	248	9	ADX01990	SARS coro
312	48.5	59.1	227	9	AEa13910	VEGF rela	385	48	58.5	263	2	AAW97889	Kabat con
313	48.5	59.1	227	9	AEa13859	VEGF rela	386	48	58.5	283	5	AAU75160	Kabat con
314	48.5	59.1	227	9	AEa13908	VEGF rela	387	48	58.5	283	6	ABG73148	Kabat con
315	48.5	59.1	295	8	ADN07004	Human EFG	388	48	58.5	283	6	ABG73868	Kabat con
316	48	58.5	16	8	ADH17906	Human 15H	389	48	58.5	283	9	ADZ59470	L19 antib

390	48	58.5	307	4	AAU14225	AAU14225 Human nov	463	47.5	57.9	17	8	ADO58072	S2 cell d
391	48	58.5	363	4	AAU14228	AAU14228 Human nov	464	47.5	57.9	17	8	ADP47149	Human pho
392	48	58.5	365	9	AD259471	Ad259471 Tagged pr	465	47.5	57.9	17	8	ADP47170	Human pho
393	48	58.5	443	2	AAW13564	AAW13564 Humanised	466	47.5	57.9	17	8	ADQ91433	CDR2 of t
394	48	58.5	445	7	ADP11421	ADP11421 2E11 anti	467	47.5	57.9	17	8	ADQ91433	Human Myo
395	48	58.5	474	9	ADW44413	ADW44413 Dog immun	468	47.5	57.9	17	8	ADS92908	Anti-IL-2
396	48	58.5	533	7	ADB65070	ADB65070 Human pro	469	47.5	57.9	17	8	ADS82665	Fab targe
397	48	58.5	650	6	ABR62591	ABR62591 Anti-CD7	470	47.5	57.9	17	8	ADS52406	Peptide d
398	48	58.5	651	6	ABR62590	ABR62590 Anti-CD7	471	47.5	57.9	17	9	ADU86616	Anti-huma
399	47.5	57.9	17	2	AAW16651	AAW16651 Anti-canc	472	47.5	57.9	17	9	ADW87167	Anti-huma
400	47.5	57.9	17	3	AAW95213	AAW95213 Anti-plat	473	47.5	57.9	17	9	ADW87265	Anti-huma
401	47.5	57.9	17	4	AAW95213	AAW95213 Anti-IL-1	474	47.5	57.9	17	9	ADW87265	Anti-huma
402	47.5	57.9	17	6	ABR01548	ABR01548 Human ant	475	47.5	57.9	17	9	ADW77425	Human pla
403	47.5	57.9	17	6	ADA90032	ADA90032 Anti-Abet	476	47.5	57.9	17	9	ADW77337	Human pla
404	47.5	57.9	17	6	ADA90594	ADA90594 MS-Roche	477	47.5	57.9	17	9	AEA53661	Novel hum
405	47.5	57.9	17	6	ADA90100	ADA90100 Anti-Abet	478	47.5	57.9	17	9	AEA44869	Apolipop
406	47.5	57.9	17	6	ADA90421	ADA90421 MS-Roche	479	47.5	57.9	17	9	AEA44878	Apolipop
407	47.5	57.9	17	6	ADA90575	ADA90575 MS-Roche	480	47.5	57.9	17	9	AEA44878	Human CDR
408	47.5	57.9	17	6	ADA90587	ADA90587 MS-Roche	481	47.5	57.9	19	8	ADS54245	Anti-huma
409	47.5	57.9	17	6	ADA90591	ADA90591 MS-Roche	482	47.5	57.9	19	8	ADS54239	Anti-huma
410	47.5	57.9	17	6	ADA91300	ADA91300 MS-R Fab/	483	47.5	57.9	56	2	AAW02509	Clone s
411	47.5	57.9	17	6	ADA91306	ADA91306 MS-R Fab/	484	47.5	57.9	56	2	AAW02478	Clone s
412	47.5	57.9	17	6	ADA90574	ADA90574 MS-Roche	485	47.5	57.9	56	2	AAW02486	Clone s
413	47.5	57.9	17	6	ADA90576	ADA90576 MS-Roche	486	47.5	57.9	56	2	AAW02496	Clone s
414	47.5	57.9	17	6	ADA90714	ADA90714 MS-Roche	487	47.5	57.9	56	2	AAW02516	Clone s
415	47.5	57.9	17	6	ADA90716	ADA90716 MS-Roche	488	47.5	57.9	56	2	AAW02484	Clone s
416	47.5	57.9	17	6	ADA90718	ADA90718 MS-Roche	489	47.5	57.9	56	2	AAW02487	Clone s
417	47.5	57.9	17	6	ADA90419	ADA90419 MS-Roche	490	47.5	57.9	56	2	AAW02524	Clone s
418	47.5	57.9	17	6	ADA90705	ADA90705 MS-Roche	491	47.5	57.9	56	2	AAW02504	Clone s
419	47.5	57.9	17	6	ADA90907	ADA90907 MS-Roche	492	47.5	57.9	56	2	AAW02508	Clone s
420	47.5	57.9	17	6	ADA91315	ADA91315 MS-R Fab/	493	47.5	57.9	56	2	AAW02520	Clone s
421	47.5	57.9	17	6	ADA90715	ADA90715 MS-Roche	494	47.5	57.9	56	2	AAW02488	Clone s
422	47.5	57.9	17	6	ADA90966	ADA90966 MS-R Fab/	495	47.5	57.9	56	2	AAW02505	Clone s
423	47.5	57.9	17	6	ADA91074	ADA91074 MS-R Fab/	496	47.5	57.9	56	2	AAW02512	Clone s
424	47.5	57.9	17	6	ADA91185	ADA91185 MS-R Fab/	497	47.5	57.9	56	2	AAW02518	Clone s
425	47.5	57.9	17	6	ADA90416	ADA90416 MS-Roche	498	47.5	57.9	56	2	AAW02493	Clone s
426	47.5	57.9	17	6	ADA90417	ADA90417 MS-Roche	499	47.5	57.9	56	2	AAW02494	Clone s
427	47.5	57.9	17	6	ADA90588	ADA90588 MS-Roche	500	47.5	57.9	56	2	AAW02497	Clone s
428	47.5	57.9	17	6	ADA90906	ADA90906 MS-Roche	501	47.5	57.9	56	2	AAW02522	Clone s
429	47.5	57.9	17	6	ADA90589	ADA90589 MS-Roche	502	47.5	57.9	56	2	AAW02525	Clone s
430	47.5	57.9	17	6	ADA90592	ADA90592 MS-Roche	503	47.5	57.9	56	2	AAW02485	Clone s
431	47.5	57.9	17	6	ADA90597	ADA90597 MS-Roche	504	47.5	57.9	56	2	AAW02495	Clone s
432	47.5	57.9	17	6	ADA91182	ADA91182 MS-R Fab/	505	47.5	57.9	56	2	AAW02474	Clone s
433	47.5	57.9	17	6	ADA91197	ADA91197 MS-R Fab/	506	47.5	57.9	56	2	AAW02517	Clone s
434	47.5	57.9	17	6	ADA91303	ADA91303 MS-R Fab/	507	47.5	57.9	96	8	ADU04233	Human imm
435	47.5	57.9	17	6	ADA91384	ADA91384 MS-R Fab/	508	47.5	57.9	96	9	AEA54023	Novel hum
436	47.5	57.9	17	6	ADA89985	ADA89985 Anti-Abet	509	47.5	57.9	96	9	AEA54127	Novel hum
437	47.5	57.9	17	6	ADA90908	ADA90908 MS-Roche	510	47.5	57.9	96	9	AEA54143	Novel hum
438	47.5	57.9	17	6	ADA91191	ADA91191 MS-R Fab/	511	47.5	57.9	96	9	AEA54163	Novel hum
439	47.5	57.9	17	6	ADA90590	ADA90590 MS-Roche	512	47.5	57.9	96	9	AEA54047	Novel hum
440	47.5	57.9	17	6	ADA90826	ADA90826 MS-Roche	513	47.5	57.9	96	9	AEA54051	Novel hum
441	47.5	57.9	17	6	ADA90913	ADA90913 MS-Roche	514	47.5	57.9	96	9	AEA54063	Novel hum
442	47.5	57.9	17	6	ADA91188	ADA91188 MS-R Fab/	515	47.5	57.9	96	9	AEA54087	Novel hum
443	47.5	57.9	17	6	ADA90827	ADA90827 MS-Roche	516	47.5	57.9	96	9	AEA54175	Novel hum
444	47.5	57.9	17	6	ADA90837	ADA90837 MS-Roche	517	47.5	57.9	96	9	AEA54179	Novel hum
445	47.5	57.9	17	6	ADA90418	ADA90418 MS-Roche	518	47.5	57.9	96	9	AEA54043	Novel hum
446	47.5	57.9	17	6	ADA90420	ADA90420 MS-Roche	519	47.5	57.9	96	9	AEA54115	Novel hum
447	47.5	57.9	17	6	ADA91068	ADA91068 MS-R Fab/	520	47.5	57.9	96	9	AEA54015	Novel hum
448	47.5	57.9	17	6	ADA91071	ADA91071 MS-R Fab/	521	47.5	57.9	96	9	AEA54055	Novel hum
449	47.5	57.9	17	6	ADA90577	ADA90577 MS-Roche	522	47.5	57.9	96	9	AEA54083	Novel hum
450	47.5	57.9	17	6	ADA90596	ADA90596 MS-Roche	523	47.5	57.9	96	9	AEA54195	Novel hum
451	47.5	57.9	17	6	ADA90598	ADA90598 MS-Roche	524	47.5	57.9	96	9	AEA54011	Novel hum
452	47.5	57.9	17	6	ADA91194	ADA91194 MS-R Fab/	525	47.5	57.9	96	9	AEA54059	Novel hum
453	47.5	57.9	17	6	ADA90422	ADA90422 MS-Roche	526	47.5	57.9	96	9	AEA54119	Novel hum
454	47.5	57.9	17	6	ADA90585	ADA90585 MS-Roche	527	47.5	57.9	96	9	AEA54159	Novel hum
455	47.5	57.9	17	6	ADA90586	ADA90586 MS-Roche	528	47.5	57.9	96	9	AEA54167	Novel hum
456	47.5	57.9	17	6	ADA90593	ADA90593 MS-Roche	529	47.5	57.9	96	9	AEA54187	Novel hum
457	47.5	57.9	17	6	ADA90595	ADA90595 MS-Roche	530	47.5	57.9	96	9	AEA54191	Novel hum
458	47.5	57.9	17	6	ADA91200	ADA91200 MS-R Fab/	531	47.5	57.9	96	9	AEA54004	Novel hum
459	47.5	57.9	17	6	ADA91312	ADA91312 MS-R Fab/	532	47.5	57.9	96	9	AEA54039	Novel hum
460	47.5	57.9	17	6	ADA91387	ADA91387 MS-R Fab/	533	47.5	57.9	96	9	AEA54067	Novel hum
461	47.5	57.9	17	7	ADD93791	ADD93791 Antibody	534	47.5	57.9	96	9	AEA54075	Novel hum
462	47.5	57.9	17	7	ADJ32091	ADJ32091 Human int	535	47.5	57.9	96	9	AEA54107	Novel hum

682	47.5	57.9	120	8	ADL923395	Adl923395 Single do	755	57.9	127	8	ADSL12493	Adsl12493 Human IGF
683	47.5	57.9	120	8	ADL923384	Adl923384 Anti-HSA	756	47.5	128	2	AAW06242	Aaw06242 Heavy cha
684	47.5	57.9	120	8	ADQ77003	Adq77003 TAR2-10 P	757	47.5	128	4	Aae07014	Aae07014 Human hea
685	47.5	57.9	120	8	ADQ77189	Adq77189 Dummy VH	758	47.5	128	7	ADL91322	Adl91322 VH chain
686	47.5	57.9	120	8	ADQ89307	Adq89307 Human imm	759	47.5	128	8	ADQ89299	Adq89299 Human imm
687	47.5	57.9	120	8	ADU86702	Adu86702 TNFR1 bin	760	47.5	128	8	ADQ89301	Adq89301 Human imm
688	47.5	57.9	120	9	ADW87134	Adw87134 Anti-huma	761	47.5	128	9	AEB09572	Aeb09572 Human hea
689	47.5	57.9	120	9	ADX01830	Adx01830 SARS coro	762	47.5	128	9	AEB09574	Aeb09574 Human hea
690	47.5	57.9	120	9	ADX01771	Adx01771 SARS coro	763	47.5	129	9	AEA53364	Aea53364 Novel hum
691	47.5	57.9	120	9	ADX01763	Adx01763 SARS coro	764	47.5	129	9	AEA44944	Aea44944 Apolipop
692	47.5	57.9	120	9	ADY070833	Ady070833 MS-GPC-6	765	47.5	130	2	AAW71048	Aaw71048 scFv-Bli
693	47.5	57.9	120	9	ADZ411143	Adz411143 Dummy VH	766	47.5	131	2	AAW13520	Aaw13520 Anti-mela
694	47.5	57.9	120	9	AEA41074	Aea41074 Germline	767	47.5	136	5	ADI45736	Adi45736 Single st
695	47.5	57.9	120	9	AEB09580	Aeb09580 Human hea	768	47.5	136	6	ABP55473	Abp55473 Synthetic
696	47.5	57.9	121	2	AAW47180	Aaw47180 Variable	769	47.5	137	9	ADW77344	Adw77344 Human pla
697	47.5	57.9	121	4	AAE07029	Aae07029 Human hea	770	47.5	140	2	AAW13524	Aaw13524 Anti-mela
698	47.5	57.9	121	5	ABG76929	Abg76929 Humanised	771	47.5	142	9	AEA45199	Aea45199 Apolipop
699	47.5	57.9	121	5	AB57571	Ab57571 HLA-DR-sp	772	47.5	142	9	AEA45019	Aea45019 Apolipop
700	47.5	57.9	121	6	ABP56507	Abp56507 Human ant	773	47.5	142	9	AEA45201	Aea45201 Apolipop
701	47.5	57.9	121	6	ABP56504	Abp56504 Human ant	774	47.5	142	9	AEA45200	Aea45200 Apolipop
702	47.5	57.9	121	6	ABP56506	Abp56506 Human ant	775	47.5	147	6	ABR55912	AbR55912 Human mAb
703	47.5	57.9	121	8	ADQ89314	Adq89314 Human imm	776	47.5	156	6	ABR55911	AbR55911 Human mAb
704	47.5	57.9	121	8	ADS12497	AdS12497 Human IGF	777	47.5	177	6	ABJ36939	AbJ36939 Anti-CD40
705	47.5	57.9	121	8	ADR88413	AdR88413 Human pro	778	47.5	217	6	ABR01503	AbR01503 Human ant
706	47.5	57.9	121	9	ABE09587	Aeb09587 Human hea	779	47.5	217	6	ABR01504	AbR01504 Human ant
707	47.5	57.9	121	9	ABE45962	Aeb45962 Human non	780	47.5	217	6	ABR01505	AbR01505 Human ant
708	47.5	57.9	122	2	AAU43253	Aau43253 VH domain	781	47.5	217	6	ABR01509	AbR01509 Human ant
709	47.5	57.9	122	4	AAU02589	Aau02589 Anti-adip	782	47.5	218	6	ABR01507	AbR01507 Human ant
710	47.5	57.9	122	4	AAU02621	Aau02621 Anti-adip	783	47.5	220	6	ABR01519	AbR01519 Human ant
711	47.5	57.9	122	6	ADA89889	Ada89889 MS-Roche	784	47.5	220	6	ABR01517	AbR01517 Human ant
712	47.5	57.9	122	8	ABG75345	Abg75345 Antibody	785	47.5	221	6	ABR01534	AbR01534 Human ant
713	47.5	57.9	122	8	ADP22356	Adp22356 Human ant	786	47.5	221	6	ABR01536	AbR01536 Human ant
714	47.5	57.9	122	8	ADQ77068	Adq77068 TAR2h-10-	787	47.5	222	6	ABR01515	AbR01515 Human ant
715	47.5	57.9	122	8	ADS12503	AdS12503 Human IGF	788	47.5	222	6	ABR01518	AbR01518 Human ant
716	47.5	57.9	122	8	ADW87144	Adw87144 Anti-huma	789	47.5	223	7	ADJ32132	AdJ32132 Human int
717	47.5	57.9	123	2	AAW54811	Aaw54811 SpA-react	790	47.5	224	6	ABR01511	AbR01511 Human ant
718	47.5	57.9	123	4	AAW62748	Aaw62748 Human HIV	791	47.5	224	6	ABR01513	AbR01513 Human ant
719	47.5	57.9	123	6	ABR55827	AbR55827 Heavy cha	792	47.5	224	7	ADJ32114	AdJ32114 Human int
720	47.5	57.9	123	6	ABR55791	AbR55791 Heavy cha	793	47.5	227	9	ADX18560	AdX18560 VEGF-spec
721	47.5	57.9	123	6	ABR55769	AbR55769 Heavy cha	794	47.5	227	9	ADX40895	AdX40895 Humanized
722	47.5	57.9	123	8	ADO36381	Ado36381 Intracell	795	47.5	231	9	ADX40895	AdX40895 Humanized
723	47.5	57.9	123	8	ADO75231	Ado75231 Immunoglo	796	47.5	235	4	AAAG65320	AaG65320 Anti-IL-1
724	47.5	57.9	124	2	AAW13537	Aaw13537 Anti-mela	797	47.5	235	8	ADR28079	AdR28079 NPB poly
725	47.5	57.9	124	4	AAE07026	Aae07026 Human hea	798	47.5	236	4	AAAB99386	AaB99386 Human int
726	47.5	57.9	124	6	ADA89893	Ada89893 MS-Roche	799	47.5	236	4	AAAB99362	AaB99362 Human int
727	47.5	57.9	124	8	ABG75342	Abg75342 Antibody	800	47.5	236	4	AAW74995	Aaw74995 Anti-IL8
728	47.5	57.9	124	8	ADO36358	Ado36358 Intracell	801	47.5	236	4	AAW75019	Aaw75019 Anti-IL8
729	47.5	57.9	124	8	ADQ89311	Adq89311 Human imm	802	47.5	237	3	AAAY95219	AaY95219 Anti-plat
730	47.5	57.9	124	8	ADS92868	AdS92868 Human Myo	803	47.5	238	8	ADR28078	AdR28078 NPB poly
731	47.5	57.9	124	9	ABE09584	Aeb09584 Human hea	804	47.5	238	8	ADS09239	AdS09239 Human c-M
732	47.5	57.9	125	2	AAK54784	Aak54784 SpA-react	805	47.5	239	4	AAAB46054	AaB46054 Human TF
733	47.5	57.9	125	4	AAE07021	Aae07021 Human hea	806	47.5	239	5	ABP46011	Abp46011 Human Bly
734	47.5	57.9	125	4	AAE07013	Aae07013 Human hea	807	47.5	239	5	ABP45911	Abp45911 Human Bly
735	47.5	57.9	125	4	ABG77142	Abg77142 Anti-IGF-	808	47.5	239	5	ABP46024	Abp46024 Human Bly
736	47.5	57.9	125	6	ABU56827	Abu56827 Human imm	809	47.5	239	5	ABP46012	Abp46012 Human Bly
737	47.5	57.9	125	8	ADQ36377	Adq36377 Intracell	810	47.5	239	5	ABP46012	Abp46012 Human Bly
738	47.5	57.9	125	8	ADQ91429	Adq91429 Amino aci	811	47.5	239	7	ADG96838	AdG96838 Single ch
739	47.5	57.9	125	8	ADQ89306	Adq89306 Human imm	812	47.5	239	7	ADG96839	AdG96839 Single ch
740	47.5	57.9	125	8	ADQ89298	Adq89298 Human imm	813	47.5	239	7	ADG96851	AdG96851 Single ch
741	47.5	57.9	125	8	ADR28550	AdR28550 Human ant	814	47.5	239	7	ADG96834	AdG96834 Single ch
742	47.5	57.9	125	8	ADW78339	Adw78339 TAR2-10-2	815	47.5	239	7	ADG96738	AdG96738 Single ch
743	47.5	57.9	125	9	ADZ41221	Adz41221 Anti-TNFR	816	47.5	239	8	ADR28076	AdR28076 NPB poly
744	47.5	57.9	125	9	AEB09571	Aeb09571 Human hea	817	47.5	240	2	AAAY02472	AaY02472 A single
745	47.5	57.9	125	9	AEB09579	Aeb09579 Human hea	818	47.5	240	3	AAAY15124	AaY15124 Anti-mur1
746	47.5	57.9	126	4	AAU02600	Aau02600 Anti-adip	819	47.5	240	3	AAAY15125	AaY15125 Human TF
747	47.5	57.9	126	6	ADA89891	Ada89891 MS-Roche	820	47.5	240	4	AAAB46052	AaB46052 Human Bly
748	47.5	57.9	126	7	ADL91331	Adl91331 VH chain	821	47.5	240	5	AAU79563	Aau79563 Monoclon
749	47.5	57.9	126	8	ADO36349	Ado36349 Intracell	822	47.5	240	5	AAU79563	Aau79563 Monoclon
750	47.5	57.9	126	8	ADP46964	Adp46964 Murine he	823	47.5	240	5	ABP95997	Abp95997 Human ser
751	47.5	57.9	126	8	ADQ75222	Adq75222 Immunoglo	824	47.5	240	6	ADG96863	AdG96863 Single ch
752	47.5	57.9	127	6	ADA90120	Ada90120 Anti-Abet	825	47.5	240	7	ADG96863	AdG96863 Single ch
753	47.5	57.9	127	6	AAQ31085	AaQ31085 Human ant	826	47.5	240	8	ADL92369	AdL92369 Human pha
754	47.5	57.9	127	8	ADP46950	Adp46950 Murine he	827	47.5	241	5	ABP46049	Abp46049 Human Bly

828	47.5	57.9	241	7	ADG96876	Adg96876 Single ch	901	47.5	57.9	248	8	ADH13874	Adh13874 Human vas
829	47.5	57.9	241	9	AEA62548	Aea62548 Her-2/neu	902	47.5	57.9	248	8	ADI58096	Adi58096 Reg IV-sp
830	47.5	57.9	241	9	AEA62549	Aea62549 Her-2/neu	903	47.5	57.9	248	8	ADI58104	Adi58104 Reg IV-sp
831	47.5	57.9	241	9	AEA62549	Aea62549 Her-2/neu	903	47.5	57.9	248	8	ADI58104	Adi58104 Reg IV-sp
832	47.5	57.9	242	2	AEA62549	Aea62549 Her-2/neu	904	47.5	57.9	248	8	ADI58051	Adi58051 Reg IV-sp
833	47.5	57.9	242	4	AAy21881	Aay21881 Amino aci	905	47.5	57.9	248	8	ADI58045	Adi58045 Reg IV-sp
834	47.5	57.9	242	4	AAy21881	Aay21881 Amino aci	906	47.5	57.9	248	8	ADI58103	Adi58103 Reg IV-sp
835	47.5	57.9	242	8	ADH158106	Adh158106 Reg IV-sp	907	47.5	57.9	248	8	ADI58087	Adi58087 Reg IV-sp
836	47.5	57.9	242	8	ADH158098	Adh158098 Reg IV-sp	908	47.5	57.9	248	8	ADI58086	Adi58086 Reg IV-sp
837	47.5	57.9	242	8	ADH158098	Adh158098 Reg IV-sp	908	47.5	57.9	248	8	ADI58091	Adi58091 Reg IV-sp
838	47.5	57.9	243	5	ABP46045	Abp46045 Human Bly	910	47.5	57.9	248	8	ADI58058	Adi58058 Reg IV-sp
839	47.5	57.9	243	5	ABP45958	Abp45958 Human Bly	911	47.5	57.9	248	8	ADR28065	Adr28065 NPB polyP
840	47.5	57.9	243	6	AAO311149	Aao311149 Human CMO	912	47.5	57.9	248	8	ADR28060	Adr28060 NPB polyP
841	47.5	57.9	243	6	AAO311145	Aao311145 Human CMO	913	47.5	57.9	248	8	ADR28059	Adr28059 NPB polyP
842	47.5	57.9	243	7	ADG304336	Adg304336 Human GMB	914	47.5	57.9	248	8	ADR28070	Adr28070 NPB polyP
843	47.5	57.9	243	7	ADG96872	Adg96872 Single ch	915	47.5	57.9	249	6	AAE36257	Aae36257 TRAIL rec
844	47.5	57.9	243	7	ADG96872	Adg96872 Single ch	916	47.5	57.9	249	8	ADI58102	Adi58102 Reg IV-sp
845	47.5	57.9	243	9	ADG96872	Adg96872 Single ch	917	47.5	57.9	249	8	ADI58055	Adi58055 Reg IV-sp
846	47.5	57.9	243	9	ADY34218	Ady34218 TRAIL rec	918	47.5	57.9	249	8	ADI58094	Adi58094 Reg IV-sp
847	47.5	57.9	243	9	ADY34222	Ady34222 TRAIL rec	919	47.5	57.9	249	8	ADR28202	Adr28202 T1008F07
848	47.5	57.9	244	6	ABJ19831	Abj19831 Human VEG	920	47.5	57.9	249	9	AEA27585	Aea27585 Antibody
849	47.5	57.9	244	6	AAO311139	Aao311139 Human CMO	921	47.5	57.9	249	9	AEA55201	Aea55201 TRAIL rec
850	47.5	57.9	244	7	ADG30488	Adg30488 Human GMC	922	47.5	57.9	250	4	AAU00212	Aau00212 Monoclonal
851	47.5	57.9	244	7	ADH13872	Adh13872 Human vas	923	47.5	57.9	250	5	ABP45409	Abp45409 Human Bly
852	47.5	57.9	244	8	ADI58089	Adi58089 Reg IV-sp	924	47.5	57.9	250	6	ABJ19826	Abj19826 Human VEG
853	47.5	57.9	244	8	ADR28082	Adr28082 NPB polyP	925	47.5	57.9	250	7	ADG96236	Adg96236 Single ch
854	47.5	57.9	244	9	ADY34212	Ady34212 TRAIL rec	926	47.5	57.9	250	8	ADH13868	Adh13868 Human vas
855	47.5	57.9	245	4	AAE67620	Aae67620 Human leu	927	47.5	57.9	250	8	ADH13868	Adh13868 Human vas
856	47.5	57.9	245	6	AAO311137	Aao311137 Human CMO	928	47.5	57.9	251	5	ABP45594	Abp45594 Human Bly
857	47.5	57.9	245	8	ADI58088	Adi58088 Reg IV-sp	929	47.5	57.9	251	5	ABP45729	Abp45729 Human Bly
858	47.5	57.9	245	8	ADI58105	Adi58105 Reg IV-sp	930	47.5	57.9	251	5	ABP45697	Abp45697 Human Bly
859	47.5	57.9	245	8	ADI58093	Adi58093 Reg IV-sp	931	47.5	57.9	251	5	ABP44897	Abp44897 Human Bly
860	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	932	47.5	57.9	251	5	ADG96556	Adg96556 Single ch
861	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	933	47.5	57.9	251	7	ADG95724	Adg95724 Single ch
862	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	934	47.5	57.9	251	7	ADG96421	Adg96421 Single ch
863	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	935	47.5	57.9	251	7	ADG96524	Adg96524 Single ch
864	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	936	47.5	57.9	251	7	ADG96524	Adg96524 Single ch
865	47.5	57.9	245	8	ADG92927	Adg92927 Human c-M	937	47.5	57.9	251	8	ADI58101	Adi58101 Reg IV-sp
866	47.5	57.9	245	9	ADW90309	Adw90309 Phage scf	938	47.5	57.9	251	8	ADI58099	Adi58099 Reg IV-sp
867	47.5	57.9	245	9	ADW90305	Adw90305 Phage scf	939	47.5	57.9	251	8	ADI58123	Adi58123 Human IGF
868	47.5	57.9	245	9	ADX01795	Adx01795 SARS coro	940	47.5	57.9	252	5	ABP45420	Abp45420 Human Bly
869	47.5	57.9	245	9	ADY34210	Ady34210 TRAIL rec	941	47.5	57.9	252	7	ADG96247	Adg96247 Single ch
870	47.5	57.9	246	5	ABP45964	Abp45964 Human Bly	942	47.5	57.9	252	8	ADI58052	Adi58052 Reg IV-sp
871	47.5	57.9	246	5	ABP45313	Abp45313 Human Bly	943	47.5	57.9	252	8	ADG96556	Adg96556 Single ch
872	47.5	57.9	246	6	ABJ19834	Abj19834 Human VEG	944	47.5	57.9	252	9	ADG96556	Adg96556 Single ch
873	47.5	57.9	246	7	ADG96140	Adg96140 Single ch	945	47.5	57.9	252	9	ADX01974	Adx01974 SARS coro
874	47.5	57.9	246	7	ADG96791	Adg96791 Single ch	946	47.5	57.9	252	9	ADX02024	Adx02024 SARS coro
875	47.5	57.9	246	8	ADH13876	Adh13876 Human vas	947	47.5	57.9	252	9	ADX01968	Adx01968 SARS coro
876	47.5	57.9	246	8	ADR28084	Adr28084 NPB polyP	948	47.5	57.9	252	9	ADX01970	Adx01970 SARS coro
877	47.5	57.9	246	8	ADR28081	Adr28081 NPB polyP	949	47.5	57.9	252	9	ADX02010	Adx02010 SARS coro
878	47.5	57.9	246	8	ADR28080	Adr28080 NPB polyP	950	47.5	57.9	252	9	ADX01998	Adx01998 SARS coro
879	47.5	57.9	246	8	ADG92925	Adg92925 Human c-M	951	47.5	57.9	252	9	ADX02000	Adx02000 SARS coro
880	47.5	57.9	246	8	ADG92925	Adg92925 Human c-M	952	47.5	57.9	252	9	ADX02004	Adx02004 SARS coro
881	47.5	57.9	247	5	ABP45912	Abp45912 Human Bly	953	47.5	57.9	252	9	ADX02006	Adx02006 SARS coro
882	47.5	57.9	247	6	ABJ19835	Abj19835 Human Bly	954	47.5	57.9	252	9	ADX02002	Adx02002 SARS coro
883	47.5	57.9	247	6	ABJ19835	Abj19835 Human Bly	955	47.5	57.9	252	9	ADX02014	Adx02014 SARS coro
884	47.5	57.9	247	7	ADG95812	Adg95812 Single ch	956	47.5	57.9	252	9	ADX01976	Adx01976 SARS coro
885	47.5	57.9	247	7	ADG96739	Adg96739 Single ch	957	47.5	57.9	252	9	ADX01972	Adx01972 SARS coro
886	47.5	57.9	247	8	ADH13877	Adh13877 Human vas	958	47.5	57.9	252	9	ADX02008	Adx02008 SARS coro
887	47.5	57.9	247	8	ADI58107	Adi58107 Reg IV-sp	959	47.5	57.9	252	9	ADX02032	Adx02032 SARS coro
888	47.5	57.9	247	8	ADI58056	Adi58056 Reg IV-sp	960	47.5	57.9	252	9	ADX02012	Adx02012 SARS coro
889	47.5	57.9	247	8	ADI58090	Adi58090 Reg IV-sp	961	47.5	57.9	252	9	ADX02016	Adx02016 SARS coro
890	47.5	57.9	247	8	ADI58100	Adi58100 Reg IV-sp	962	47.5	57.9	253	5	ABP44847	Abp44847 Human Bly
891	47.5	57.9	247	8	ADR28072	Adr28072 NPB polyP	963	47.5	57.9	253	5	ABP44847	Abp44847 Human Bly
892	47.5	57.9	247	8	ADR28091	Adr28091 NPB polyP	964	47.5	57.9	253	6	ABJ19830	Abj19830 Human VEG
893	47.5	57.9	247	9	ADW90316	Adw90316 Phage scf	965	47.5	57.9	253	7	ADG95674	Adg95674 Single ch
894	47.5	57.9	247	9	ADX01840	Adx01840 SARS coro	966	47.5	57.9	253	7	ADG95805	Adg95805 Single ch
895	47.5	57.9	248	5	ABP45445	Abp45445 Human Bly	967	47.5	57.9	253	8	ADH13872	Adh13872 Human vas
896	47.5	57.9	248	5	ABP44910	Abp44910 Human Bly	968	47.5	57.9	253	8	ADI58097	Adi58097 Reg IV-sp
897	47.5	57.9	248	6	ABJ19832	Abj19832 Human VEG	969	47.5	57.9	253	8	ADI58057	Adi58057 Reg IV-sp
898	47.5	57.9	248	7	ADG96272	Adg96272 Single ch	970	47.5	57.9	253	8	ADI58060	Adi58060 Reg IV-sp
899	47.5	57.9	248	7	ADG95737	Adg95737 Single ch	971	47.5	57.9	253	8	ADH13878	Adh13878 Human IGF
900	47.5	57.9	248	8	ADG34309	Adg34309 Neurokini	972	47.5	57.9	254	5	ABP45690	Abp45690 Human Bly
							973	47.5	57.9	254	5	ABP45728	Abp45728 Human Bly

974 47.5 57.9 254 7 ADG96555 Single ch
 975 47.5 57.9 254 7 ADG96517 Single ch
 976 47.5 57.9 254 8 ADI58092 Reg IV-sp
 977 47.5 57.9 254 8 ADI58085 Reg IV-sp
 978 47.5 57.9 254 8 ADI58042 Reg IV-sp
 979 47.5 57.9 255 8 ADH34561 scFv SC02
 980 47.5 57.9 255 8 ADI58044 Reg IV-sp
 981 47.5 57.9 256 5 ABP45172 Human Bly
 982 47.5 57.9 256 7 ADG95999 Single ch
 983 47.5 57.9 260 5 ABG92023 Antibody
 984 47.5 57.9 262 8 ADG92866 Human Myo
 985 47.5 57.9 263 5 ABG92024 Antibody
 986 47.5 57.9 274 8 ADO25153 Melanoma
 987 47.5 57.9 275 8 ADO25155 Melanoma
 988 47.5 57.9 276 8 ADO25149 Melanoma
 989 47.5 57.9 277 8 ADO25150 Melanoma
 990 47.5 57.9 278 8 ADO25151 Melanoma
 991 47.5 57.9 281 2 AAW27560 Consensus
 992 47.5 57.9 281 8 ADO25156 Melanoma
 993 47.5 57.9 288 8 ADR28055 NPB polyp
 994 47.5 57.9 290 6 ABP55318 Pelb/5AF/
 995 47.5 57.9 290 7 ADI99518 Single ch
 996 47.5 57.9 291 5 AAE29202 Single ch
 997 47.5 57.9 291 5 ABG60632 Immunoglo
 998 47.5 57.9 291 8 ADN06993 Human BFG
 999 47.5 57.9 291 8 ADN06992 Human BFG
 1000 47.5 57.9 293 4 AAG65715 Amino aci

ALIGNMENTS

RESULT 1
 AAW23430 standard; peptide; 16 AA.
 ID AAW23430 standard; peptide; 16 AA.
 AC AAW23430;
 XX
 XX
 DT 23-APR-1998 (first entry)
 DE CDR-2 of rW12 heavy chain.
 XX
 KW Antibody; complementarity determining region; CDR; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Rattus sp.
 XX
 XX WO9734636-A1.
 XX
 XX
 PD 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX
 PS Claim 3; Page 30; 46pp; English.
 XX
 CC This sequence represents the complementarity determining region-2 (CDR-2)
 CC of the rW12 heavy chain. This sequence is used in an antibody of the
 CC invention. The antibody of the invention is a chimeric or humanised anti-
 CC idiotype antibodies (cab and hab, respectively) or a fragment which
 CC specifically binds to the idiotype region of an anti-carcinoembryonic

CC antigen (CEA), where: (i) cab comprises the rW12 light (L) and heavy (H)
 CC chain variable regions, or silent mutations; and (ii) hab comprises rW12
 CC complementarity determining regions (CDR) and humanised framework (FR)
 CC regions. The hab is used as a vaccine to stimulate an immune response in
 CC a patient against cancers expressing CEA. The hab, can be used to clear
 CC non-targeted antibody in a method of diagnosis or treatment of a patient
 CC where a CEA antibody is used as a (pre-)targeting or therapy agent. The
 CC cab is used to detect the presence of an antibody that specifically binds
 CC to CEA in a sample
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 82; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SITSTGGTYHAESVKG 16
 |||||
 Db 1 SITSTGGTYHAESVKG 16
 |||||
 RESULT 2
 AAW23432
 ID AAW23432 standard; protein; 122 AA.
 XX
 AC AAW23432;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE rW12 heavy chain.
 XX
 KW Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Rattus sp.
 XX
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /note= "complementarity determining region-1"
 FT Region 50..66
 FT /note= "complementarity determining region-2"
 FT Region 99..111
 FT /note= "complementarity determining region-3"
 FT Misc-difference 100
 FT /note= "encoded by AGAC"
 XX
 XX WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86286.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX
 PS Claim 5; Fig 7; 46pp; English.
 XX
 CC This sequence represents the rat rW12 heavy chain. This sequence is used
 CC in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotypic antibodies (cab and hab,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cab

CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The CAB is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample
 XX
 XX Sequence 122 AA;

Query Match 87.2%; Score 71.5; DB 2; Length 122;

Best Local Similarity 94.1%; Pred. No. 0.00037; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16

Db 50 SITSTGGTYHAESVKG 66

RESULT 3

AAW23437

ID AAW23437 standard; protein; 122 AA.

XX AC AAW23437;

XX 23-APR-1998 (first entry)

XX Modified heavy chain variable region KOLWI2VH-1.

XX Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.

XX Synthetic.

XX Rattus sp.

XX Key Location/Qualifiers

FT Misc-difference 10 /note= "D to G mutation"

FT Misc-difference 11 /note= "L to V mutation"

FT Misc-difference 19 /note= "K to R mutation"

FT Misc-difference 23 /note= "V to S mutation"

FT Misc-difference 24 /note= "A to S mutation"

FT Region 31..35

FT Misc-difference 43 /note= "complementarity determining region-1"

FT Region 50..66

FT Misc-difference 77 /note= "complementarity determining region-2"

FT Misc-difference 80 /note= "S to N mutation"

FT Misc-difference 84 /note= "Y to P mutation"

FT Misc-difference 92 /note= "N to D mutation"

FT Misc-difference 93 /note= "A to G mutation"

FT Region 99..111

FT Misc-difference 116 /note= "complementarity determining region-3"

FT Misc-difference 117 /note= "S to T mutation"

FT /note= "S to P mutation"

XX WO9734636-A1.

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XX

PD 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Losman MJ, Hansen H;

XX WPI; 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic

XX antibodies - useful in detection of anti-CEA antibodies and as vaccine to

XX stimulate immune response against cancer.

XX Claim 7; Fig 1; 46pp; English.

XX This sequence represents a modified version of the rat rW12 heavy chain

XX variable region, designated KOLWI2VH-1. This sequence is used in an

XX antibody of the invention. The antibody of the invention is a chimeric or

XX humanised anti-idiotypic antibodies (cAb and hAb, respectively) or a

XX fragment which specifically binds to the idiotype region of an anti-

XX carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light

XX (L) and heavy (H) chain variable regions, or silent mutations; and (ii)

XX hAb comprises rW12 complementarity determining regions (CDR) and

XX humanised framework (FR) regions. The hAb is used as a vaccine to

XX stimulate an immune response in a patient against cancers expressing CEA.

XX The hAb, can be used to clear non-targeted antibody in a method of

XX diagnosis or treatment of a patient where a CEA antibody is used as a

XX (pre-)targeting or therapy agent. The cAb is used to detect the presence

XX of an antibody that specifically binds to CEA in a sample

XX Sequence 122 AA;

XX Query Match 87.2%; Score 71.5; DB 2; Length 122;

XX Best Local Similarity 94.1%; Pred. No. 0.00037;

XX Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16

Db 50 SITSTGGTYHAESVKG 66

RESULT 4

AAW23441

ID AAW23441 standard; protein; 122 AA.

XX AC AAW23441;

XX 23-APR-1998 (first entry)

XX hW12 heavy chain.

XX Antibody; complementarity determining region; heavy chain; human; CEA;

XX hW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;

XX therapy; idiotype region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 31..35

FT /note= "complementarity determining region-1"

FT Region 50..66

FT /note= "complementarity determining region-2"

FT Region 99..111

FT /note= "complementarity determining region-3"

FT /note= "S to T mutation"

FT /note= "S to P mutation"

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

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XX PR 20-MAR-1996; 96US-0013708P.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Leung S, Losman MJ, Hansen H;
XX DR WPI; 1997-479997/44.
XX DR N-PSDB; AAT86299.
XX FT Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
PT stimulate immune response against cancer.
XX PS Disclosure; Fig 3; 46pp; English.
XX CC This sequence represents the human hW12 heavy chain. This sequence is
CC used in an antibody of the invention. The antibody of the invention is a
CC chimeric or humanised anti-idiotypic antibodies (cAb and hAb,
CC respectively) or a fragment which specifically binds to the idiotype
CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb
CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
CC vaccine to stimulate an immune response in a patient against cancers
CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
CC method of diagnosis or treatment of a patient where a CEA antibody is
CC used as a (pre-)targeting or therapy agent. The cAb is used to detect the
CC presence of an antibody that specifically binds to CEA in a sample
XX Sequence 122 AA;
SQ
Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00037;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
Db ||||| ||||| ||||| |||||
50 SITSTGGGTYHAESVKG 66

RESULT 5
AAW23438
ID AAW23438 standard; protein; 122 AA.
XX AC AAW23438;
XX DT 23-APR-1998 (first entry)
XX DE Modified heavy chain variable region KOLWI2VH-2.
XX KW Antibody; complementarity determining region; heavy chain; rat; CEA;
KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
KW therapy; idiotype region; mutein; variable region.
XX OS Synthetic.
OS Rattus sp.
XX Key Location/Qualifiers
FH Misc-difference 5 /note= "Q to V mutation"
FT Misc-difference 10 /note= "D to G mutation"
FT Misc-difference 11 /note= "L to V mutation"
FT Misc-difference 19 /note= "K to R mutation"
FT Misc-difference 23 /note= "V to S mutation"
FT Misc-difference 24 /note= "A to S mutation"
FT Region 31.35 /note= "complementarity determining region-1"
FT

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FT Misc-difference 43 /note= "E to K mutation"
FT Region 50.66 /note= "complementarity determining region-2"
FT Misc-difference 77 /note= "S to N mutation"
FT Misc-difference 80 /note= "Y to F mutation"
FT Misc-difference 84 /note= "N to D mutation"
FT Misc-difference 92 /note= "A to G mutation"
FT Misc-difference 93 /note= "T to V mutation"
FT Region 99.111 /note= "complementarity determining region-3"
FT Misc-difference 116 /note= "S to T mutation"
FT Misc-difference 117 /note= "S to P mutation"
XX WO9734636-A1.
XX 25-SEP-1997.
XX 19-MAR-1997; 97WO-US004696.
XX 20-MAR-1996; 96US-0013708P.
XX (IMMU-) IMMUNOMEDICS INC.
XX Leung S, Losman MJ, Hansen H;
XX WPI; 1997-479997/44.
XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
PT stimulate immune response against cancer.
XX Claim 7; Fig 1; 46pp; English.
XX This sequence represents a modified version of the rat rW12 heavy chain
CC variable region, designated KOLWI2VH-2. This sequence is used in an
CC antibody of the invention. The antibody of the invention is a chimeric or
CC humanised anti-idiotypic antibodies (cAb and hAb, respectively) or a
CC fragment which specifically binds to the idiotype region of an anti-
CC carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light
CC (L) and heavy (H) chain variable regions, or silent mutations; and (ii)
CC hAb comprises rW12 complementarity determining regions (CDR) and
CC humanised framework (FR) regions. The hAb is used as a vaccine to
CC stimulate an immune response in a patient against cancers expressing CEA.
CC The hAb, can be used to clear non-targeted antibody in a method of
CC diagnosis or treatment of a patient where a CEA antibody is used as a
CC (pre-)targeting or therapy agent. The cAb is used to detect the presence
CC of an antibody that specifically binds to CEA in a sample
XX Sequence 122 AA;
SQ
Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00037;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
Db ||||| ||||| ||||| |||||
50 SITSTGGGTYHAESVKG 66

RESULT 6
ADM07764
ID ADM07764 standard; peptide; 16 AA.
XX AC ADM07764;
XX

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DT 20-MAY-2004 (first entry)
 DE Canine immunoglobulin heavy chain variable domain CDR2 peptide 8.
 XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW antiallergic; allergy; IgE; gene therapy;
 KW complementarity determining region; CDR2.
 XX Canis familiaris.
 XX WO2003060080-A2.
 XX 24-JUL-2003.
 XX 20-DEC-2002; 2002WO-US041362.
 XX 21-DEC-2001; 2001US-0344874P.
 XX (IDEX-) IDEX LAB INC.
 XX Krah ER, Guo H, Aiyappa A, Lawton R;
 XX WPI; 2003-598521/56.
 XX New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 PT Claim 16; Page 95; 130pp; English.
 PS The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a canine
 CC immunoglobulin heavy chain variable domain complementarity determining
 CC region (CDR) peptide of the invention.
 XX Sequence 16 AA;
 SQ
 Query Match 70.7%; Score 58; DB 7; Length 16;
 Best Local Similarity 62.5%; Pred. No. 0.0073; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 6;
 QY 1 SITSTGCTYHAESVKG 16
 Db 1 SITSSGCTFYADAVKG 16
 RESULT 7
 ADU86658
 ID ADU86658 standard; peptide; 16 AA.
 XX ADU86658;
 AC ADU86658;
 XX 10-FEB-2005 (first entry)
 DT Peptide display system related CDR 2 #15.
 DE antinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;
 KW antidiabetic; vasotropic; vaccine; protein purification; protein folding;
 KW diagnosis; inflammation; immune disorder; allergic hypersensitivity;
 KW infection; autoimmune disease; asthma; psoriasis;
 KW insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; myasthenia gravis; hematological disease;
 KW neoplasm; complementarity determining region 2; CDR2.
 XX Homo sapiens.
 OS WO2004101790-A1.
 XX 25-NOV-2004.
 PD 14-MAY-2004; 2004WO-GB002102.
 XX

PR 14-MAY-2003; 2003US-0470340P.
 XX 17-MAR-2004; 2004US-0554021P.
 PA (DOMA-) DOMANTIS LTD.
 XX Jespers LS, Jones PC, Famm KHJ, Winter GP;
 PI WPI; 2004-821888/81.
 XX Recovering a polypeptide that unfolds reversibly from a repertoire of
 PT polypeptides for treating e.g., cancer, by unfolding a portion of the
 PT displayed polypeptides and refolding a portion of the unfolded
 PT polypeptides.
 XX Disclosure; SEQ ID NO 147; 222pp; English.
 PS The invention describes a method of recovering a polypeptide that unfolds
 CC reversibly from a repertoire of polypeptides that unfolds reversibly and
 CC has a common selectable characteristic that distinguishes folded
 CC polypeptides from unfolded or misfolded polypeptides. The method
 CC comprises: providing a polypeptide display system comprising the
 CC repertoire of displayed polypeptides; unfolding at least a portion of the
 CC displayed polypeptides; refolding at least a portion of the unfolded
 CC polypeptides; and recovering at least one polypeptide that unfolds
 CC reversibly and has the selectable characteristic from the refolded
 CC portion. The method is useful in recovering a polypeptide that unfolds
 CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
 CC library or repertoire is useful for selecting a polypeptide comprising an
 CC antibody variable domain that unfolds reversibly or a polypeptide that
 CC refolds reversibly and comprising an antibody format. The polypeptide is
 CC useful in the manufacture of a medicament for diagnosing, treating or
 CC preventing a disease or medical condition mediated by a cytokine,
 CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
 CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
 CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
 CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
 CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
 CC tumor. This is the amino acid sequence of complementarity determining
 CC region (CDR) used in a polypeptide display system for selection of
 CC reversibly folding peptides.
 XX Sequence 16 AA;
 SQ
 Query Match 69.5%; Score 57; DB 8; Length 16;
 Best Local Similarity 68.8%; Pred. No. 0.011;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SITSTGCTYHAESVKG 16
 Db 1 SITODGSTYADSVKG 16
 RESULT 8
 AEB46921
 ID AEB46921 standard; protein; 117 AA.
 XX AEB46921;
 AC AEB46921;
 XX 22-SEP-2005 (first entry)
 DT Human variable heavy chain 02-118.
 XX cytostatic; gene therapy; protein interaction; pharmaceutical;
 KW immunoconjugate; diagnosis; neurological disease;
 KW acute myelogenous leukemia; hematological disease; neoplasm;
 KW chronic myelocytic leukemia; acute promyelocytic leukemia;
 KW myelodysplastic syndrome; immunostimulant; acute lymphoblastic leukemia;
 KW t-cell acute lymphoblastic leukemia; variable heavy chain; ds.
 XX Homo sapiens.
 OS WO2005063819-A2.
 XX

KW antibody therapy; tumor; cancer; antibody 8.
XX Homo sapiens.
XX WO2004087756-A2.
XX 14-OCT-2004.
XX 01-APR-2004; 2004WO-EP003442.
XX 02-APR-2003; 2003US-0459837P.
XX 15-APR-2003; 2003US-0463003P.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
PI Schumacher R, Van De Winkel J, Van Vugt M;
XX WPI; 2004-737667/72.
XX
PT New antibody binding to insulin-like growth factor I receptor (IGF-IR)
PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for
PT treating cancers of the colon, breast, prostate and lung.
XX
PS Disclosure; SEQ ID NO 3; 81pp; English.
XX
CC The invention relates to a novel antibody binding to insulin-like growth
CC factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II
CC to IGF-IR. An antibody binding to insulin-like growth factor I receptor
CC (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where
CC the antibody is of IgG1 isotype and shows a ratio of inhibition of the
CC binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-
CC IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a
CC preparation of IGF-IR expressing cells after 24 hours at a concentration
CC of the antibody of 100 nM by ADCC, is new. An antibody of the invention
CC has cytostatic activity, and may have a use in antibody therapy. The
CC methods and compositions of the present invention are useful for the
CC treatment of tumors and cancers of the colon, breast, prostate and lung
CC using antibodies against human insulin-like growth factor I receptor (IGF
CC -IR). The present sequence represents the heavy chain variable region of
CC the IGF-IR antibody 8 of the invention.
XX
SQ Sequence 119 AA;
Query Match 68.3%; Score 56; DB 8; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.17;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SITSTGGTYHAESVKG 16
: | | | | | : | | | | |
DB 50 AIGSGGGTYADSVKG 65
RESULT 11
ADT88866
ID ADT88866 standard; protein; 119 AA.
XX
AC ADT88866;
XX
XX 30-DEC-2004 (first entry)
XX
DE Human IGF-IR antibody 23 heavy chain variable region SEQ ID NO:5.
XX
XX antibody; IGF-IR; Insulin-like growth factor I receptor; cytostatic;
KW antibody therapy; tumor; cancer; antibody 23.
XX
XX Homo sapiens.
XX
XX WO2004087756-A2.
XX
XX 14-OCT-2004.
XX
XX 01-APR-2004; 2004WO-EP003442.

XX
PR 02-APR-2003; 2003US-0459837P.
PR 15-APR-2003; 2003US-0463003P.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
PI Schumacher R, Van De Winkel J, Van Vugt M;
XX WPI; 2004-737667/72.
XX
XX New antibody binding to insulin-like growth factor I receptor (IGF-IR)
PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for
PT treating cancers of the colon, breast, prostate and lung.
XX
XX Disclosure; SEQ ID NO 5; 81pp; English.
XX
CC The invention relates to a novel antibody binding to insulin-like growth
CC factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II
CC to IGF-IR. An antibody binding to insulin-like growth factor I receptor
CC (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where
CC the antibody is of IgG1 isotype and shows a ratio of inhibition of the
CC binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-
CC IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a
CC preparation of IGF-IR expressing cells after 24 hours at a concentration
CC of the antibody of 100 nM by ADCC, is new. An antibody of the invention
CC has cytostatic activity, and may have a use in antibody therapy. The
CC methods and compositions of the present invention are useful for the
CC treatment of tumors and cancers of the colon, breast, prostate and lung
CC using antibodies against human insulin-like growth factor I receptor (IGF
CC -IR). The present sequence represents the heavy chain variable region of
CC the IGF-IR antibody 23 of the invention.
XX
SQ Sequence 119 AA;
Query Match 68.3%; Score 56; DB 8; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.17;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 SITSTGGTYHAESVKG 16
: | | | | | : | | | | |
DB 50 AIGSGGGTYADSVKG 65
RESULT 12
ADT88862
ID ADT88862 standard; protein; 119 AA.
XX
AC ADT88862;
XX
XX 30-DEC-2004 (first entry)
XX
DE Human IGF-IR antibody 1A heavy chain variable region SEQ ID NO:1.
XX
XX antibody; IGF-IR; Insulin-like growth factor I receptor; cytostatic;
KW antibody therapy; tumor; cancer; antibody 1A.
XX
XX Homo sapiens.
XX
XX WO2004087756-A2.
XX
XX 14-OCT-2004.
XX
XX 01-APR-2004; 2004WO-EP003442.
XX
XX 02-APR-2003; 2003US-0459837P.
PR 15-APR-2003; 2003US-0463003P.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
PI Schumacher R, Van De Winkel J, Van Vugt M;
XX

DR WPI; 2004-737667/72.
 XX New antibody binding to insulin-like growth factor I receptor (IGF-IR)
 PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for
 PT treating cancers of the colon, breast, prostate and lung.
 XX
 XX Claim 5; SEQ ID NO 1; 81pp; English.
 XX
 CC The invention relates to a novel antibody binding to insulin-like growth
 CC factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II
 CC to IGF-IR. An antibody binding to insulin-like growth factor I receptor
 CC (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where
 CC the antibody is of IgG1 isotype and shows a ratio of inhibition of the
 CC binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-
 CC IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a
 CC preparation of IGF-IR expressing cells after 24 hours at a concentration
 CC of the antibody of 100 nM by ADCC, is new. An antibody of the invention
 CC has cytostatic activity, and may have a use in antibody therapy. The
 CC methods and compositions of the present invention are useful for the
 CC treatment of tumors and cancers of the colon, breast, prostate and lung
 CC using antibodies against human insulin-like growth factor I receptor (IGF
 CC -IR). The present sequence represents the heavy chain variable region of
 CC the IGF-IR antibody 1A of the invention.
 XX
 SQ Sequence 119 AA;

Query Match 68.3%; Score 56; DB 8; Length 119;
 Best Local Similarity 68.8%; Pred. No. 0.17;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 :|||:||||:||||
 Db 50 AIGSGGGTYADSVKG 65

RESULT 13
 ADT88873
 ID ADT88873 standard; protein; 119 AA.
 XX
 AC ADT88873;
 XX
 XX 30-DEC-2004 (first entry)
 DT
 XX Human IGF-IR antibody 1A VH R30S/Y94H/D104E variant.
 DE
 XX antibody; IGF-IR; Insulin-like growth factor I receptor; cytostatic;
 KW antibody therapy; tumor; cancer; antibody 1A.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 30
 FT /note= "Wild-type Arg substituted by Ser"
 FT Misc-difference 94
 FT /note= "Wild-type Tyr substituted by His"
 FT Misc-difference 104
 FT /note= "Wild-type Asp substituted by Glu"
 FT
 XX WO2004087756-A2.
 PN
 XX 14-OCT-2004.
 PD
 XX
 XX 01-APR-2004; 2004WO-EP003442.
 PF
 XX 02-APR-2003; 2003US-0459837P.
 PR
 XX 15-APR-2003; 2003US-0463003P.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Graus Y, Kopetzki E, Kuenkele K, Mundigl O, Parren P, Rebers F;
 PI Schumacher R, Van De Winkel J, Van Vugt M;
 XX WPI; 2004-737667/72.
 DR

XX New antibody binding to insulin-like growth factor I receptor (IGF-IR)
 PT and inhibiting the binding of IGF-I and IGF-II to IGF-IR, useful for
 PT treating cancers of the colon, breast, prostate and lung.
 XX
 XX Claim 7; Page; 81pp; English.
 XX
 CC The invention relates to a novel antibody binding to insulin-like growth
 CC factor I receptor (IGF-IR) and inhibiting the binding of IGF-I and IGF-II
 CC to IGF-IR. An antibody binding to insulin-like growth factor I receptor
 CC (IGF-IR) and inhibiting the binding of IGF-I and IGF-II to IGF-IR, where
 CC the antibody is of IgG1 isotype and shows a ratio of inhibition of the
 CC binding of IGF-I to IGF-IR to the inhibition of binding of IGF-II to IGF-
 CC IR of 1:3 to 3:1 and induces cell death of 20% or more cells of a
 CC preparation of IGF-IR expressing cells after 24 hours at a concentration
 CC of the antibody of 100 nM by ADCC, is new. An antibody of the invention
 CC has cytostatic activity, and may have a use in antibody therapy. The
 CC methods and compositions of the present invention are useful for the
 CC treatment of tumors and cancers of the colon, breast, prostate and lung
 CC using antibodies against human insulin-like growth factor I receptor (IGF
 CC -IR). The present sequence represents a variant of the heavy chain
 CC variable region of the IGF-IR antibody 1A of the invention. Note: The
 CC present sequence is not represented in the specification, but has been
 CC created by the indexer using sequence information supplied in SEQ ID NO:1
 CC (ADT88862) and Claim 7.
 XX
 SQ Sequence 119 AA;

Query Match 68.3%; Score 56; DB 8; Length 119;
 Best Local Similarity 68.8%; Pred. No. 0.17;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 :|||:||||:||||
 Db 50 AIGSGGGTYADSVKG 65

RESULT 14
 AAR27053
 ID AAR27053 standard; protein; 139 AA.
 XX
 AC AAR27053;
 XX
 XX 01-MAR-1993 (first entry)
 DT
 XX Anti-CEA specific heavy chain variable region.
 DE
 XX Human; carcinoembryonic antigen; heavy chain; light chain; variable;
 KW region; diagnostic; tumor; markers; targeting.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..139
 FT /note= "mature peptide"
 FT
 XX JP04234987-A.
 PN
 XX 24-AUG-1992.
 PD
 XX 28-DEC-1990; 90JP-00408810.
 PF
 XX 28-DEC-1990; 90JP-00408810.
 PR
 XX (MITU) MITSUBISHI KASEI CORP.
 PA
 XX WPI; 1992-327631/40.
 DR N-FSDB; AAQ28746.
 DR
 XX New DNA fragments encoding variable regions of ABS specific for human CEA
 PT - for diagnosing and monitoring tumours, as tumour markers and for
 PT

PT treatment of tumours.
 XX Disclosure; Fig 1; 7pp; Japanese.
 PS
 CC The anti-CEA murine monoclonal antibody heavy chain variable region was
 CC obtd. by screening a cDNA library prepd. from mRNA obtd. from hybridomas
 CC producing anti-CEA-specific antibodies with a probe based on the constant
 CC region of the H-chain. The antibodies reacts specifically with human CEA
 CC and are useful as a diagnostic agents, as tumour markers for digestive
 CC organs, for diagnosis of malignant tumours, for monitoring after cancer
 CC operations, to follow up bloodless therapy or as therapeutic agents in
 CC passive immune therapy and targetting therapy. See also AAR27054
 XX
 SQ Sequence 139 AA;

Query Match 68.3%; Score 56; DB 2; Length 139;
 Best Local Similarity 68.8%; Pred. No. 0.2;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 DB 69 SITSDGSTVYPSVKG 84
 ||||| |||: |||||
 ||||| |||: |||||

RESULT 15
 AAR30480
 ID AAR30480 standard; protein; 139 AA.
 XX
 AC AAR30480;
 XX
 XX 06-MAY-1993 (first entry)
 DT
 DE hCEA specific mouse heavy chain variable chain region.
 XX
 KW Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;
 KW cancer.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT 20..139
 FT /note= "mature peptide"
 FT
 XX JP04330295-A.
 PN
 XX 18-NOV-1992.
 PD
 XX 28-DEC-1990; 90JP-00408811.
 PF
 XX 28-DEC-1990; 90JP-00408811.
 PR
 XX (MITU) MITSUBISHI KASEI CORP.
 PA
 XX WPI; 1993-003502/01.
 DR N-PSDB; AAQ33052.
 XX
 XX Mouse-human chimeric antibody for diagnosis and treatment of cancer -
 PT obtd. by combining variable region of mouse antibody specifically
 PT combining to human cancer embryonic antigen with constant region of human
 PT antibody.
 XX
 PS Disclosure; Page 6; 10pp; Japanese.
 XX
 CC The sequence is that of the heavy chain variable region of a mouse
 CC antibody specific to human cancer embryonal antigen (hCEA). The region is
 CC used, with the corresponding mouse light chain variable region and the
 CC constant region of a human antibody, to prepare a mouse-human chimeric
 CC antibody which can be used for the diagnosis and treatment of cancer
 XX
 SQ Sequence 139 AA;

Query Match 68.3%; Score 56; DB 2; Length 139;
 Best Local Similarity 68.8%; Pred. No. 0.2;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 DB 69 SITSDGSTVYPSVKG 84
 ||||| |||: |||||
 ||||| |||: |||||

RESULT 16
 AEB46939
 ID AEB46939 standard; protein; 240 AA.
 XX
 AC AEB46939;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 DE Human CD1a specific scFv SC02-118.
 XX
 KW cytostatic; gene therapy; protein interaction; pharmaceutical;
 KW immunoconjugate; diagnosis; neurological disease;
 KW acute myelogenous leukemia; hematological disease; neoplasm;
 KW chronic myelocytic leukemia; acute promyelocytic leukemia;
 KW myelodysplastic syndrome; immunostimulant; acute lymphoblastic leukemia;
 KW t-cell acute lymphoblastic leukemia; single chain variable fragment;
 KW scFv.
 XX
 OS Homo sapiens.
 XX
 PN WO2005063819-A2.
 XX
 XX 14-JUL-2005.
 PD
 XX 21-DEC-2004; 2004WO-EP053639.
 PF
 XX 23-DEC-2003; 2003WO-EP051096.
 PR 09-SEP-2004; 2004WO-EP052110.
 PR
 XX (CRUC-) CRUCELL HOLLAND BV.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Throsby M, Van Meijer M, Germersaad WTV, Arceci RJ, Kruisbeek AM;
 PI WPI; 2005-563676/57.
 DR N-PSDB; AEB46938.
 XX
 XX New human binding molecule against CD1a, useful for diagnosing,
 PT preventing, or and/or treating neoplastic disorder, leukemia, or
 PT Langerhans cell histiocytosis.
 XX
 XX Example 4; SEQ ID NO 36; 172pp; English.
 PS
 XX The invention describes a human binding molecule capable of binding to
 CC human CD1a. Also described are: a functional variant of a human binding
 CC molecule above, where the functional variant is capable of competing for
 CC specifically binding to human CD1a; an immunoconjugate comprising a human
 CC binding molecule above, or a functional variant of (1), the
 CC immunoconjugate further comprising at least one tag; a nucleic acid
 CC molecule encoding a human binding molecule above or a functional variant
 CC of (1); a vector comprising at least one nucleic acid molecule; a host
 CC comprising at least one vector; a method of producing a human binding
 CC molecule above or a functional variant of (1); a method of identifying a
 CC human binding molecule specifically binding to human CD1a or a nucleic
 CC acid molecule encoding a human binding molecule specifically binding to
 CC CD1a; a method of obtaining a human binding molecule specifically binding
 CC to the human CD1a or a nucleic acid molecule encoding a human binding
 CC molecule specifically binding to the human CD1a; a composition comprising
 CC a binding molecule above, a functional variant of (1), an immunoconjugate
 CC of (2), or a nucleic acid molecule of (3); a pharmaceutical composition
 CC comprising a binding molecule above, a functional variant of (1), an
 CC immunoconjugate of (2), or a composition of (9), the pharmaceutical
 CC composition further comprising at least one pharmaceutical excipient; and
 CC a method of detecting CD1a. The binding molecule, functional variant,

CC immunoconjugate, composition, or a pharmaceutical composition is useful
 CC for preparing a medicament for the diagnosis, prevention, treatment, or
 CC their combination, of a neoplastic disorder or disease, e.g. acute
 CC myeloid leukemia, chronic myeloid leukemia, chronic myelogenous leukemia
 CC in blast crisis, chronic myelomonocytic leukemia, acute promyelocytic
 CC leukemia, myelodysplastic syndrome, juvenile myelomonocytic leukemia,
 CC acute lymphoblastic leukemia, acute non-lymphocytic leukemia, T-cell
 CC acute lymphoblastic leukemia, large granular lymphocytic leukemia, B-cell
 CC chronic lymphocytic leukemia and Langerhans cell histiocytosis. This is
 CC the amino acid sequence of a human CD1a specific single chain variable
 CC fragment (scFv) antibody.

XX Sequence 240 AA;

Query Match 68.3%; Score 56; DB 9; Length 240;

Best Local Similarity 62.5%; Pred. No. 0.39;

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16

Db 50 AISTGGGTYADSVKG 65

RESULT 17

AEBA6964

ID AEB46964 standard; protein; 447 AA.

XX AC AEB46964;

XX 22-SEP-2005 (first entry)

XX CD1a specific scFv 02-118 (CR2118) heavy chain SEQ ID NO 61.

XX cytostatic; gene therapy; protein interaction; pharmaceutical;

XX immunoconjugate; diagnosis; neurological disease;

KW acute myelogenous leukemia; hematological disease; neoplasm;

KW chronic myelocytic leukemia; acute promyelocytic leukemia;

KW myelodysplastic syndrome; immunostimulant; acute lymphoblastic leukemia;

KW t-cell acute lymphoblastic leukemia; single chain variable fragment;

KW scFv.

XX Homo sapiens.

XX WO2005063819-A2.

XX 14-JUL-2005.

XX 21-DEC-2004; 2004WO-EP053639.

XX 23-DEC-2003; 2003WO-EP051096.

PR 09-SEP-2004; 2004WO-EP052110.

XX (CRUC-) CRUCCELL HOLLAND BV.

PA (UYJO) UNIV JOHNS HOPKINS.

XX Throsby M, Van Meijer M, Germeeraad WTV, Arceci RJ, Kruisbeek AM,

XX WPI; 2005-563676/57.

DR N-PSDB; AEB46963.

XX New human binding molecule against CD1a, useful for diagnosing,

PT preventing, or and/or treating neoplastic disorder, leukemia, or

PT Langerhans cell histiocytosis.

XX Example 5; SEQ ID NO 61; 172pp; English.

PS The invention describes a human binding molecule capable of binding to

CC human CD1a. Also described are: a functional variant of a human binding

CC molecule above, where the functional variant is capable of competing for

CC specifically binding to human CD1a; an immunoconjugate comprising a human

CC binding molecule above, or a functional variant of (1), the

CC immunoconjugate further comprising at least one tag; a nucleic acid

CC molecule encoding a human binding molecule above or a functional variant

CC of (1); a vector comprising at least one nucleic acid molecule; a host
 CC comprising at least one vector; a method of producing a human binding
 CC molecule above or a functional variant of (1); a method of identifying a
 CC human binding molecule specifically binding to human CD1a or a nucleic
 CC acid molecule encoding a human binding molecule specifically binding to
 CC CD1a; a method of obtaining a human binding molecule specifically binding
 CC to the human CD1a or a nucleic acid molecule encoding a human binding
 CC molecule specifically binding to the human CD1a; a composition comprising
 CC a binding molecule above, a functional variant of (1), an immunoconjugate
 CC of (2), or a nucleic acid molecule of (3); a pharmaceutical composition
 CC comprising a binding molecule above, a functional variant of (1), an
 CC immunoconjugate of (2), or a composition of (9), the pharmaceutical
 CC composition further comprising at least one pharmaceutical excipient; and
 CC a method of detecting CD1a. The binding molecule, functional variant,
 CC immunoconjugate, composition, or a pharmaceutical composition is useful
 CC for preparing a medicament for the diagnosis, prevention, treatment, or
 CC their combination, of a neoplastic disorder or disease, e.g. acute
 CC myeloid leukemia, chronic myeloid leukemia, chronic myelogenous leukemia
 CC in blast crisis, chronic myelomonocytic leukemia, acute promyelocytic
 CC leukemia, myelodysplastic syndrome, juvenile myelomonocytic leukemia,
 CC acute lymphoblastic leukemia, acute non-lymphocytic leukemia, T-cell
 CC acute lymphoblastic leukemia, large granular lymphocytic leukemia, B-cell
 CC chronic lymphocytic leukemia and Langerhans cell histiocytosis. This is
 CC the amino acid sequence of human CD1a specific single chain variable
 CC fragment (scFv) 02-118 (CR2118).

XX Sequence 447 AA;

Query Match 68.3%; Score 56; DB 9; Length 447;

Best Local Similarity 62.5%; Pred. No. 0.8;

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16

Db 50 AISTGGGTYADSVKG 65

RESULT 18

ADO25822 ID ADO25822 standard; protein; 125 AA.

XX AC ADO25822;

XX 12-AUG-2004 (first entry)

XX Camelidae VHH anti-IgE protein sequence SeqID11.

XX protein therapeutic molecule; VHH antibody; Camelidae antibody;

KW antiinflammatory; cytostatic; gastrointestinal-Gen; antitubercular;

KW tuberculostatic; virucide; anti-allergic; immunosuppressive; gene therapy;

KW inflammation; colon; head; neck; lung cancer; indigestion; gastritis;

KW tuberculosis; flu; allergy; transplant rejection; autoimmune disorder.

XX Lama glama.

XX WO2004041867-A2.

XX 21-MAY-2004.

XX 07-NOV-2003; 2003WO-BE000190.

XX 08-NOV-2002; 2002US-0425063P.

PR 08-NOV-2002; 2002US-0425073P.

PR 10-JAN-2003; 2003EP-00447005.

PR 23-JUN-2003; 2003WO-EP006581.

PR 08-JUL-2003; 2003WO-EP007313.

XX (ABLY-) ABLYNX NV.

XX Silence K, Vaeck M, Van Bergen En Henegouwen PPM;

XX WPI; 2004-400649/37.

PT New VHH polypeptides derived from Camelidae antibodies directed against
 PT IggE, useful for preventing, treating or alleviating disorders such as
 PT inflammation, cancer, gastritis, tuberculosis, allergies or transplant
 PT rejection.

XX Claim 3; SEQ ID NO 11; 125pp; English.

PS This invention relates to novel methods for administration of protein
 CC therapeutic molecules so as to avoid inactivation through use of VHH
 CC antibodies derived from Camelidae antibodies. The invention may be useful
 CC for the production of compounds with antiinflammatory, cytostatic,
 CC gastrointestinal-Gen, antitubercular, tuberculosis, flu, allergies,
 CC antiallergic or immunosuppressive activity or for gene therapy. The
 CC polypeptide construct and method are useful for treating, preventing
 CC lung cancer, indigestion, gastritis, tuberculosis, flu, allergies,
 CC transplant rejection or autoimmune disorder. These may also be used in
 CC preparing a medicament for treating, preventing and/or alleviating the
 CC above disorders. The present sequence is that of a Camelidae-derived VHH
 CC protein which may be used during the method of the invention.

XX Sequence 125 AA;

Query Match 67.7%; Score 55.5; DB 8; Length 125;
 Best Local Similarity 76.5%; Pred. No. 0.22;
 Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTG-GTYHAESVKG 16
 ||||| ||||| |||||
 Db 50 SITWTGTYADSVKG 66

RESULT 19

AD025845
 ID AD025845 standard; protein; 133 AA.

XX AC AD025845;

XX DT 12-AUG-2004 (first entry)

XX DE Camelidae VHH anti-EGFR protein sequence SeqID34.

XX protein therapeutic molecule; VHH antibody; Camelidae antibody;
 KW antiinflammatory; cytostatic; gastrointestinal-Gen; antitubercular;
 KW tuberculosis; virucide; antiallergic; immunosuppressive; gene therapy;
 KW inflammation; colon; head; neck; lung cancer; indigestion; gastritis;
 KW tuberculosis; flu; allergy; transplant rejection; autoimmune disorder.

XX OS Lama glama.

XX PN WO2004041867-A2.

XX PD 21-MAY-2004.

XX PF 07-NOV-2003; 2003WO-BE000190.

XX PR 08-NOV-2002; 2002US-0425063P.

XX PR 08-NOV-2002; 2002US-0425073P.

XX PR 10-JAN-2003; 2003EP-00447005.

XX PR 23-JUN-2003; 2003WO-BP006581.

XX PR 08-JUL-2003; 2003WO-BP007313.

XX PA (ABLY-) ABLYNX NV.

XX PI Silence K, Vaeck M, Van Bergen En Henegouwen PPM;

XX DR WPI; 2004-400649/37.

XX New VHH polypeptides derived from Camelidae antibodies directed against
 PT IggE, useful for preventing, treating or alleviating disorders such as
 PT inflammation, cancer, gastritis, tuberculosis, allergies or transplant
 PT rejection.

XX

PS Claim 29; SEQ ID NO 34; 125pp; English.

XX This invention relates to novel methods for administration of protein
 CC therapeutic molecules so as to avoid inactivation through use of VHH
 CC antibodies derived from Camelidae antibodies. The invention may be useful
 CC for the production of compounds with antiinflammatory, cytostatic,
 CC gastrointestinal-Gen, antitubercular, tuberculosis, flu, allergies,
 CC antiallergic or immunosuppressive activity or for gene therapy. The
 CC polypeptide construct and method are useful for treating, preventing
 CC and/or alleviating disorders such as inflammation, colon, head, neck or
 CC lung cancer, indigestion, gastritis, tuberculosis, flu, allergies,
 CC transplant rejection or autoimmune disorder. These may also be used in
 CC preparing a medicament for treating, preventing and/or alleviating the
 CC above disorders. The present sequence is that of a Camelidae-derived VHH
 CC protein which may be used during the method of the invention.

XX Sequence 133 AA;

Query Match 67.7%; Score 55.5; DB 8; Length 133;
 Best Local Similarity 70.6%; Pred. No. 0.23;
 Matches 12; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITSTG-TYHAESVKG 16

Db 50 AITSSGGSTYADSVKG 66

RESULT 20

ABP45942

ID ABP45942 standard; protein; 247 AA.

XX AC ABP45942;

XX DT 19-AUG-2002 (first entry)

XX DE Human BlyS binding scFv SEQ ID 1953.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240818P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIPODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2731-2732; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SQ Sequence 247 AA;

Query Match 67.7%; Score 55.5; DB 5; Length 247;
Best Local Similarity 70.6%; Pred. No. 0.49;
Matches 12; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
:||||| ||:|||||
Db 50 AITSSGGATYADSVKG 66

RESULT 21
ADG96769
ID ADG96769 standard; protein; 247 AA.

XX AC ADG96769;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1953.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1953; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The

CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

SQ Sequence 247 AA;

Query Match 67.7%; Score 55.5; DB 7; Length 247;
Best Local Similarity 70.6%; Pred. No. 0.49;
Matches 12; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
:||||| ||:|||||
Db 50 AITSSGGATYADSVKG 66

RESULT 22
AD004876
ID AD004876 standard; protein; 251 AA.

XX AC AD004876;

XX DT 12-AUG-2004 (first entry)

XX DE Anti-mouse serum albumin/anti-IgE antibody MSA210/EV2H11 SEQ ID NO:24.

XX KW mouse; albumin; antibody; antiinflammatory; antirheumatic; antiarthritic;
KW neuroprotective; cerebroprotective; vasotropic; antianginal; cardiant;
KW antiallergic; gene therapy; IgE; immunoglobulin E.

XX OS Synthetic.

XX PN WO2004041865-A2.

XX PD 21-MAY-2004.

XX PF 07-NOV-2003; 2003WO-BE000193.

XX PR 08-NOV-2002; 2002US-0425063P.

XX PR 08-NOV-2002; 2002US-0425073P.

XX PR 10-JAN-2003; 2003EP-00447005.

XX PR 23-JUN-2003; 2003WO-EP006581.

XX PR 08-JUL-2003; 2003WO-EP007313.

XX PA (ABLY-) ABLYNX NV.

XX PI Silence K, Lauwereys M, Dreier T;

XX DR WPI; 2004-400647/37.

XX New heterospecific polypeptide constructs, useful for preventing or
PT treating, for e.g. inflammation or allergies, comprises single domain
PT antibodies directed against a therapeutic or diagnostic target or against
PT a serum protein.

XX Claim 28; SEQ ID NO 24; 95pp; English.

XX The invention relates to a novel polypeptide construct comprising at
CC least one single domain antibody directed against a therapeutic and/or
CC diagnostic target, and at least one single domain antibody directed
CC against a serum protein. An antibody of the invention has
CC antiinflammatory, antirheumatic, antiarthritic, neuroprotective,
CC cerebroprotective, vasotropic, antianginal, cardiant, and antiallergic

CC activity, and may have a use in gene therapy. The composition and methods
 CC of the invention are useful for treating, preventing and/or alleviating
 CC disorders relating to inflammatory processes, rheumatoid arthritis,
 CC Crohn's disease, ulcerative colitis, multiple sclerosis, diseases or
 CC conditions relating to platelet-mediated aggregation or dysfunction (e.g.
 CC cerebral ischaemic attack, unstable angina pectoris, cerebral infarction,
 CC myocardial infarction, peripheral arterial occlusive disease, restenosis,
 CC conditions arising from coronary by-pass graft or coronary artery valve
 CC replacement and coronary interventions such as angioplasty, stenting or
 CC atherectomy), allergic reactions (e.g. hay fever, asthma, atopic
 CC dermatitis, allergic skin reactions, allergic eye reactions or food
 CC allergies), or disorders or conditions where the immune system is
 CC overactive (e.g. autoimmune disorders or organ transplant rejection). In
 CC addition, these are used for treating, preventing or alleviating
 CC disorders or conditions in which the above targets are involved, or for
 CC preparing a medicament for treating, preventing or alleviating the above
 CC disorders or conditions or the symptoms of a disease requiring a
 CC therapeutic or diagnostic compound that is not rapidly cleared from the
 CC circulation or that remains active in the circulation for extended
 CC periods of time. The present sequence represents an antibody of the
 CC invention.

XX SQ Sequence 251 AA;

Query Match 67.7%; Score 55.5; DB 8; Length 251;

Best Local Similarity 76.5%; Pred. No. 0.49;

Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTG-GTYHAEVSKG 16

Db 176 SITWTGTYADSVKG 192

RESULT 23

AD004874

ID AD004874 standard; protein; 252 AA.

XX AC AD004874;

XX DT 12-AUG-2004 (first entry)

XX DE Anti-mouse serum albumin/anti-IgE antibody MSA21/EV2H11 SEQ ID NO:22.

XX KW mouse; albumin; antibody; antiinflammatory; antirheumatic; antiarthritic;
 KW neuroprotective; cerebroprotective; vasotropic; antianginal; cardiant;
 KW antiallergic; gene therapy; IgE; immunoglobulin E.

XX OS Synthetic.

XX PN WO2004041865-A2.

XX PD 21-MAY-2004.

XX PF 07-NOV-2003; 2003WO-BE000193.

XX PR 08-NOV-2002; 2002US-0425063P.

XX PR 08-NOV-2002; 2002US-0425073P.

XX PR 10-JAN-2003; 2003EP-00447005.

XX PR 23-JUN-2003; 2003WO-BE006581.

XX PR 08-JUL-2003; 2003WO-BE007313.

XX PA (ABLY-) ABLYNX NV.

XX PI Silence K, Lauwereys M, Dreier T;

XX DR WPI; 2004-400647/37.

XX PT New heterospecific polypeptide constructs, useful for preventing or
 PT treating, for e.g. inflammation or allergies, comprises single domain
 PT antibodies directed against a therapeutic or diagnostic target or against
 PT a serum protein.

XX PS Claim 28; SEQ ID NO 22; 95pp; English.

XX

CC The invention relates to a novel polypeptide construct comprising at
 CC least one single domain antibody directed against a therapeutic and/or
 CC diagnostic target, and at least one single domain antibody directed
 CC against a serum protein. An antibody of the invention has
 CC antiinflammatory, antirheumatic, antiarthritic, neuroprotective,
 CC cerebroprotective, vasotropic, antianginal, cardiant, and antiallergic
 CC activity, and may have a use in gene therapy. The composition and methods
 CC of the invention are useful for treating, preventing and/or alleviating
 CC disorders relating to inflammatory processes, rheumatoid arthritis,
 CC Crohn's disease, ulcerative colitis, multiple sclerosis, diseases or
 CC conditions relating to platelet-mediated aggregation or dysfunction (e.g.
 CC cerebral ischaemic attack, unstable angina pectoris, cerebral infarction,
 CC myocardial infarction, peripheral arterial occlusive disease, restenosis,
 CC conditions arising from coronary by-pass graft or coronary artery valve
 CC replacement and coronary interventions such as angioplasty, stenting or
 CC atherectomy), allergic reactions (e.g. hay fever, asthma, atopic
 CC dermatitis, allergic skin reactions, allergic eye reactions or food
 CC allergies), or disorders or conditions where the immune system is
 CC overactive (e.g. autoimmune disorders or organ transplant rejection). In
 CC addition, these are used for treating, preventing or alleviating
 CC disorders or conditions in which the above targets are involved, or for
 CC preparing a medicament for treating, preventing or alleviating the above
 CC disorders or conditions or the symptoms of a disease requiring a
 CC therapeutic or diagnostic compound that is not rapidly cleared from the
 CC circulation or that remains active in the circulation for extended
 CC periods of time. The present sequence represents an antibody of the
 CC invention.

XX SQ Sequence 252 AA;

Query Match 67.7%; Score 55.5; DB 8; Length 252;

Best Local Similarity 76.5%; Pred. No. 0.5;

Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTG-GTYHAEVSKG 16

Db 177 SITWTGTYADSVKG 193

RESULT 24

AD004875

ID AD004875 standard; protein; 252 AA.

XX AC AD004875;

XX DT 12-AUG-2004 (first entry)

XX DE Anti-mouse serum albumin/anti-IgE antibody MSA24/EV2H11 SEQ ID NO:23.

XX KW mouse; albumin; antibody; antiinflammatory; antirheumatic; antiarthritic;
 KW neuroprotective; cerebroprotective; vasotropic; antianginal; cardiant;
 KW antiallergic; gene therapy; IgE; immunoglobulin E.

XX OS Synthetic.

XX PN WO2004041865-A2.

XX PD 21-MAY-2004.

XX PF 07-NOV-2003; 2003WO-BE000193.

XX PR 08-NOV-2002; 2002US-0425063P.

XX PR 08-NOV-2002; 2002US-0425073P.

XX PR 10-JAN-2003; 2003EP-00447005.

XX PR 23-JUN-2003; 2003WO-BE006581.

XX PR 08-JUL-2003; 2003WO-BE007313.

XX PA (ABLY-) ABLYNX NV.

XX PI Silence K, Lauwereys M, Dreier T;

XX DR WPI; 2004-400647/37.

XX New heterospecific polypeptide constructs, useful for preventing or
PT treating, for e.g. inflammation or allergies, comprises single domain
PT antibodies directed against a therapeutic or diagnostic target or against
XX a serum protein.

XX Claim 28; SEQ ID NO 23; 95pp; English.

XX The invention relates to a novel polypeptide construct comprising at
CC least one single domain antibody directed against a therapeutic and/or
CC diagnostic target, and at least one single domain antibody directed
CC against a serum protein. An antibody of the invention has
CC antiinflammatory, antirheumatic, antiarthritic, neuroprotective,
CC cerebroprotective, vasotropic, antianginal, cardiant, and antiallergic
CC activity, and may have a use in gene therapy. The composition and methods
CC of the invention are useful for treating, preventing and/or alleviating
CC disorders relating to inflammatory processes, rheumatoid arthritis,
CC Crohn's disease, ulcerative colitis, multiple sclerosis, diseases or
CC conditions relating to platelet-mediated aggregation or dysfunction (e.g.
CC cerebral ischaemic attack, unstable angina pectoris, cerebral infarction,
CC myocardial infarction, peripheral arterial occlusive disease, restenosis,
CC conditions arising from coronary by-pass graft or coronary artery valve
CC replacement and coronary interventions such as angioplasty, stenting or
CC atherectomy), allergic reactions (e.g. hay fever, asthma, atopic
CC dermatitis), allergic skin reactions, allergic eye reactions or food
CC allergies), or disorders or conditions where the immune system is
CC overactive (e.g. autoimmune disorders or organ transplant rejection). In
CC addition, these are used for treating, preventing or alleviating
CC disorders or conditions in which the above targets are involved, or for
CC preparing a medicament for treating, preventing or alleviating the above
CC disorders or conditions or the symptoms of a disease requiring a
CC therapeutic or diagnostic compound that is not rapidly cleared from the
CC circulation or that remains active in the circulation for extended
CC periods of time. The present sequence represents an antibody of the
CC invention.

XX Sequence 252 AA;

Query Match 67.7%; Score 55.5; DB 8; Length 252;
Best Local Similarity 76.5%; Pred. No. 0.5;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Oy 1 SITSTG-GTYHAESVKG 16
||||| :|||:|||||
Db 177 SITWTGTGYADSVKG 193

RESULT 25
AAU82610
ID AAU82610 standard; peptide; 16 AA.
XX
XX AAU82610;
XX
XX 29-AUG-2003 (revised)
DT 23-APR-2002 (first entry)
XX
XX Llama CDR2 region variable heavy chain fragment #64.
DE
XX Llama; phage display library; variable heavy domain fragment; VHH; VH;
XX sdAb fragment; single domain anti-idiotypic antibody fragment;
XX phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
XX complementarity determining region.

OS Lama glama.
XX
XX WO200190190-A2.
XX
XX 29-NOV-2001.
PD
XX 25-MAY-2001; 2001WO-CA000763.
XX
XX 26-MAY-2000; 2000US-0207234P.
XX
XX

PA (CANA) NAT RES COUNCIL CANADA.
XX
XX Tanha J, Dubuc G, Narang S;
XX WPI; 2002-083093/11.
XX
XX New phage display library of variable heavy domain antigen-binding
PT fragments derived from llama antibodies, useful for in vitro selection
PT against any antigen of interest as a target.
XX
XX Disclosure; Page 19a; 46pp; English.

XX The present invention relates to a phage display library of variable
CC heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama
CC antibodies. The library is useful for in vitro selection against any
CC antigen of interest as a target. Single domain anti-idiotypic antibody
CC fragments are isolated from the library using phage display technology
CC and an antibody serving as an antigen. Such anti-idiotypic antibody
CC fragments have great potential in evoking the immune system response to
CC pathological antigens and in vaccine development. The large size of the
CC library considerably increases the probability of isolating from it
CC antigen-binding fragments having high affinity to almost any
CC predetermined target (antigen of interest). The library eliminates the
CC development of anti-idiotypic antibodies by immunisation and allows
CC isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the
CC llama heavy chain domain fragments of the invention. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX Sequence 16 AA;

Query Match 67.1%; Score 55; DB 5; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.024;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ITSTGGTYHAESVKG 16
||||| :|||:|||||
Db 2 ITSSGGTDYADSVKG 16

RESULT 26
ADP22214
ID ADP22214 standard; protein; 115 AA.
XX
XX ADP22214;
XX
XX 09-SEP-2004 (first entry)
DT
XX Human anti-TNFa antibody light chain variable region SEQ ID NO:120.
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
XX anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
XX antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
XX neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
XX prostate cancer; immuno-mediated inflammatory disease;
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
XX septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.
OS
XX
XX WO2004050683-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038281.
XX
XX 02-DEC-2002; 2002US-0430729P.
XX
XX (ABGE-) ABGENIX INC.
XX

XX Babcock JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX WPI: 2004-480601/45.
 DR N-PSDB; ADP22213.
 XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 120; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22416) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFa
 CC antibody light chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 115 AA;

Query Match 67.1%; Score 55; DB 8; Length 115;
 Best Local Similarity 73.3%; Pred. No. 0.24;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYSTGTYHAESVKG 16
 DB 51 IYSGGTYADSVKG 65
 |||||:|||||

RESULT 27
 ADRI6818
 ID ADRI6818 standard; protein; 217 AA.

XX ADR16818;
 AC
 XX 21-OCT-2004 (first entry)

XX Human breast cancer-specific antibody Fab fragment, Fab14.6.20 #1.

XX Breast cancer; diagnosis; therapy; human; antibody; Fab 14.6.20.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 109.110

FT Misc-difference 216.217
 FT /note= "Encoded by TTGTAGGAA"
 FT /notes= "Encoded by CCAGG"

XX US2004151724-A1.

XX 05-AUG-2004.

XX 30-OCT-2003; 2003US-00698041.

XX 31-OCT-2002; 2002US-0423052P.

XX (CORO/) CORONELLA-WOOD J.

XX Coronella-Wood J;

XX WPI: 2004-570704/55.

XX N-PSDB; ADRI6815.

XX New isolated polynucleotides encoding breast cancer-specific antibody Fab
 PT fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing
 PT or treating breast cancer.

XX Claim 9; SEQ ID NO 5; 36pp; English.

XX The invention provides a breast cancer-specific antibody fragment
 CC polynucleotide and its corresponding polypeptide. The invention is useful
 CC as clinical reagents for the diagnosis and therapy of breast cancer. The
 CC present sequence is human breast cancer-specific antibody Fab fragment,
 CC Fab14.6.20.

XX Sequence 217 AA;

Query Match 67.1%; Score 55; DB 8; Length 217;
 Best Local Similarity 80.0%; Pred. No. 0.51;
 Matches 12; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 4 STGG--TYHAESVKG 16
 DB 54 STGGSSTYHADSVKG 68
 |||||:|||||

RESULT 28
 ADU86691
 ID ADU86691 standard; peptide; 17 AA.

XX AC ADU86691;

XX 10-FEB-2005 (first entry)

XX Peptide display system related CDR 2 #26.

XX antinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;
 KW antidiabetic; vasotropic; vaccine; protein purification; protein folding;
 KW diagnosis; inflammation; immune disorder; allergic hypersensitivity;
 KW infection; autoimmune disease; asthma; psoriasis;
 KW insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; myasthenia gravis; hematological disease;
 KW neoplasm; complementarity determining region 2; CDR2.

XX Homo sapiens.

XX WO2004101790-A1.

XX 25-NOV-2004.

XX 14-MAY-2004; 2004WO-GB002102.

XX 14-MAY-2003; 2003US-0470340P.

XX 17-MAR-2004; 2004US-0554021P.

XX (DOMA-) DOMANTIS LTD.

antiasthmatic; heavy chain variable region; inflammation;
 antiinflammatory; cancer; cytostatic; arthritis; antiarthritic;
 dermatitis; dermatological; urticaria; ulcerative colitis; antiulcer;
 gastrointestinal-gen; scleroderma; scarring; vulnary;
 prostate hyperplasia; pulmonary disease; respiratory-gen;
 gastrointestinal function disorder; Kawasaki disease; antipyretic;
 cardiac; sickle cell anemia; antianemic; antischlicking; Graves disease;
 antithyroid; pre-eclampsia; gynecological; Sjogrens syndrome;
 immunosuppressive; autoimmune disease; Barrett's esophagus;
 mycobacterium tuberculosis infection; antibacterial; cystic fibrosis;
 cns-gen; chronic obstructive pulmonary disease;
 respiratory distress syndrome; pemphigus vulgaris; myasthenia gravis;
 muscular-gen; neuroprotective; chronic fatigue syndrome; immunomodulator;
 immunotherapy.
 XX
 OS unidentified.
 XX
 XX WO2005047331-A2.
 PN
 XX 26-MAY-2005.
 XX
 XX 04-NOV-2004; 2004WO-US037242.
 XX
 XX 07-NOV-2003; 2003US-0518166P.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Carter PJ, Zhou H;
 PI
 XX
 XX WPI; 2005-367002/37.
 DR
 XX
 XX New antibody that binds to the human IL-4 receptor, useful for asthma,
 PT septic arthritis, dermatitis herpetiformis, chronic idiopathic urticaria,
 PT ulcerative colitis, scleroderma, hypertrophic scarring.
 PT
 XX Disclosure; SEQ ID NO 68; 148pp; English.
 PS
 XX
 CC The present invention relates to new interleukin-4 (IL-4) receptor
 CC antagonists, and in particular to antibodies and antibody derivatives
 CC that bind to interleukin-4 receptor alpha (IL-4R alpha). IL-4 stimulates
 CC the growth of T cells, mast cells, granulocytes, megakaryocytes, and
 CC erythrocytes. IL-4 also stimulates the proliferation of several IL-2 and
 CC IL-3-dependent cell lines, induces expression of class II major
 CC histocompatibility complex molecules on resting B cells, and enhances the
 CC secretion of IgE and IgG1 isotypes by stimulated B cells. IL-4 is
 CC associated with a TH2-type immune response. IL-4 has been implicated in a
 CC number of disorders, such as allergy and asthma. Provided is an antibody
 CC comprising a light chain variable domain or a heavy chain variable
 CC domain, where the antibody binds to the human interleukin (IL)-4
 CC receptor. The antibody domains each have various amino acid
 CC substitutions. Also disclosed is a method of inhibiting an IL-4 receptor
 CC by contacting a cell expressing an the receptor with the antibody under
 CC binding conditions, where binding inhibits signal transduction through
 CC the IL-4 receptor. The antibody is useful for treating a condition such
 CC as such as an inflammatory or cancerous condition, e.g. asthma,
 CC arthritis, dermatitis, urticaria, ulcerative colitis, scleroderma,
 CC scarring, prostate hyperplasia, a lung disorder, condition of the
 CC epithelial barrier, digestive system disorder, allergic reaction to a
 CC drug, Kawasaki disease, sickle cell anemia, Grave's disease, pre-
 CC eclampsia, Sjogren's syndrome, autoimmune disease, Barrett's esophagus,
 CC tuberculosis, cystic fibrosis, chronic obstructive pulmonary disease,
 CC adult respiratory distress syndrome, hyper IgE syndrome, pemphigus
 CC vulgaris, myasthenia gravis, chronic fatigue syndrome, or nephrosis. The
 CC antibody has a mutation in a hinge region that alleviates a tendency to
 CC form intra-H chain disulfide bond antibody. The preferred sequence is an
 CC undefined antibody heavy chain variable region, designated 63.
 CC
 XX Sequence 117 AA;
 XX
 Query Match 66.5%; Score 54.5; DB 9; Length 117;
 Best Local Similarity 70.6%; Pred. No. 0.3;
 Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAEVSKG 16
 |||:| |||:| |||
 Db 50 SITSGSGGYADSVKG 66
 RESULT 31
 ADZ41229
 ID ADZ41229 standard; protein; 118 AA.
 XX
 AC ADZ41229;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Anti-HAS domain antibody TAR3h-23.
 XX
 KW Single chain antibody; antibody engineering; inflammation;
 KW antiinflammatory; sepsis; antibacterial; immunosuppressive; infection;
 KW hypersensitivity; antiallergic; immunosuppressive; immune disorder;
 KW cancer; cytostatic; neoplasm; autoimmune disease; diabetes; antidiabetic;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW rheumatoid arthritis; antiarthritic; antirheumatic;
 KW musculoskeletal disease; multiple sclerosis; neuroprotective;
 KW neurological disease; Crohns disease; gastrointestinal-gen;
 KW gastrointestinal disease; ulcerative colitis; antiulcer; aplastic anemia;
 KW antianemic; hematological disease; hashimoto's disease; antithyroid;
 KW graves disease; reiter's syndrome; ophthalmological; uropathic;
 KW transplant rejection; graft versus host disease; pulmonary disease;
 KW respiratory-gen.; respiratory disease; pulmonary fibrosis;
 KW myocardial ischemia; cardiac; vasotropic; cardiovascular disease;
 KW bone disease; osteopathic; hepatitis; hepatotropic; reperfusion injury;
 KW injury; fever; antipyretic; temperature disorder.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2005035572-A2.
 XX
 XX 21-APR-2005.
 XX
 XX 08-OCT-2004; 2004WO-GB004253.
 XX
 XX 08-OCT-2003; 2003US-0509613P.
 PR 08-JAN-2004; 2004US-0535076P.
 PR 30-JUN-2004; 2004WO-GB002829.
 PR
 PA (DOMA-) DOMANTIS LTD.
 XX
 XX Tomlinson I, Baaran A, Jones P;
 PI WPI; 2005-306343/31.
 XX
 CC Composition useful for treating or preventing sepsis, autoimmune
 CC disorders and pulmonary disorders, comprises polypeptide having single
 CC human immunoglobulin variable domain that binds polypeptide antigen, e.g.
 CC human cytokine.
 CC
 XX Example 11; SEQ ID NO 90; 169pp; English.
 XX
 CC The invention relates to a composition comprising a polypeptide having a
 CC single human immunoglobulin variable domain that binds a polypeptide
 CC antigen with Kd less than or equal to 100 nM, where the polypeptide is
 CC present at a concentration of at least 400 microm as determined by
 CC absorbance of light at 280 nm wavelength. The polypeptides are termed
 CC domain antibodies (dab) and may occur as homodimers or heterodimers
 CC (where the second polypeptide is a partner dab which does not bind to the
 CC target protein, linked via (Gly4Ser)n linkers. The dab polypeptides
 CC contain human framework regions, synthetic/modified complementarity
 CC domains (CDR) or contain mutations at positions defined in the
 CC specification. dab antibodies were created which bind to TNFalpha, TNF
 CC receptor (p55), mouse serum albumin (MSA) and human serum albumin (HSA).
 CC The polypeptide is useful for treating or preventing a disease or
 CC disorder in an individual in need of treatment, which involves
 CC administering the polypeptide to the individual. The polypeptide (or an

CC extended release dosage formulation containing it) is useful for
 CC preventing or treating diseases or disorders related to target antigens,
 CC such as inflammation, sepsis, allergic hypersensitivity, cancer,
 CC autoimmune disorders (e.g., diabetes, rheumatoid arthritis, multiple
 CC sclerosis, Crohn's disease, ulcerative colitis, aplastic anemia,
 CC Hashimoto's disease, Graves disease, Reiter's syndrome), transplant
 CC rejection, graft versus host disease, pulmonary disorder (e.g., pneumonia
 CC fibrosis, pulmonary sarcoidosis), cardiac disorders (e.g., ischemia of
 CC heart), inflammatory bone disorders, hepatitis, reperfusion injury and
 CC pyrexia. The polypeptide comprises single immunoglobulin variable domain
 CC polypeptides that bind target antigen with high affinity and are soluble
 CC at high concentration, without aggregation or precipitation. The present
 CC sequence represents a dAb antibody of the invention.

XX SQ Sequence 118 AA;

Query Match 66.5%; Score 54.5; DB 9; Length 118;
 Best Local Similarity 70.6%; Pred. No. 0.3;
 Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 Db 50 TITHTGGVTYYADSVKG 66

RESULT 32

ADP09930
 ID ADP09930 standard; protein; 125 AA.

XX AC ADP09930;

XX DT 12-AUG-2004 (first entry)

XX DE Anti-human IFN gamma protein sequence #34.

XX anti-interferon-gamma; anti-IFN- ϵ ggr; Antiinflammatory; Antirheumatic;
 KW Neuroprotective; Anabolic; Hypertensive; Hepatotrophic; Immunosuppressive;
 KW Antidiabetic; Nephrotropic; Antithyroid; CNS-Gen.; Antianemic;
 KW Dermatological; Antinfertility; Antipsoriatic; Antipyretic; Vasotropic;
 KW inflammation; rheumatoid arthritis; diabetes type I;
 KW systemic lupus erythematosus; anti-IFN-gamma.

XX OS Homo sapiens.

XX FN WO2004041863-A2.

XX PD 21-MAY-2004.

XX PF 07-NOV-2003; 2003WO-BE000194.

XX PR 08-NOV-2002; 2002US-0425063P.

PR 08-NOV-2002; 2002US-0425073P.

PR 10-JAN-2003; 2003EP-00447005.

PR 23-JUN-2003; 2003WO-EP006581.

PR 08-JUL-2003; 2003WO-EP007313.

XX (ABLY-) ABLYNX NV.

XX PI Beirnaert E;

XX DR WPI; 2004-400646/37.

XX New polypeptides derived from single domain heavy chain antibodies
 PT directed to interferon-gamma, useful for preventing, treating or
 PT alleviating disorders such as inflammation, multiple sclerosis, diabetes
 PT or Grave's disease.

XX PS Claim 3; SEQ ID NO 34; 86pp; English.

XX The present invention relates to an anti-interferon-gamma (anti-IFN- ϵ ggr;
 CC) polypeptide comprising at least one anti-IFN- ϵ ggr; single domain
 CC antibody. The composition and methods are useful for treating, preventing
 CC and/or alleviating disorders related to inflammatory processes, disorders

CC requiring the delivery of an IFN- ϵ ggr; modulating polypeptide that is
 CC able to pass through the gastric environment without being inactivated,
 CC disorders requiring the delivery of an IFN- ϵ ggr; modulator or a
 CC therapeutic compound to the vaginal and/or rectal tract, to the upper
 CC respiratory tract and lung, through the tissues beneath the tongue or
 CC through the skin, or disorders increasing the permeability of the
 CC intestinal mucosa. These may also be used for preparing a medicament for
 CC treating, preventing and/or alleviating the disorders cited above,
 CC particularly inflammation, rheumatoid arthritis, Crohn's disease,
 CC ulcerative colitis, inflammatory bowel syndrome, multiple sclerosis,
 CC Addison's disease, autoimmune hepatitis, autoimmune parotitis, diabetes
 CC type I, epidiidymitis, glomerulonephritis, Grave's disease, Guillain-Barre
 CC syndrome, Hashimoto's disease, hemolytic anemia, systemic lupus
 CC erythematosus, male infertility, myasthenia gravis, pemphigus, psoriasis,
 CC rheumatic fever, sarcoidosis, scleroderma, Sjogren's syndrome,
 CC spondyloarthropathies, thyroiditis or vasculitis. The anti-IFN- ϵ ggr;
 CC polypeptide is also used for purifying IFN- ϵ ggr; or for inhibiting the
 CC interaction between the IFN- ϵ ggr; and IFN- ϵ ggr; receptors. The present
 CC sequence represents an anti human -IFN-gamma polypeptide.

XX SQ Sequence 125 AA;

Query Match 66.5%; Score 54.5; DB 8; Length 125;
 Best Local Similarity 75.0%; Pred. No. 0.32;
 Matches 12; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 2 ITSTGG-TYHAESVKG 16
 Db 51 ITSSGGVTYYADSVKG 66

RESULT 33

ADF11393
 ID ADF11393 standard; protein; 116 AA.

XX AC ADF11393;

XX DT 12-FEB-2004 (first entry)

XX DE 22B3 anti-OPGL antibody heavy chain variable region SEQ ID NO:6.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX OS Homo sapiens.

XX FN WO2003086289-A2.

XX PD 23-OCT-2003.

XX PF 07-APR-2003; 2003WO-US010749.

XX PR 05-APR-2002; 2002US-0370407P.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX DR WPI; 2003-845253/78.

XX N-PSDB; ADF11392.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX PS Claim 1; SEQ ID NO 6; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical

CC composition of (1) or a pharmaceutical amount of (1); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (1) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (1) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 XX Sequence 116 AA;

Query Match 65.9%; Score 54; DB 7; Length 116;
 Best Local Similarity 66.7%; Pred. No. 0.36;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
 | : ||||:||||
 Db 51 IGTAGGTYADSVKG 65

RESULT 34
 ADF11413
 ID ADF11413 standard; protein; 116 AA.
 XX
 AC ADF11413;
 DT 12-FEB-2004 (first entry)
 XX
 DE 9H7 anti-OPGL antibody heavy chain variable region SEQ ID NO:26.
 XX
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX
 OS Homo sapiens.
 XX WO2003086289-A2.
 PN
 XX 23-OCT-2003.
 PD
 XX 07-APR-2003; 2003WO-US010749.
 PF
 XX 05-APR-2002; 2002US-0370407P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 PI WPI; 2003-845253/78.
 XX N-PSDB; ADF11412.
 DR
 XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 PT
 XX Claim 1; SEQ ID NO 26; 156pp; English.

CC The present invention describes an isolated human antibody (1) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (1); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (1); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (1) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (1) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (1) may also be used for

CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 XX Sequence 116 AA;
 QY Query Match 65.9%; Score 54; DB 7; Length 116;
 Best Local Similarity 66.7%; Pred. No. 0.36;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 51 IGTAGGTYADSVKG 65

RESULT 35
 ADF11437
 ID ADF11437 standard; protein; 116 AA.

QY 2 ITSTGGTYHAESVKG 16
 | : ||||:||||
 Db 51 IGTAGGTYADSVKG 65

RESULT 35
 ADF11437
 ID ADF11437 standard; protein; 116 AA.
 XX
 AC ADF11437;
 DT 24-MAR-2005 (first entry)
 XX
 DE Melanin tumor monoclonal antibody associated protein SEQ ID NO 1.
 KW monoclonal antibody; antibody production; melanin.
 XX
 OS Homo sapiens.
 XX CN1470530-A.
 PN
 XX 28-JAN-2004.
 PD
 XX 22-JUL-2002; 2002CN-00136147.
 PF
 XX 22-JUL-2002; 2002CN-00136147.
 PR
 XX (GUOJ-) GUOJIAN PHARM IND CO LTD ZHONGXIN GROUP.
 PA
 XX Ma J, Wang H, Liu Q;
 PI WPI; 2004-296029/28.
 DR N-PSDB; ADF11437.
 XX
 PT Human machine tumor monoclonal antibody, and its preparing method and
 PT use.
 XX
 PS Claim 1; SEQ ID NO 1; 14pp; Chinese.

CC The present invention discloses a novel human melanin tumor monoclonal
 CC antibody, the polynucleotide encoding said antibody and its application,
 CC and the monoclonal antibody preparation method. This is the amino acid
 CC sequence of a melanin tumor monoclonal antibody associated protein.
 XX
 XX Sequence 116 AA;

Query Match 65.9%; Score 54; DB 8; Length 116;
 Best Local Similarity 76.9%; Pred. No. 0.36;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 STGGTYHAESVKG 16
 | : ||||:||||
 Db 54 STGGTYADSVKG 66

RESULT 36
 ADF11437
 ID ADF11437 standard; protein; 446 AA.

QY 12-FEB-2004 (first entry)
 XX

DE 9H7 anti-OPGL antibody heavy chain SEQ ID NO:50.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 141 /note= "encoded by TG"

FT

XX WO2003086289-A2.

XX 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADF11436.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX Claim 11; SEQ ID NO 50; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.

XX Sequence 446 AA;

Query Match 65.9%; Score 54; DB 7; Length 446;

Best Local Similarity 66.7%; Pred. No. 1.8;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16

Db 51 IGTAGGTYADSVKG 65

RESULT 37

ADFL1417

ID ADF11417 standard; protein; 446 AA.

XX ADF11417;

XX 12-FEB-2004 (first entry)

XX 22B3 anti-OPGL antibody heavy chain SEQ ID NO:30.
 DE human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;

KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 141 /note= "encoded by TG"

FT

XX WO2003086289-A2.

XX 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADF11416.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX Claim 11; SEQ ID NO 30; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.

XX Sequence 446 AA;

Query Match 65.9%; Score 54; DB 7; Length 446;

Best Local Similarity 66.7%; Pred. No. 1.8;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16

Db 51 IGTAGGTYADSVKG 65

RESULT 38

ABP96588

ID ABP96588 standard; protein; 567 AA.

XX ABP96588;

XX 28-MAY-2003 (first entry)

DE Pig IgE heavy chain amino acid sequence SEQ ID NO:33.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

KW urticaria hives.
 XX
 OS Sus scrofa.
 XX
 PN WO2003015716-A2.
 XX
 PD 27-FEB-2003.
 XX
 XX
 PF 08-AUG-2002; 2002WO-US026986.
 XX
 PR 13-AUG-2001; 2001US-0312120P.
 XX
 PA (IGET-) IGE THERAPEUTICS INC.
 XX
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
 XX
 DR WPI; 2003-268242/26.
 XX
 XX
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IGE, by identifying peptide eliciting CTL response to IGE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 XX Example 7; Page 164-167; 187pp; English.
 PS
 XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 XX Sequence 567 AA;
 SQ
 Query Match 65.9%; Score 54; DB 6; Length 567;
 Best Local Similarity 71.4%; Pred. No. 2.3;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 TSTGGTYHAESVKG 16
 ||| |||:|:|
 DB 72 TSAGSTYADSVKG 85
 RESULT 39
 ABG70430
 ID ABG70430 standard; peptide; 16 AA.
 XX
 AC ABG70430;
 XX
 XX 29-AUG-2003 (revised)
 DT 05-NOV-2002 (first entry)
 XX
 XX CDR2 region of Llama single-domain antibody, #4 (C5).
 DE
 XX Llama; human; blood-brain barrier; BBB; transmigration;
 KW

KW single-domain antibody; dAB; sDAB; antibody; phage display;
 KW antigen-binding antibody; cerebrovascular endothelial cell; HCBC;
 KW variable heavy domain; VH; hypervariable region; hypervariable loop;
 KW complementarity determining region; CDR1/H1; CDR1; CDR2; CDR3;
 KW therapeutic; diagnostic; drug delivery; gene delivery; CNS;
 KW central nervous system.
 XX
 OS Lama glama.
 XX
 PN WO200257445-A1.
 XX
 PD 25-JUL-2002.
 XX
 XX 25-MAY-2001; 2001WO-CA0000783.
 PF
 XX 26-MAY-2000; 2000US-0207234P.
 PR
 XX 22-JAN-2001; 2001US-0263108P.
 XX
 PA (CANADA) NAT RES COUNCIL CANADA.
 XX
 PI Muruganandam A, Tanha J, Narang S, Stanimirovic D;
 XX
 XX WPI; 2002-590739/63.
 DR
 XX
 XX Preparing a blood brain barrier (BBB) transmigration llama antibody
 PT fragment (LF) by enriching phages displaying LF, for species internalized
 PT by endothelial cells expressing BBB antigens, and which transigrate
 PT across in vitro BBB.
 XX
 PS Disclosure; Page 20; 70pp; English.
 XX
 XX The invention discloses the preparation of a human blood-brain barrier
 CC (BBB) transmigration single-domain antibody (dAB or sDAB) fragment
 CC derived from a llama antibody. Preparation involves providing a phage
 CC display library of antigen-binding antibody fragments derived from llama
 CC antibodies, enriching the library for phage species selectively binding
 CC to, and internalized into, human cerebrovascular endothelial cells
 CC (HCBC) expressing BBB antigens and then recovering these enriched library
 CC phage particles. The DNA of the phage particles identified is then cloned
 CC into an expression vector and the antigen-binding antibody fragments can
 CC then be prepared. Each antigen-binding fragment comprises at least a part
 CC of the variable heavy domain (VH or VH) of a llama antibody. The
 CC variable domains are not uniformly variable throughout their length and
 CC three regions, known as hypervariable regions (loops) or complementarity
 CC determining regions (CDR1, CDR2 and CDR3), show more variability than the
 CC rest of the domain. It is these regions that determine the specificity of
 CC the antigen-antibody interaction. The antigen-binding antibody fragments
 CC are useful as therapeutic or diagnostic agents, when linked, directly or
 CC indirectly, covalently or non-covalently, to a therapeutic or diagnostic
 CC entity. Due to their small size, and selectivity of binding to brain
 CC endothelium and ability to cross the BBB, the antigen-binding antibody
 CC fragments are useful, not only as vectors for the delivery of therapeutic
 CC and diagnostic agents into the brain, but also as molecular templates for
 CC designing drug and gene delivery vectors targeting the central nervous
 CC system. The peptides in AB851973-AB852059 show the CDR1/H1, CDR2 and CDR3
 CC variable sequences from 28 sDABs from the llama phage display library.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 64.6%; Score 53; DB 5; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.053;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ITSGGTTHAESVKG 16
 ||| |||:|:|
 DB 2 ITSGGTTHAESVKG 16
 RESULT 40
 AAU82466
 ID AAU82466 standard; peptide; 16 AA.
 XX

AC AAU82466;
 XX
 XX
 DT 29-AUG-2003 (revised)
 DT 23-APR-2002 (first entry)
 XX
 XX
 DE Llama CDR2 region variable heavy chain fragment #4.
 XX
 XX
 XX Llama; phage display library; variable heavy domain fragment; VHH; VH;
 KW sdbb fragment; single domain anti-idiotypic antibody fragment;
 KW phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
 KW complementarity determining region.
 XX
 XX
 OS Lama glama.
 XX
 PN WO200190190-A2.
 XX
 XX
 PD 29-NOV-2001.
 XX
 XX
 PF 25-MAY-2001; 2001WO-CA000763.
 XX
 XX 26-MAY-2000; 2000US-0207234P.
 PR
 XX (CANA) NAT RES COUNCIL CANADA.
 PA
 XX Tanha J, Dubuc G, Narang S;
 PI
 XX WPI; 2002-083093/11.
 DR
 XX
 XX New phage display library of variable heavy domain antigen-binding
 PT fragments derived from llama antibodies, useful for in vitro selection
 PT against any antigen of interest as a target.
 PT
 XX
 XX Disclosure; Page 13a; 46pp; English.
 PS
 XX The present invention relates to a phage display library of variable
 CC heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama
 CC antibodies. The library is useful for in vitro selection against any
 CC antigen of interest as a target. Single domain anti-idiotypic antibody
 CC fragments are isolated from the library using phage display technology
 CC and an antibody serving as an antigen. Such anti-idiotypic antibody
 CC fragments have great potential in evoking the immune system response to
 CC pathological antigens and in vaccine development. The large size of the
 CC library considerably increases the probability of isolating from it
 CC antigen-binding fragments having high affinity to almost any
 CC predetermined target (antigen of interest). The library eliminates the
 CC development of anti-idiotypic antibodies by immunisation and allows
 CC isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent
 CC llama heavy chain domain fragments of the invention. (Updated on 29-AUG-
 CC 2003 to standardise OS field)
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 64.6%; Score 53; DB 5; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.053;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ITSGGTTHAESVKG 16
 ||| |||:|:|:
 Db 2 ITSGGATYADSMKG 16
 RESULT 41
 AEA45760
 ID AEA45760 standard; peptide; 17 AA.
 XX
 AC AEA45760;
 XX
 XX 11-AUG-2005 (first entry)
 DT
 XX Apolipoprotein E C-terminal domain antibody VH-CDR2 peptide #57.
 DE
 XX Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
 KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
 KW

KW Alzheimer's disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
 KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KW motor neurone disease; chronic obstructive pulmonary disease.
 XX
 XX Homo sapiens.
 OS
 XX GB2408508-A.
 PN
 XX 01-JUN-2005.
 PD
 XX 26-NOV-2004; 2004GB-00026043.
 PF
 XX 28-NOV-2003; 2003US-0525174P.
 PR
 XX (ASTR) ASTRAZENECA AB.
 PA (DYAX-) DYAX CORP.
 XX
 XX Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
 PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
 XX WPI; 2005-408785/42.
 DR
 XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.
 XX
 XX Example 8; Page 101; 392pp; English.
 PS
 XX The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 XX illustrate the invention.
 XX Sequence 17 AA;
 SQ
 Query Match 64.6%; Score 53; DB 9; Length 17;
 Best Local Similarity 76.9%; Pred. No. 0.057;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 STGGTYHAESVKG 16
 ||| |||:|:|:
 Db 5 SGGGTYADSVKG 17
 RESULT 42
 AAM33349
 ID AAM33349 standard; protein; 95 AA.
 XX
 AC AAM33349;
 XX
 XX 17-OCT-2001 (first entry)
 DT
 XX Peptide #7386 encoded by probe for measuring placental gene expression.
 DE
 XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 KW

CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (1) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 95 AA;

Query Match 64.6%; Score 53; DB 4; Length 95;
 Best Local Similarity 62.5%; Pred. No. 0.43;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 DB 46 AIGTGGGTYADSVKG 61

RESULT 45
 ABG42982
 ID ABG42982 standard; peptide; 95 AA.

XX AC ABG42982;

XX DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 32647.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW Chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

XX OS Homo sapiens.

XX FN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 XX Claim 27; SEQ ID NO 32647; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12367 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types comprising one
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 95 AA;

Query Match 64.6%; Score 53; DB 5; Length 95;

Best Local Similarity 62.5%; Pred. No. 0.43;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 DB 46 AIGTGGGTYADSVKG 61

RESULT 46

AAB40091

ID AAB40091 standard; protein; 97 AA.

XX AC AAB40091;

XX DT 05-FEB-2001 (first entry)

XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 617.

XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritis;
 KW antisclerotic; neuroprotective; antipsoriatic; antiaschmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX OS Homo sapiens.

XX FN WO200056772-A1.

XX PD 28-SEP-2000.

XX PF 24-MAR-2000; 2000WO-US007946.

XX PR 25-MAR-1999; 99US-0126603P.

PA (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 XX Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX
 SQ Sequence 97 AA;
 Query Match 64.6%; Score 53; DB 3; Length 97;
 Best Local Similarity 62.5%; Pred. No. 0.44;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SITSTGGTYHAESVKG 16
 : : ||||: ||||
 Db 50 AIGTGGTYADSVKG 65
 RESULT 47
 AAB40092
 ID AAB40092 standard; protein; 97 AA.
 XX
 AC AAB40092;
 XX
 XX 05-FEB-2001 (first entry)
 DT
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 618.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 XX WO200056772-A1.
 PN
 XX
 XX 28-SEP-2000.
 PD
 XX
 XX 24-MAR-2000; 2000NO-US007946.
 PF
 XX
 XX 25-MAR-1999; 99US-0126603P.
 PR

XX (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 XX Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX
 SQ Sequence 97 AA;
 Query Match 64.6%; Score 53; DB 3; Length 97;
 Best Local Similarity 62.5%; Pred. No. 0.44;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SITSTGGTYHAESVKG 16
 : : ||||: ||||
 Db 50 AIGTGGTYADSVKG 65
 RESULT 48
 AABG78195
 ID AABG78195 standard; protein; 97 AA.
 XX
 AC AABG78195;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 XX
 DE Human Fv molecule hypervariable region related peptide #70.
 XX
 KW Human; Fv molecule; hypervariable region; single chain Fv; cyostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200259264-A2.
 PN
 XX
 XX 01-AUG-2002.
 PD
 XX
 XX 31-DEC-2001; 2001WO-US049440.
 PF
 XX
 XX 29-DEC-2000; 2000US-00751181.
 PR

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI; 2002-619166/66.
 DR
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 XX Claim 13; Page 183; 232pp; English.
 PS
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX Sequence 97 AA;
 SQ

Query Match 64.6%; Score 53; DB 5; Length 97;
 Best Local Similarity 62.5%; Pred. No. 0.44;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 SITSTGGTYHAESVKG 16
 :|: ||||:||||
 DB 50 AIGTGGTYADSVKG 65

RESULT 49
 ABG78196
 ID ABG78196 standard; protein; 97 AA.
 XX
 AC ABG78196;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #71.
 XX
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI; 2002-619166/66.
 XX
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX Claim 13; Page 183-184; 232pp; English.
 XX
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX Sequence 97 AA;
 SQ

Query Match 64.6%; Score 53; DB 5; Length 97;
 Best Local Similarity 62.5%; Pred. No. 0.44;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 SITSTGGTYHAESVKG 16
 :|: ||||:||||
 DB 50 AIGTGGTYADSVKG 65

RESULT 50
 ABG91886
 ID ABG91886 standard; protein; 97 AA.
 XX
 AC ABG91886;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #70.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Page 260; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 97 AA;

Query Match 64.6%; Score 53; DB 5; Length 97;
 Best Local Similarity 62.5%; Pred. No. 0.44;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
 Db : | : ||| : |||
 50 AIGTGGGTYADSVKG 65

Search completed: May 11, 2006, 16:25:54
 Job time : 172.934 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 23.6066 Seconds
(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82
Sequence: 1 SITSTGGTYHAESVKG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	70.7	137	2 I47193	Ig heavy chain var
2	53.5	65.2	115	2 S09382	Ig heavy chain - c
3	53	64.6	97	2 S26885	Ig heavy chain v r
4	53	64.6	97	2 S26886	Ig heavy chain v r
5	53	64.6	116	2 S12557	Ig heavy chain - h
6	53	64.6	147	2 I47183	Ig heavy chain var
7	52	63.4	145	2 I47203	Ig heavy chain var
8	51	62.2	97	1 HVMS91	Ig heavy chain v r
9	51	62.2	112	2 S26327	Ig heavy chain v r
10	51	62.2	148	2 I47180	Ig heavy chain var
11	50	61.0	117	1 MHDMO	Ig heavy chain v r
12	50	61.0	145	2 I47185	Ig heavy chain var
13	50	61.0	146	2 I47184	Ig heavy chain var
14	49	59.8	92	2 S56009	Ig heavy chain v r
15	49	59.8	97	2 S26935	Ig heavy chain v r
16	49	59.8	97	2 S46462	Ig heavy chain v r
17	49	59.8	116	2 B28966	Ig heavy chain pre
18	49	59.8	116	2 S31110	Ig heavy chain - h
19	48.5	59.1	143	2 I47202	Ig heavy chain var
20	48	58.5	86	2 S26788	Ig heavy chain v r
21	47.5	57.9	98	2 S26889	Ig heavy chain v r
22	47.5	57.9	99	2 S24259	Ig heavy chain v r
23	47.5	57.9	100	2 S24258	Ig heavy chain v r
24	47.5	57.9	101	2 S24257	Ig heavy chain v r
25	47.5	57.9	102	2 S24260	Ig heavy chain v r
26	47.5	57.9	104	2 S24255	Ig heavy chain v r
27	47.5	57.9	105	2 S24249	Ig heavy chain v r
28	47.5	57.9	106	2 S24256	Ig heavy chain v r
29	47.5	57.9	108	2 PH1648	Ig heavy chain v r

30	47.5	57.9	109	2 S24254	Ig heavy chain v r
31	47.5	57.9	109	2 PH1653	Ig heavy chain v r
32	47.5	57.9	109	2 S24253	Ig heavy chain v r
33	47.5	57.9	109	2 PH1649	Ig heavy chain v r
34	47.5	57.9	110	2 S24250	Ig heavy chain v r
35	47.5	57.9	111	2 S69911	Ig V-D-J region (R
36	47.5	57.9	112	2 PH1647	Ig heavy chain v r
37	47.5	57.9	113	2 S24247	Ig heavy chain v r
38	47.5	57.9	113	2 S25571	Ig heavy chain v r
39	47.5	57.9	117	2 A45953	Ig heavy chain pre
40	47.5	57.9	118	2 S31121	Ig heavy chain - h
41	47.5	57.9	119	2 D36005	Ig heavy chain v r
42	47.5	57.9	119	2 S31107	Ig heavy chain - h
43	47.5	57.9	119	2 C36005	Ig heavy chain v r
44	47.5	57.9	119	2 S31108	Ig heavy chain - h
45	47.5	57.9	120	2 S48798	Ig heavy chain v r
46	47.5	57.9	121	2 S31113	Ig heavy chain - h
47	47.5	57.9	121	2 I55673	Ig heavy chain - h
48	47.5	57.9	123	2 S31114	Ig heavy chain - h
49	47.5	57.9	125	2 S72665	Ig V-D-J region (R
50	47.5	57.9	127	2 S38489	Ig heavy chain - h
51	47.5	57.9	138	2 S31666	Ig heavy chain v r
52	47.5	57.9	140	2 S31588	Ig heavy chain v r
53	47.5	57.9	160	2 S05271	Ig heavy chain pre
54	47	57.3	90	2 S24248	Ig heavy chain v r
55	47	57.3	120	2 S36278	Ig heavy chain v r
56	47	57.3	140	2 A30532	Ig heavy chain pre
57	46	56.1	143	2 I47201	Ig heavy chain var
58	46	56.1	676	1 A39379	hatching-suppresse
59	45	54.9	98	2 S26929	Ig heavy chain v r
60	45	54.9	98	2 S4856	Ig heavy chain v r
61	45	54.9	118	2 S00700	Ig heavy chain v r
62	45	54.9	120	2 S44111	Ig heavy chain v r
63	45	54.9	122	2 A33989	Ig heavy chain V-D
64	45	54.9	138	2 I47205	Ig heavy chain var
65	45	54.9	145	2 I47186	Ig heavy chain var
66	45	54.9	152	2 I47188	Ig heavy chain var
67	44.5	54.3	97	2 S24252	Ig heavy chain v r
68	44.5	54.3	98	2 S26891	Ig heavy chain v r
69	44.5	54.3	98	2 S26930	Ig heavy chain v r
70	44.5	54.3	110	2 PH1652	Ig heavy chain v r
71	44.5	54.3	114	2 S31120	Ig heavy chain - h
72	44.5	54.3	118	2 S31105	Ig heavy chain (su
73	44.5	54.3	128	2 S26790	Ig heavy chain v r
74	44.5	54.3	134	2 S31699	Ig heavy chain v r
75	44.5	54.3	140	2 S31686	Ig heavy chain v r
76	44.5	54.3	572	2 B46529	Ig heavy chain (
77	44	53.7	92	2 S56008	Ig heavy chain var
78	44	53.7	116	2 S17080	Ig heavy chain v r
79	44	53.7	119	2 PH0098	Ig heavy chain v r
80	44	53.7	139	2 S38808	Ig heavy chain - m
81	44	53.7	148	2 I47210	Ig heavy chain var
82	44	53.7	577	2 T15445	hypothetical prote
83	43.5	53.0	108	2 PL0248	Ig heavy chain v r
84	43.5	53.0	117	1 H3HU26	Ig heavy chain pre
85	43.5	53.0	118	2 S20641	Ig heavy chain v r
86	43.5	53.0	138	2 S09258	Ig heavy chain v r
87	43	52.4	98	2 PH0874	Ig heavy chain v r
88	43	52.4	115	1 A2HUBU	Ig heavy chain V-I
89	43	52.4	678	2 C86495	hypothetical prote
90	43	52.4	678	2 H72128	3-methyl-2-oxobuta
91	42.5	51.8	97	2 PH0875	Ig heavy chain v r
92	42.5	51.8	111	2 PH1007	Ig heavy chain v r
93	42.5	51.8	151	2 A60943	Ig heavy chain pre
94	42	51.2	96	2 S20781	Ig heavy chain v r
95	42	51.2	113	2 A34792	Ig heavy chain pre
96	42	51.2	114	2 B34792	Ig heavy chain pre
97	42	51.2	116	2 A38291	Ig heavy chain pre
98	42	51.2	118	2 PH0097	Ig heavy chain v r
99	42	51.2	120	1 M3HUBW	Ig heavy chain V-I
100	42	51.2	121	2 S09958	Ig heavy chain V-D
101	42	51.2	139	2 PC1213	Ig heavy chain pre
102	42	51.2	141	2 I47209	Ig heavy chain var

103	42	51.2	146	2	I47196	Ig heavy chain var	176	39	47.6	111	2	B28071	hypothetical prote
104	42	51.2	235	2	JC4603	conserved hypoteth	177	39	47.6	120	2	PH1650	Ig heavy chain V r
105	41.5	50.6	97	2	S54855	Ig heavy chain V r	178	39	47.6	122	2	S20772	Ig heavy chain V r
106	41.5	50.6	97	2	S26895	Ig heavy chain V r	179	39	47.6	150	2	I47200	Ig heavy chain var
107	41.5	50.6	105	2	S38488	Ig heavy chain - h	180	39	47.6	227	2	C89808	exotoxin 15 [impor
108	41.5	50.6	113	2	S02717	Ig heavy chain V r	181	39	47.6	373	2	AG3191	amide hydrolase [i
109	41.5	50.6	115	2	PH1538	Ig H chain V regio	182	39	47.6	425	2	AH1041	Vi polysaccharide
110	41.5	50.6	117	1	HVMSRF	Ig heavy chain pre	183	39	47.6	425	2	B36892	Vi polysaccharide
111	41.5	50.6	117	2	A34964	Ig heavy chain pre	184	39	47.6	531	2	B96966	beta-mannanase Man
112	41.5	50.6	117	2	PH1553	Ig H chain V regio	185	39	47.6	714	2	A40614	penicillin-binding
113	41.5	50.6	119	2	PH1548	Ig H chain V regio	186	39	47.6	804	2	AI2157	hypothetical prote
114	41.5	50.6	119	2	PH1549	Ig H chain V regio	187	39	47.6	906	2	G75362	aconitate hydratase
115	41.5	50.6	124	2	S20782	Ig heavy chain V r	188	39	47.6	1325	1	S73723	probable lipoprote
116	41.5	50.6	140	2	I47182	Ig heavy chain var	189	39	47.6	1615	2	JC6510	ras-responsive ele
117	41.5	50.6	140	2	I47204	Ig heavy chain var	190	39	47.6	1820	2	A55494	latent transformin
118	41.5	50.6	141	2	I47197	Ig heavy chain var	191	39	47.6	1848	2	S37771	ankyrin, erythrocy
119	41.5	50.6	141	2	I47179	Ig heavy chain var	192	39	47.6	1856	2	B35049	ankyrin 1, erythro
120	41	50.0	96	2	S54854	Ig heavy chain V r	193	39	47.6	1862	2	I49502	ankyrin 1, mouse
121	41	50.0	117	2	PH1552	Ig H chain V regio	194	39	47.6	1880	2	A35049	ankyrin 1, erythro
122	41	50.0	118	2	S38491	Ig heavy chain - h	195	39	47.6	1881	1	S7HUK	ankyrin 1, erythro
123	41	50.0	119	1	AIHUBR	Ig heavy chain V-I	196	39	47.6	2248	2	A35938	profilaggrin - hum
124	41	50.0	214	2	S74663	peptide methionine	197	38.5	47.0	98	2	S26894	Ig heavy chain V r
125	41	50.0	216	2	AG2591	hypothetical prote	198	38.5	47.0	110	2	S36282	Ig heavy chain V r
126	41	50.0	228	2	H97373	probable transcrip	199	38.5	47.0	110	2	S69897	Ig heavy chain V r
127	41	50.0	1146	2	S64402	hypothetical prote	200	38.5	47.0	111	2	S51211	Ig heavy chain V r
128	41	50.0	1388	2	T17269	hypothetical prote	201	38.5	47.0	117	2	S21980	Ig heavy chain V-g
129	40.5	49.4	115	2	PG6026	acetylcholine recep	202	38.5	47.0	117	2	B34964	Ig heavy chain V r
130	40.5	49.4	120	2	S49590	Ig heavy chain V r	203	38.5	47.0	123	2	S26794	Ig heavy chain V r
131	40.5	49.4	120	2	S55538	Ig heavy chain V r	204	38.5	47.0	125	2	S30531	Ig heavy chain V r
132	40.5	49.4	120	2	S55539	Ig heavy chain V r	205	38.5	47.0	143	2	S23624	Ig heavy chain V r
133	40.5	49.4	142	2	C34903	Ig heavy chain pre	206	38	46.3	98	1	HVMS96	Ig heavy chain V r
134	40.5	49.4	254	2	B31790	Ig heavy chain V r	207	38	46.3	101	2	C27889	Ig heavy chain V r
135	40	48.8	70	2	PL0250	Ig heavy chain V r	208	38	46.3	111	2	PH1659	Ig heavy chain V r
136	40	48.8	83	2	C25913	Ig heavy chain V r	209	38	46.3	119	2	B27889	Ig heavy chain pre
137	40	48.8	94	2	S14580	Ig heavy chain V r	210	38	46.3	139	2	S01158	Ig heavy chain pre
138	40	48.8	102	2	S14581	Ig heavy chain V r	211	38	46.3	139	2	G29380	Ig heavy chain pre
139	40	48.8	108	2	PH1010	Ig heavy chain V r	212	38	46.3	142	2	I47194	Ig heavy chain var
140	40	48.8	117	1	HVMS57	Ig heavy chain pre	213	38	46.3	152	2	B26471	Ig heavy chain pre
141	40	48.8	117	2	PL0252	Ig heavy chain V r	214	38	46.3	187	2	G97426	hypothetical prote
142	40	48.8	117	2	PL0249	Ig heavy chain V r	215	38	46.3	187	2	AG2644	conserved hypoteth
143	40	48.8	119	2	F27888	Ig heavy chain V r	216	38	46.3	232	2	T09821	expansin (clone pp
144	40	48.8	120	2	S55537	Ig heavy chain V r	217	38	46.3	232	2	T09818	expansin (clone pp
145	40	48.8	120	2	S55536	Ig heavy chain V r	218	38	46.3	232	2	T09825	expansin (clone pp
146	40	48.8	121	2	S26798	Ig heavy chain V r	219	38	46.3	260	2	D82316	transcription regu
147	40	48.8	121	2	I27887	Ig heavy chain V r	220	38	46.3	309	2	C72368	hypothetical prote
148	40	48.8	122	2	E27888	Ig heavy chain V r	221	38	46.3	331	2	F86633	fatty acid/phospho
149	40	48.8	123	2	S63597	Ig heavy chain, V	222	38	46.3	349	2	E70640	hypothetical prote
150	40	48.8	124	2	C27888	Ig heavy chain V r	223	38	46.3	411	2	AB0199	peptidase 1 (BC 3.
151	40	48.8	200	2	A82071	3-isopropylmalate	224	38	46.3	435	2	T08454	hypothetical prote
152	40	48.8	293	2	A12775	conserved hypoteth	225	38	46.3	519	2	S36471	L2 protein - human
153	40	48.8	293	2	G37555	hypothetical prote	226	38	46.3	575	2	T52420	dehydrin 5 [impor
154	40	48.8	332	2	C48835	kinesin-like prote	227	38	46.3	575	2	S27761	dehydrin Dhn5 - ba
155	40	48.8	514	2	AG1170	amidophosphoribos	228	38	46.3	590	2	A41335	microbial metallo
156	40	48.8	514	2	G81935	amidophosphoribos	229	38	46.3	1203	2	A49175	Motch B protein -
157	40	48.8	516	2	S64120	TATA box-binding p	230	38	46.3	1712	1	CGHU28	collagen alpha 2(I
158	40	48.8	548	2	S38864	Ig epsilon chain C	231	38	46.3	2471	2	A49128	cell-fate determin
159	40	48.8	582	2	T38743	hypothetical zinc	232	38	46.3	3068	1	A44062	conserved hypoteth
160	40	48.8	747	1	A57107	kinesin-related pr	233	37.5	45.7	114	1	H3HUNE	Ig heavy chain V-I
161	40	48.8	987	2	H81722	polymorphic membra	234	37.5	45.7	118	2	PH1536	Ig H chain V regio
162	40	48.8	1311	2	A56390	mannosyl-glycoprot	235	37.5	45.7	122	1	AIHUTR	Ig heavy chain V-I
163	40	48.8	1312	2	E95006	beta-N-acetylhexos	236	37.5	45.7	137	2	I47181	Ig heavy chain var
164	40	48.8	1312	2	A37879	beta-N-acetylhexos	237	37.5	45.7	504	2	S00390	Ig gamma chain (cl
165	39.5	48.2	83	2	S21593	Ig heavy chain V r	238	37.5	45.7	1000	2	D87244	conserved hypoteth
166	39.5	48.2	108	2	S24251	Ig heavy chain V r	239	37	45.1	96	2	C47624	Ig heavy chain V-V
167	39.5	48.2	113	2	S26468	Ig heavy chain V r	240	37	45.1	101	2	S26460	Ig heavy chain V r
168	39.5	48.2	117	1	HVMS34	Ig heavy chain pre	241	37	45.1	102	2	S14486	Ig heavy chain V r
169	39.5	48.2	130	2	I37783	Ig variable region	242	37	45.1	106	2	S24521	Ig heavy chain V r
170	39.5	48.2	136	2	S31615	hypothetical prote	243	37	45.1	108	2	PH1006	Ig heavy chain V r
171	39.5	48.2	140	2	I47208	Ig heavy chain var	244	37	45.1	110	2	PH1093	Ig heavy chain V-I
172	39	47.6	60	2	J70512	Ig heavy chain V-I	245	37	45.1	111	1	HMMS76	Ig heavy chain V-I
173	39	47.6	97	2	S26890	Ig heavy chain V r	246	37	45.1	113	1	AVMS09	Ig heavy chain V-I
174	39	47.6	98	2	S31692	Ig heavy chain V r	247	37	45.1	113	1	AVMS57	Ig heavy chain V-I
175	39	47.6	108	2	PH1651	Ig heavy chain V r	248	37	45.1	113	1	AVMS61	Ig heavy chain V-I

249	37	45.1	113	1	AVMSAB	Ig heavy chain V-I	322	36	43.9	125	2	S67945	Ig heavy chain BrE
250	37	45.1	113	1	AVMSB7	Ig heavy chain V-I	323	36	43.9	127	2	P0369	Ig gamma chain pre
251	37	45.1	113	2	S22555	Ig heavy chain V r	324	36	43.9	137	2	B34903	Ig heavy chain pre
252	37	45.1	115	1	AVMS06	Ig heavy chain V-I	325	36	43.9	137	2	A34903	Ig heavy chain pre
253	37	45.1	115	1	AVMS82	Ig heavy chain V-I	326	36	43.9	137	2	D34903	Ig heavy chain pre
254	37	45.1	115	2	A25803	Ig heavy chain V r	327	36	43.9	137	2	F34903	Ig heavy chain pre
255	37	45.1	115	2	S38714	Ig heavy chain V r	328	36	43.9	152	2	H95928	probable transcrip
256	37	45.1	117	1	HVMS84	Ig heavy chain pre	329	36	43.9	157	2	S57995	probable olfactory
257	37	45.1	117	2	E34792	Ig heavy chain pre	330	36	43.9	161	2	S05547	dehydrin 17 - barl
258	37	45.1	118	2	G34792	Ig heavy chain pre	331	36	43.9	230	2	A12659	ATP phosphoribosyl
259	37	45.1	119	2	PH1544	Ig H chain V regio	332	36	43.9	230	2	G97441	ATP phosphoribosyl
260	37	45.1	119	2	A43413	Ig heavy chain V r	333	36	43.9	231	2	SL7367	rab15B protein - w
261	37	45.1	119	2	D27889	Ig heavy chain V r	334	36	43.9	231	2	AF3555	histidine ammonia-
262	37	45.1	119	2	PH1555	Ig H chain V regio	335	36	43.9	232	2	JC7577	endo-1,4-beta-xyla
263	37	45.1	121	2	H27887	Ig heavy chain V r	336	36	43.9	269	2	AC0727	rRNA (guanine-N1-)
264	37	45.1	128	1	GFHUC	glycophorin C - hu	337	36	43.9	291	2	T23595	hypothetical prote
265	37	45.1	135	1	I37778	Ig variable region	338	36	43.9	297	1	A30586	B-cell surface ant
266	37	45.1	142	2	I47206	Ig heavy chain var	339	36	43.9	297	2	A83469	probable transcrip
267	37	45.1	197	2	F69359	conserved hypothet	340	36	43.9	300	2	S75692	hypothetical prote
268	37	45.1	231	2	AE3641	ATP phosphoribosyl	341	36	43.9	303	2	T00969	probable mitochond
269	37	45.1	240	1	JS0591	endo-1,4-beta-xyla	342	36	43.9	314	2	C85090	probable phi-1-lik
270	37	45.1	241	2	T37005	endo-1,4-beta-xyla	343	36	43.9	320	2	A40660	outer membrane pro
271	37	45.1	257	2	G82951	probable transcrip	344	36	43.9	333	1	JS0590	endo-1,4-beta-xyla
272	37	45.1	327	2	D89331	branched-chain alp	345	36	43.9	335	2	T50601	endo-1,4-beta-xyla
273	37	45.1	359	2	T21247	hypothetical prote	346	36	43.9	351	2	B82496	immunogenic protei
274	37	45.1	395	2	S44454	transcription fact	347	36	43.9	360	2	G91108	membrane-bound lyt
275	37	45.1	400	2	C90791	probable integrase	348	36	43.9	360	2	B85954	membrane-bound lyt
276	37	45.1	400	2	E85600	probable P4-family	349	36	43.9	372	2	JC7865	fructosyl-amino ac
277	37	45.1	429	2	T00907	hypothetical prote	350	36	43.9	379	2	G87023	cell division prot
278	37	45.1	432	1	D64773	trigger factor [va	351	36	43.9	444	2	S73831	trigger factor tlg
279	37	45.1	432	2	AB0558	trigger factor [im	352	36	43.9	471	2	JC1403	glutamate-ammonia
280	37	45.1	432	2	B85540	hypothetical prote	353	36	43.9	472	2	A60330	protein A precurs
281	37	45.1	432	2	B90690	trigger factor [im	354	36	43.9	487	2	E90251	aspartate oxidase
282	37	45.1	432	2	C64088	trigger factor [im	355	36	43.9	499	2	H97071	aiCAR transformat
283	37	45.1	433	2	H82139	trigger factor [ei	356	36	43.9	501	1	RGEUCB	sensor protein uhp
284	37	45.1	434	2	AP0383	Trigger factor [im	357	36	43.9	506	2	AE0596	histidine ammonia-
285	37	45.1	448	2	C95257	choline binding pr	358	36	43.9	507	2	S05542	hypothetical prote
286	37	45.1	464	2	AG2774	glutathione-disulf	359	36	43.9	509	2	G83009	histidine ammonia-
287	37	45.1	464	2	E97554	glutathione-disulf	360	36	43.9	509	2	C87368	histidine ammonia-
288	37	45.1	534	2	B87278	sensor histidine k	361	36	43.9	510	1	A35251	histidine ammonia-
289	37	45.1	632	2	E84157	glucose-inhibited	362	36	43.9	510	2	AG0488	histidine ammonia-
290	37	45.1	671	2	T23015	hypothetical prote	363	36	43.9	511	2	G95945	probable histidine
291	37	45.1	680	2	T27078	hypothetical prote	364	36	43.9	511	2	B82228	histidine ammonia-
292	37	45.1	732	2	AF0439	probable Rhs acces	365	36	43.9	514	2	AG3040	histidine ammonia-
293	37	45.1	764	2	T45793	hypothetical prote	366	36	43.9	514	2	E98245	hucH gene homolog
294	37	45.1	800	2	AG0438	probable Rhs acces	367	36	43.9	535	2	F83040	phosphoribosylamin
295	37	45.1	860	2	T27084	hypothetical prote	368	36	43.9	538	2	I51560	ribonucleoprotein
296	37	45.1	909	2	G69599	aconitate hydratase	369	36	43.9	581	2	S49098	penicillin-binding
297	37	45.1	914	2	T08081	probable myrosinase	370	36	43.9	581	2	S49096	penicillin-binding
298	37	45.1	988	2	T08102	myrosinase-binding	371	36	43.9	581	2	S49093	penicillin-binding
299	37	45.1	1000	2	AB3467	sarcosine oxidase	372	36	43.9	582	2	S49097	penicillin-binding
300	37	45.1	2706	2	T28155	variant-specific s	373	36	43.9	582	2	A36190	penicillin-binding
301	37	45.1	5232	2	A45086	HC-toxin synthetas	374	36	43.9	607	2	C95503	conserved hypothet
302	36.5	44.5	98	2	S26940	Ig heavy chain V r	375	36	43.9	644	1	I40712	endo-1,4-beta-xyla
303	36.5	44.5	115	2	S36284	Ig heavy chain V r	376	36	43.9	654	2	B84689	hypothetical prote
304	36.5	44.5	116	2	S21979	Ig heavy chain V-g	377	36	43.9	711	2	E89953	hypothetical prote
305	36.5	44.5	121	2	S55540	Ig heavy chain V r	378	36	43.9	768	2	JC6564	cellobiose oxidase
306	36.5	44.5	122	2	PH1537	Ig H chain V regio	379	36	43.9	784	1	A55236	kinesin-related pr
307	36.5	44.5	141	2	S31669	Ig heavy chain V r	380	36	43.9	840	2	G83052	translation initia
308	36.5	44.5	1197	2	T13956	timeless protein h	381	36	43.9	892	2	B82831	translation initia
309	36.5	44.5	1205	2	T13959	timeless protein t	382	36	43.9	953	2	T08961	hypothetical prote
310	36	43.9	50	2	D26747	hypothetical prote	383	36	43.9	962	2	C81060	translation initia
311	36	43.9	56	2	B30518	Ig heavy chain V-A	384	36	43.9	1000	2	T22391	hypothetical prote
312	36	43.9	96	2	A28555	Ig heavy chain V r	385	36	43.9	1027	2	C86300	protein F309.28 [i
313	36	43.9	116	1	GAR815	Ig heavy chain V-A	386	36	43.9	1063	2	D86731	hypothetical prote
314	36	43.9	116	2	H29380	Ig heavy chain pre	387	36	43.9	1070	2	A10484	probable autocrans
315	36	43.9	118	2	F34792	Ig heavy chain pre	388	36	43.9	1372	2	T25933	hypothetical prote
316	36	43.9	118	2	E27889	Ig heavy chain V r	389	36	43.9	1829	2	T34239	hypothetical prote
317	36	43.9	118	2	A31485	Ig heavy chain V r	390	36	43.9	1946	2	AB1449	hypothetical prote
318	36	43.9	120	2	D97857	hypothetical prote	391	36	43.9	2020	2	A43932	mucin 2 precursor,
319	36	43.9	121	2	A27888	Ig heavy chain V r	392	35.5	43.3	107	2	S60590	Ig heavy chain var
320	36	43.9	121	2	D27888	Ig heavy chain V r	393	35.5	43.3	108	2	PH1011	Ig heavy chain v r
321	36	43.9	121	2	B27888	Ig heavy chain V r	394	35.5	43.3	117	1	HVMS39	Ig heavy chain pre

395	35.5	43.3	120	1	GIHUBD	Ig heavy chain V-I	468	35	42.7	495	1	S75895	probable L-xyloio
396	35.5	43.3	142	2	I47190	Ig heavy chain var	469	35	42.7	515	2	T03070	hypothetical prote
397	35.5	43.3	263	2	H82015	probable pyroline	470	35	42.7	523	2	T12198	sucrose transport
398	35.5	43.3	263	2	E81243	pyroline-5-carbox	471	35	42.7	529	2	F70550	probable accDl pro
399	35.5	43.3	677	2	S32816	potassium channel	472	35	42.7	535	2	AF3452	methylcrotonoyl-Co
400	35	42.7	53	2	I50832	Ig heavy chain - L	473	35	42.7	548	1	HYBST	thermolysin (EC 3.
401	35	42.7	98	2	A49021	Ig heavy chain V-X	474	35	42.7	551	2	B36706	neutrol proteinase
402	35	42.7	98	2	S26928	Ig heavy chain V-X	475	35	42.7	552	2	A46564	thermolysin (EC 3.
403	35	42.7	98	2	S26933	Ig heavy chain V r	476	35	42.7	581	2	S00916	penicillin-binding
404	35	42.7	98	2	A37632	Ig heavy chain V r	477	35	42.7	581	2	S04857	penicillin-binding
405	35	42.7	99	2	S20765	hypothetical prote	478	35	42.7	582	2	S49050	penicillin-binding
406	35	42.7	100	2	D48223	Ig heavy chain V r	479	35	42.7	582	2	S49095	penicillin-binding
407	35	42.7	104	2	S69899	Ig heavy chain V r	480	35	42.7	582	2	S49092	penicillin-binding
408	35	42.7	104	2	E82360	cyav protein VC012	481	35	42.7	582	2	S49091	penicillin-binding
409	35	42.7	110	2	PH1014	Ig heavy chain V r	482	35	42.7	614	2	G69481	hypothetical prote
410	35	42.7	112	2	PH1654	Ig heavy chain V r	483	35	42.7	628	1	BWBSGA	glucose-inhibited
411	35	42.7	115	2	S57445	Ig heavy chain V r	484	35	42.7	629	2	AI1425	GidA protein homol
412	35	42.7	120	2	S12953	Ig heavy chain V-J	485	35	42.7	629	2	AG1799	GidA protein homol
413	35	42.7	121	1	GIHULH	Ig heavy chain V-I	486	35	42.7	667	2	A48579	trophozoite surfac
414	35	42.7	121	1	PH1661	Ig heavy chain V r	487	35	42.7	674	2	T48204	hypothetical prote
415	35	42.7	142	1	H8RB	hemoglobin alpha c	488	35	42.7	681	2	AH1409	potassium-transport
416	35	42.7	154	2	B83304	hypothetical prote	489	35	42.7	703	2	D84604	hypothetical prote
417	35	42.7	155	2	I47199	Ig heavy chain var	490	35	42.7	721	2	TI19103	hypothetical prote
418	35	42.7	165	2	F82743	hypothetical prote	491	35	42.7	721	2	B83820	hypothetical prote
419	35	42.7	169	2	E83578	disulfide bond for	492	35	42.7	741	2	AC0094	conserved hypothet
420	35	42.7	174	2	S45603	ferritin, soma - g	493	35	42.7	748	2	T35818	probable integral
421	35	42.7	205	2	T05713	dehydrin - barley	494	35	42.7	790	2	D86528	omp85 analog [limp
422	35	42.7	211	2	S25938	env protein - huma	495	35	42.7	790	2	D72094	omp85 analog - chl
423	35	42.7	214	2	B86639	acyl carrier prote	496	35	42.7	879	2	S64755	hypothetical prote
424	35	42.7	223	2	H95350	VirB8 type IV secr	497	35	42.7	879	2	F86548	polymorphic outer
425	35	42.7	223	2	E83180	agrobacterium viru	498	35	42.7	938	2	H72074	polymorphic membra
426	35	42.7	235	2	E69436	hypothetical prote	499	35	42.7	942	2	T38649	hypothetical homeo
427	35	42.7	249	1	V6XRHB	glycoprotein VP7 p	500	35	42.7	1024	2	T34517	kinesin-related pr
428	35	42.7	250	2	T10079	expansin SI precu	501	35	42.7	1081	1	WZBEA6	119K DNA helicase/
429	35	42.7	263	2	F82311	survival protein S	502	35	42.7	1421	2	T02501	hypothetical prote
430	35	42.7	265	2	G84049	hypothetical prote	503	35	42.7	1596	2	AG2501	hypothetical prote
431	35	42.7	284	2	AD1394	fructose-1,6-bisph	504	35	42.7	1795	2	T30332	avirulence protein
432	35	42.7	284	2	AG1769	fructose-1,6-bisph	505	35	42.7	1819	2	D97132	uncharacterized ph
433	35	42.7	296	2	B33823	ribosomal protein	506	35	42.7	2020	2	C48339	ABC-type transport
434	35	42.7	297	2	UC1308	hypothetical prote	507	35	42.7	2105	2	TI18968	probable serine-ty
435	35	42.7	299	2	T16137	nonstructural prote	508	35	42.7	2136	2	B84651	hypothetical prote
436	35	42.7	301	1	JQ1927	NSM protein - toma	509	35	42.7	2314	2	T28698	hypothetical prote
437	35	42.7	302	2	S72542	homoserine kinase	510	34.5	42.1	111	2	S40090	Ig heavy chain - m
438	35	42.7	306	2	AB3526	probable phosphate	511	34.5	42.1	117	2	PH1542	Ig H chain V regio
439	35	42.7	309	2	H86471	thioredoxin reduct	512	34.5	42.1	118	2	PH1530	Ig H chain V regio
440	35	42.7	310	2	D71703	bifunctional cyclo	513	34.5	42.1	128	2	PH0095	Ig kappa chain V r
441	35	42.7	316	2	S25843	transaldolase PA27	514	34.5	42.1	137	2	S78054	Ig heavy chain pre
442	35	42.7	321	2	H98181	transaldolase talB	515	34.5	42.1	392	2	D91185	probable regulator
443	35	42.7	321	2	AD3105	serine/threonine-p	516	34.5	42.1	392	2	B86032	xylose operon regu
444	35	42.7	327	2	H83659	transaldolase (EC	517	34.5	42.1	392	2	S47790	probable regulator
445	35	42.7	334	2	S39870	probable cysteine	518	34.5	42.1	582	2	D82146	transport ATP-bind
446	35	42.7	341	2	T45839	succinate-CoA liga	519	34.5	42.1	636	2	H87789	protein C34G6.1 [i
447	35	42.7	345	2	S30579	immunogenic protei	520	34	41.5	64	2	T77394	Ig heavy chain V r
448	35	42.7	346	2	A84017	succinate-CoA liga	521	34	41.5	70	2	S24495	Ig heavy chain V r
449	35	42.7	347	2	T51816	3beta-hydroxy-Delt	522	34	41.5	94	2	G32513	Ig heavy chain V r
450	35	42.7	373	2	A37404	occlusion-derived	523	34	41.5	94	2	PL0120	Ig heavy chain V-I
451	35	42.7	376	2	F72868	conserved hypothet	524	34	41.5	95	2	S20777	Ig heavy chain V r
452	35	42.7	394	2	AF2650	penicillin-binding	525	34	41.5	96	2	PH0873	Ig heavy chain V r
453	35	42.7	399	2	S49100	penicillin-binding	526	34	41.5	96	2	PH1165	Ig heavy chain V r
454	35	42.7	400	2	B36190	penicillin-binding	527	34	41.5	97	2	S44115	Ig heavy chain V-I
455	35	42.7	400	2	S29686	penicillin-binding	528	34	41.5	98	2	PL0116	Ig heavy chain V r
456	35	42.7	400	2	S49089	penicillin-binding	529	34	41.5	98	2	S29543	Ig heavy chain V r
457	35	42.7	400	2	S29687	penicillin-binding	530	34	41.5	98	2	S26934	Ig heavy chain V r
458	35	42.7	400	2	S49099	penicillin-binding	531	34	41.5	98	2	S26932	Ig heavy chain V r
459	35	42.7	401	2	S29688	hypothetical prote	532	34	41.5	98	2	S29546	Ig heavy chain V-I
460	35	42.7	406	2	G84774	hypothetical prote	533	34	41.5	98	2	F47624	Ig heavy chain V-I
461	35	42.7	420	2	E97432	UDP-N-acetylglucos	534	34	41.5	106	2	S20774	Ig heavy chain V r
462	35	42.7	426	2	B75434	hypothetical prote	535	34	41.5	106	2	PH1008	Ig heavy chain V r
463	35	42.7	433	2	T27538	probable lat prote	536	34	41.5	108	2	PH1642	Ig heavy chain V r
464	35	42.7	449	2	T36042	probable plasmid r	537	34	41.5	109	2	PH1646	Ig heavy chain V r
465	35	42.7	452	2	C70981	sigma 1 protein -	538	34	41.5	109	2	PH1644	Ig heavy chain V r
466	35	42.7	462	2	C34829	fimbrial assembly	539	34	41.5	110	2	PL1000	Ig heavy chain V r
467	35	42.7	490	2	F82546		540	34	41.5	111	2	PL0199	anti-DNA autoantib

541	34	41.5	111	2	PH1643	Ig heavy chain V r	614	34	41.5	295	2	JB0051	SC01 protein precu
542	34	41.5	111	2	PH1645	Ig heavy chain V r	615	34	41.5	296	2	A33823	ribosomal protein
543	34	41.5	113	2	S38490	Ig heavy chain - h	616	34	41.5	297	2	S55912	ribosomal protein
544	34	41.5	114	2	S46390	Ig heavy chain V r	617	34	41.5	305	2	P95965	probable thiolgula
545	34	41.5	114	2	S46391	Ig heavy chain V r	618	34	41.5	313	2	T33849	hypothetical prote
546	34	41.5	114	2	S46392	Ig heavy chain V r	619	34	41.5	314	2	AG0485	2-dehydro-3-deoxyg
547	34	41.5	115	2	S44112	Ig heavy chain V r	620	34	41.5	315	2	A36944	outer membrane pro
548	34	41.5	117	2	S36259	Ig heavy chain V r	621	34	41.5	317	2	E83380	probable transcrip
549	34	41.5	117	2	S36270	Ig heavy chain V r	622	34	41.5	325	2	S74512	cystathionine beta
550	34	41.5	118	2	S31677	Ig heavy chain V r	623	34	41.5	326	2	AH0054	phosphoserine phos
551	34	41.5	118	2	PH0096	Ig heavy chain V r	624	34	41.5	330	2	S37595	mucin JUL10 - huma
552	34	41.5	118	2	S31116	Ig heavy chain - h	625	34	41.5	332	2	AH3054	succinoglycan bios
553	34	41.5	119	2	S31111	Ig heavy chain - h	626	34	41.5	333	2	T23618	hypothetical prote
554	34	41.5	119	2	PH1533	Ig H chain V regio	627	34	41.5	334	2	D72381	dehydrogenase - Th
555	34	41.5	119	2	P36005	Ig heavy chain V r	628	34	41.5	336	2	D72243	rod shape-determin
556	34	41.5	120	2	S31112	Ig heavy chain - h	629	34	41.5	338	2	E98231	succinoglycan bios
557	34	41.5	121	2	S19666	Ig heavy chain V r	630	34	41.5	340	2	T20148	probable cysteine
558	34	41.5	121	2	S36005	Ig heavy chain V r	631	34	41.5	342	2	A46529	Ig gamma chain (5.
559	34	41.5	122	2	S31117	Ig heavy chain - h	632	34	41.5	347	2	B47611	env polyprotein -
560	34	41.5	122	2	E36005	Ig heavy chain V r	633	34	41.5	350	2	B43670	sulfate-binding pr
561	34	41.5	122	2	S31119	Ig heavy chain - h	634	34	41.5	352	2	S76739	sulfate-binding pr
562	34	41.5	123	2	S25574	Ig heavy chain V r	635	34	41.5	360	1	T10716	dihydrokaempferol
563	34	41.5	123	2	S38493	Ig heavy chain - h	636	34	41.5	360	2	AE3175	hypothetical prote
564	34	41.5	123	2	D33548	Ig heavy chain V-1	637	34	41.5	368	2	A99864	conserved hypotet
565	34	41.5	125	2	S37455	Ig mu chain - huma	638	34	41.5	373	2	T13332	hypothetical prote
566	34	41.5	125	2	S20785	Ig heavy chain V r	639	34	41.5	374	2	T10415	virus envelope pro
567	34	41.5	125	2	T06804	probable dehydrin	640	34	41.5	375	2	A64300	aspartate transami
568	34	41.5	126	2	I44151	Ig heavy chain V r	641	34	41.5	381	2	E88427	protein R0785.3 [i
569	34	41.5	128	2	S48797	Ig heavy chain V r	642	34	41.5	388	2	S15591	probable transpoea
570	34	41.5	130	2	PL0098	Ig heavy chain pre	643	34	41.5	391	2	A75451	probable soluble h
571	34	41.5	132	2	S31603	Ig heavy chain V r	644	34	41.5	394	2	G84265	hypothetical prote
572	34	41.5	133	2	A49028	Ig heavy chain V-1	645	34	41.5	402	2	H88650	protein C09G12.9 [
573	34	41.5	133	2	S31510	Ig heavy chain - h	646	34	41.5	408	2	D82016	pili-like protein
574	34	41.5	134	2	S31679	Ig heavy chain V r	647	34	41.5	412	2	B97316	pectate lyase limp
575	34	41.5	134	2	S31688	Ig heavy chain V r	648	34	41.5	420	2	B97502	riboflavin-specifi
576	34	41.5	135	2	S31598	Ig heavy chain V r	649	34	41.5	420	1	S34379	glycine hydroxymet
577	34	41.5	139	2	S31674	Ig heavy chain V r	650	34	41.5	425	2	D83455	hypothetical prote
578	34	41.5	140	2	S70442	Ig heavy chain pre	651	34	41.5	442	2	C83890	beta-glucosidase b
579	34	41.5	141	2	I47177	Ig H-chain - pig (652	34	41.5	457	2	S46054	probable DNA-bindi
580	34	41.5	141	2	C83529	hypothetical prote	653	34	41.5	453	2	G69494	DNA helicase homol
581	34	41.5	141	2	T15990	hypothetical prote	654	34	41.5	466	2	H69065	5'-nucleotidase -
582	34	41.5	142	2	C39610	BET1 protein - yea	655	34	41.5	476	2	AC2306	hypothetical prote
583	34	41.5	147	2	I37780	Ig variable region	656	34	41.5	476	2	G82062	sulfate adenylate
584	34	41.5	151	2	B87163	conserved hypotet	657	34	41.5	483	2	I65219	retinoid-related o
585	34	41.5	168	2	C82670	general secretory	658	34	41.5	492	2	T36429	probable iron-sulf
586	34	41.5	182	2	C90141	hypothetical prote	659	34	41.5	505	2	C96966	beta-mannanase Man
587	34	41.5	186	2	T29117	hypothetical prote	660	34	41.5	515	2	E82267	thiamin biosynthes
588	34	41.5	191	2	JI0048	Ig heavy chain V r	661	34	41.5	518	1	P2WL5	L2 protein - human
589	34	41.5	205	2	T02385	hypothetical prote	662	34	41.5	518	1	P2WL8	L2 protein - human
590	34	41.5	206	2	T23852	hypothetical prote	663	34	41.5	520	2	B96517	L2 protein - human
591	34	41.5	209	2	T35041	hypothetical prote	664	34	41.5	520	2	S36489	hypothetical prote
592	34	41.5	209	2	G72528	hypothetical prote	665	34	41.5	522	2	D96836	L2 protein - human
593	34	41.5	213	2	E83828	thioredoxin reduct	666	34	41.5	525	2	JN0059	probable glycerol
594	34	41.5	232	2	AG2876	RNA methylase [imp	667	34	41.5	525	2	AE2984	hypothetical 57.4K
595	34	41.5	233	2	F81391	amino-acid ABC tra	668	34	41.5	529	2	S43599	Snf5 homolog R0785
596	34	41.5	238	2	A55324	agglutinin WBA1 -	669	34	41.5	533	2	AE2984	3-methylcrotonoyl-
597	34	41.5	238	2	S70468	agglutinin (WBA 1)	670	34	41.5	535	2	C83395	probable acyl-CoA
598	34	41.5	238	2	T05344	hypothetical prote	671	34	41.5	535	2	E95929	probable methylcro
599	34	41.5	240	1	S47512	endo-1,4-beta-xyla	672	34	41.5	537	2	B98299	probable acyl-CoA
600	34	41.5	247	2	F82101	DNA polymerase III	673	34	41.5	543	2	S35047	mucin JUL7 - human
601	34	41.5	249	2	JC5510	proteasome endopep	674	34	41.5	544	2	S62527	probable amino-aci
602	34	41.5	253	2	F84831	probable expansin	675	34	41.5	549	2	S04845	Ig heavy chain pre
603	34	41.5	254	2	S60038	proteasome endopep	676	34	41.5	569	2	D69374	type II secretion
604	34	41.5	259	1	TRSMG	trypsin (EC 3.4.21	677	34	41.5	595	2	B69292	type II secretion
605	34	41.5	259	2	G81352	probable oxidoredu	678	34	41.5	599	1	BVECLA	GTP-binding membra
606	34	41.5	260	2	C55230	succinate-CoA liga	679	34	41.5	599	2	AE0829	GTP-binding elonga
607	34	41.5	277	2	T19983	hypothetical prote	680	34	41.5	599	2	C91058	GTP-binding membra
608	34	41.5	277	2	H86589	hypothetical prote	681	34	41.5	599	2	A85903	GTP-binding membra
609	34	41.5	277	2	C72033	hypothetical prote	682	34	41.5	608	1	S28313	hypothetical prote
610	34	41.5	285	2	A97653	probable rRNA meth	683	34	41.5	609	2	P70872	probable acyl-coad
611	34	41.5	291	2	AH2017	lipoic acid synthe	684	34	41.5	622	2	E71312	hypothetical prote
612	34	41.5	291	2	G71300	probable protein-m	685	34	41.5	624	2	AC2588	DNA polymerase III
613	34	41.5	294	2	A87291	succinyl-CoA synth	686	34	41.5	624	2	C97370	DNA polymerase III

687 34 41.5 651 2 E83443 probable sensor/re
688 34 41.5 669 2 T13640 probable minor str
689 34 41.5 672 2 T50259 probable serine/th
690 34 41.5 678 2 G71526 3-methyl-2-oxobuta
691 34 41.5 678 2 C81683 3-methyl-2-oxobuta
692 34 41.5 691 2 A34708 vacuolar protein-s
693 34 41.5 693 2 A54847 GMP synthase (glut
694 34 41.5 693 2 E89822 translational elon
695 34 41.5 694 2 A62353 translation elonga
696 34 41.5 697 2 B44489 GT box-binding pro
697 34 41.5 707 2 D55926 DNA binding protei
698 34 41.5 707 2 T24361 hypothetical prote
699 34 41.5 714 2 S37345 pilQ protein - Pse
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701 34 41.5 726 2 A97041 exodeoxyribonuclea
702 34 41.5 735 2 T30096 hypothetical prote
703 34 41.5 747 2 T39744 conserved hypoteth
704 34 41.5 791 2 S67265 hypothetical prote
705 34 41.5 803 2 B84931 DNA topoisomerase
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707 34 41.5 840 2 A87639 TonB-dependent rec
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713 34 41.5 884 2 A10424 translation initia
714 34 41.5 890 1 F1EC2 translation initia
715 34 41.5 890 2 D85980 protein chain init
716 34 41.5 890 2 A91331 protein chain init
717 34 41.5 896 2 T51891 hypothetical prote
718 34 41.5 896 2 A82298 translation initia
719 34 41.5 899 2 A60859 outer membrane ush
720 34 41.5 952 2 E86147 Tln6.4 protein - A
721 34 41.5 1092 2 T45095 probable arabinosy
722 34 41.5 1135 2 T14803 phytochrome C - so
723 34 41.5 1175 2 T46124 hypothetical prote
724 34 41.5 1187 2 F86422 carbamoyl-phosphat
725 34 41.5 1314 2 G28770 KIAA0197 protein -
726 34 41.5 1319 1 C37335 bcsc protein - Ace
727 34 41.5 1398 2 T28159 pyrolysin (EC 3.4.
728 34 41.5 1441 2 B86807 hypothetical prote
729 34 41.5 1472 2 H82802 fibribial assembly
730 34 41.5 1588 2 A86036 probable adhesin Z
731 34 41.5 1588 2 H31188 probable adhesin E
732 34 41.5 1684 2 S10789 amyliase A-180 - al
733 34 41.5 1787 2 T20160 hypothetical prote
734 34 41.5 1787 2 AG1360 laminin beta-2 cha
735 34 41.5 1801 1 MWRTS 190-KDa cell surfa
736 34 41.5 1959 2 AG1085 hypothetical prote
737 34 41.5 2021 2 A37859 probable polyketid
738 34 41.5 2126 2 H70621 otogelin - mouse
739 34 41.5 2910 2 T42214 mucin MUC5B, trach
740 34 41.5 3570 2 T45025 Ig heavy chain V r
741 34 41.5 5149 2 F83345 Ig heavy chain V r
742 33.5 40.9 100 2 PH1016 Ig H chain V regio
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744 33.5 40.9 120 2 B49715 Ig heavy chain V r
745 33.5 40.9 120 2 PH1534 Ig H chain V regio
746 33.5 40.9 127 2 S19878 Ig heavy chain V r
747 33.5 40.9 206 1 MWBPL membrane protein l
748 33.5 40.9 218 2 A36040 Ig heavy chain V-I
749 33.5 40.9 234 2 G72758 hypothetical prote
750 33.5 40.9 234 2 C88088 protein B0454.9 [i
751 33.5 40.9 959 2 H69344 hypothetical prote
752 33 40.2 38 2 D82306 hypothetical prote
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754 33 40.2 93 2 C24672 Ig heavy chain V r
755 33 40.2 97 2 H85711 hypothetical prote
756 33 40.2 97 2 G85706 hypothetical prote
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767 33 40.2 110 2 PH1091 Ig heavy chain V r
768 33 40.2 117 2 B33989 Ig heavy chain V-2
769 33 40.2 119 2 A27630 anti-peptide Fab'
770 33 40.2 119 2 B34353 Ig heavy chain V r
771 33 40.2 121 2 A41940 Ig heavy chain V r
772 33 40.2 121 2 B34871 Ig heavy chain V-I
773 33 40.2 122 1 M3HUAM anti-tetanus toxin
774 33 40.2 122 2 PC23398 interferon gamma-i
775 33 40.2 125 2 JN0470 Ig heavy chain V r
776 33 40.2 128 2 S26786 Ig heavy chain pre
777 33 40.2 129 2 S03534 hypothetical prote
778 33 40.2 129 2 AB1933 Ig heavy chain V r
779 33 40.2 130 2 S31673 Ig heavy chain V r
780 33 40.2 132 2 AC3143 hypothetical prote
781 33 40.2 133 1 CCQFCT cytochrome c' - Rh
782 33 40.2 133 2 T14630 H+-exporting ATPas
783 33 40.2 137 2 A69019 conserved protein
784 33 40.2 140 2 A24770 hypothetical hybri
785 33 40.2 140 2 S53877 sex-regulated prot
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787 33 40.2 144 2 I47187 Ig heavy chain var
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792 33 40.2 156 2 S26202 riboflavin synthas
793 33 40.2 156 2 AF0386 riboflavin synthas
794 33 40.2 162 2 T14987 probable endonucle
795 33 40.2 169 2 E84252 flagellin B3 precu
796 33 40.2 173 2 C64115 riboflavin synthas
797 33 40.2 178 2 AH1090 protein gp20 from
798 33 40.2 178 2 AG1454 weakly protein gp2
799 33 40.2 180 2 D75484 probable adenine p
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801 33 40.2 187 2 S52654 flagellin B1 precu
802 33 40.2 193 1 C28944 flagellin B3 precu
803 33 40.2 193 1 E28944 dehydrin-like prot
804 33 40.2 193 2 S63689 flagellin B1 precu
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807 33 40.2 197 2 C81958 hypothetical prote
808 33 40.2 200 2 AB2123 conserved hypoteth
809 33 40.2 201 2 C81015 conserved hypoteth
810 33 40.2 210 2 C83762 endo-1,4-beta-xyla
811 33 40.2 215 2 F84019 transcription regu
812 33 40.2 243 2 F87246 probable MarR-fami
813 33 40.2 244 2 T37686 hypothetical prote
814 33 40.2 251 2 B64337 hypothetical prote
815 33 40.2 256 2 T27836 hypothetical prote
816 33 40.2 258 2 S71561 drought-induced pr
817 33 40.2 260 2 A75572 conserved hypoteth
818 33 40.2 261 2 AD0963 probable Deor-fami
819 33 40.2 265 2 B96993 major prion protei
820 33 40.2 267 1 UUCH prion protein homo
821 33 40.2 267 2 A37372 hypothetical prote
822 33 40.2 267 2 AB1273 hypothetical prote
823 33 40.2 269 2 AC1636 probable S-adenosy
824 33 40.2 269 2 D90949 probable enzyme li
825 33 40.2 269 2 G85793 hypothetical prote
826 33 40.2 269 2 T21407 probable cytochrom
827 33 40.2 270 2 T02955 prion protein - ch
828 33 40.2 273 2 A46280 myelin proteolipid
829 33 40.2 280 2 S31491 lipioic acid synthe
830 33 40.2 289 2 S74959 hypothetical prote
831 33 40.2 290 2 AB1126

833	33	40.2	291	2	T33426	hypothetical prote	906	33	40.2	490	2	T26171	hypothetical prote
834	33	40.2	291	2	AB1487	hypothetical prote	907	33	40.2	494	2	S11946	cellulase (EC 3.2.
835	33	40.2	301	2	A69765	tartrate dehydrog	908	33	40.2	495	2	H70598	hypothetical prote
836	33	40.2	302	2	G81158	conserved hypothet	909	33	40.2	496	2	D89808	hypothetical prote
837	33	40.2	302	2	C81947	hypothetical prote	910	33	40.2	495	2	C87194	probable transmemb
838	33	40.2	302	2	T26513	hypothetical prote	911	33	40.2	503	2	S55589	D-nopaline dehydro
839	33	40.2	304	1	SYSMFG	drpF-dihydrostrept	912	33	40.2	505	2	T07883	cellulase (EC 3.2.
840	33	40.2	304	2	E91230	hypothetical prote	913	33	40.2	508	2	T09367	cytochrome P450 ho
841	33	40.2	304	2	D86077	hypothetical prote	914	33	40.2	512	2	C96517	hypothetical prote
842	33	40.2	305	2	A70440	succinate-CoA liga	915	33	40.2	527	2	JC1267	pyruvate kinase (E
843	33	40.2	308	2	E69771	ABC transporter (A	916	33	40.2	530	1	A25091	pyruvate kinase (E
844	33	40.2	317	2	A31387	omptin (EC 3.4.21.	917	33	40.2	530	2	A54113	pyruvate kinase (E
845	33	40.2	317	2	H85694	outer membrane pro	918	33	40.2	530	2	T02995	unspecific monooxy
846	33	40.2	317	2	G90836	outer membrane pro	919	33	40.2	531	1	S64635	pyruvate kinase (E
847	33	40.2	319	2	S55434	conserved hypothet	920	33	40.2	531	1	S30038	pyruvate kinase (E
848	33	40.2	320	2	JC7929	ATP-dependent gluc	921	33	40.2	531	2	S55921	pyruvate kinase (E
849	33	40.2	320	2	E87684	ATP phosphoribosyl	922	33	40.2	531	2	B26186	pyruvate kinase (E
850	33	40.2	321	2	F98318	hypothetical prote	923	33	40.2	531	2	A26186	pyruvate kinase (E
851	33	40.2	321	2	AG2964	fibrinogen binding	924	33	40.2	536	2	T37544	hypothetical serin
852	33	40.2	321	2	T12497	hypothetical prote	925	33	40.2	540	2	B96747	probable alanine a
853	33	40.2	323	2	F75122	hypothetical prote	926	33	40.2	546	2	S56306	hypothetical prote
854	33	40.2	328	2	G82643	conserved hypothet	927	33	40.2	548	2	AH2962	cellulose biosynth
855	33	40.2	339	2	C82486	lactonizing lipase	928	33	40.2	553	2	F98320	hypothetical prote
856	33	40.2	345	2	D84089	hypothetical prote	929	33	40.2	554	2	T05476	calcium-dependent
857	33	40.2	346	2	F64153	hypothetical prote	930	33	40.2	567	2	S69778	adhesin AP65-1 pre
858	33	40.2	348	2	C26720	hypothetical prote	931	33	40.2	568	2	G85654	probable urease st
859	33	40.2	355	2	F96940	beta-mannanase (lm	932	33	40.2	568	2	D90794	urease alpha subun
860	33	40.2	356	2	G81278	probable 1-deoxy-D	933	33	40.2	574	2	G84578	probable potassium
861	33	40.2	370	2	JC7592	spinal cord-derive	934	33	40.2	576	2	H70961	hypothetical prote
862	33	40.2	372	2	T47763	hypothetical prote	935	33	40.2	583	2	G95214	ABC transporter, A
863	33	40.2	373	2	AG3400	5-amino-6-(5-phosp	936	33	40.2	583	2	F98078	hypothetical prote
864	33	40.2	374	2	H81783	hypothetical prote	937	33	40.2	584	1	I39710	cellulose biosynth
865	33	40.2	375	2	T41885	ODV-E56 orf148 - B	938	33	40.2	588	2	A46507	ig alpha chain - c
866	33	40.2	376	2	F72514	probable Glucokina	939	33	40.2	588	2	C83836	subtilisin-type pr
867	33	40.2	377	2	D81206	hypothetical prote	940	33	40.2	591	2	G90181	hypothetical prote
868	33	40.2	385	2	T36899	probable oxidoredu	941	33	40.2	591	2	T44868	probable membrane
869	33	40.2	392	2	C72783	hypothetical prote	942	33	40.2	598	2	F75212	glutamine-fructose
870	33	40.2	392	2	H96516	F16N3.10 [imported	943	33	40.2	599	2	S67495	huntingtin-associa
871	33	40.2	395	2	AG2835	sarcosine oxidase	944	33	40.2	600	2	D75569	gida protein - Del
872	33	40.2	398	2	AB2622	succinyl-diaminopi	945	33	40.2	601	2	D87232	conserved membrane
873	33	40.2	398	2	B97404	succinyl-diaminopi	946	33	40.2	601	2	D71248	glutamine-fructose
874	33	40.2	403	2	F72254	hypothetical prote	947	33	40.2	602	1	T35760	2',3'-cyclic-nucle
875	33	40.2	407	2	F87494	hypothetical prote	948	33	40.2	614	2	B83818	class I heat-shock
876	33	40.2	408	2	D64857	aminotripeptidase	949	33	40.2	618	2	A70989	hypothetical glyci
877	33	40.2	408	2	D90825	probable peptidase	950	33	40.2	624	2	T02289	probable polygalac
878	33	40.2	408	2	G85683	probable peptidase	951	33	40.2	625	2	T39019	probable mitochond
879	33	40.2	409	2	A42363	aminotripeptidase	952	33	40.2	629	2	S67492	huntingtin-associa
880	33	40.2	409	2	AD0646	aminotripeptidase	953	33	40.2	630	2	T05433	hypothetical prote
881	33	40.2	409	2	T08928	sucrose cleavage p	954	33	40.2	643	2	T03518	hypothetical prote
882	33	40.2	410	2	B84401	probable FMV oxido	955	33	40.2	655	1	A55726	RNA-binding protei
883	33	40.2	411	2	D83307	hypothetical prote	956	33	40.2	656	1	A49358	RNA-binding protei
884	33	40.2	412	2	S53783	hypothetical prote	957	33	40.2	662	1	A31349	arachidonate 15-11
885	33	40.2	417	2	D64302	L-asparaginase I -	958	33	40.2	663	1	A35087	arachidonate 12-11
886	33	40.2	426	2	A86634	O-acetylhomoserine	959	33	40.2	666	2	A42296	lysozyme 2 (EC 3.2
887	33	40.2	429	2	T29711	hypothetical prote	960	33	40.2	669	2	S75785	translation elonga
888	33	40.2	435	2	C69194	L-asparaginase I -	961	33	40.2	671	2	C96534	probable Poly-A Bi
889	33	40.2	437	2	B97613	monomeric sarcosin	962	33	40.2	674	2	A69111	cell surface glyco
890	33	40.2	441	2	C81244	probable membrane-	963	33	40.2	678	2	G75524	translation elonga
891	33	40.2	441	2	C81244	membrane-bound lyc	964	33	40.2	694	2	F82511	vgrG protein VCA00
892	33	40.2	443	2	F86890	NADH oxidase noxd	965	33	40.2	697	2	T34006	hypothetical prote
893	33	40.2	447	2	JC7153	phosphoprotein pho	966	33	40.2	718	2	T29708	hypothetical prote
894	33	40.2	447	2	S65686	protein phosphatas	967	33	40.2	720	2	AF0242	probable exported
895	33	40.2	447	2	A55836	phosphoprotein pho	968	33	40.2	726	2	B29928	ferric anguibactin
896	33	40.2	448	2	C98122	choline binding pr	969	33	40.2	729	2	A86416	probable arm repea
897	33	40.2	458	1	S77662	thioredoxin-disulf	970	33	40.2	740	2	G75477	probable general s
898	33	40.2	461	2	S01840	nitrogenase (EC 1.	971	33	40.2	741	1	A69432	ATP-dependent RNA
899	33	40.2	463	2	T29442	hypothetical prote	972	33	40.2	752	2	T48574	hypothetical prote
900	33	40.2	468	2	A82763	UDP-N-acetylmuram	973	33	40.2	769	2	D86335	T2OH2.6 protein -
901	33	40.2	469	2	D86309	hypothetical prote	974	33	40.2	770	2	A49283	outer layer protei
902	33	40.2	470	2	S22080	Ig heavy chain pre	975	33	40.2	771	2	S40966	membrane protein S
903	33	40.2	473	2	A47050	glutamate-ammonia	976	33	40.2	774	2	T00488	hypothetical prote
904	33	40.2	482	2	A25235	alanine transamina	977	33	40.2	776	1	VPXRSM	outer layer protei
905	33	40.2	482	2	S28429	alanine transamina	978	33	40.2	776	1	VPXRSM	outer layer protei

979 33 40.2 779 2 T47756 phosphatidylinositol
980 33 40.2 788 1 B4AG58 virB4 protein prec
981 33 40.2 789 1 B4AGA6 virB4 protein prec
982 33 40.2 789 2 S73357 topoisomerase IV c
983 33 40.2 789 2 AH3248 component of type
984 33 40.2 791 2 H72258 endopeptidase Clp,
985 33 40.2 799 2 T02456 protein kinase hom
986 33 40.2 818 2 A24772 alpha-glucosidase
987 33 40.2 848 2 S48273 probable transcrip
988 33 40.2 862 2 T29133 hypothetical prote
989 33 40.2 862 2 AC1214 fibrinogen-binding
990 33 40.2 880 2 G88925 protein t22H9.2 li
991 33 40.2 880 2 G86408 hypothetical prote
992 33 40.2 892 2 A00901 protein chain init
993 33 40.2 908 2 A33280 sarcosylamin precu
994 33 40.2 934 2 H71274 probable ankryrin -
995 33 40.2 937 2 S55504 hexon protein - hu
996 33 40.2 937 2 S39301 hexon protein - hu
997 33 40.2 942 2 S39298 hexon protein - hu
998 33 40.2 946 2 S48397 hypothetical prote
999 33 40.2 963 2 B3502 ribonucleoside red
1000 33 40.2 985 2 JC4217 alpha-glucosidase

ALIGNMENTS

RESULT 1

I47193
Ig heavy chain variable VDJ region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47193
R:Sun, J.; Kacskovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A:Reference number: I47177; MUID:95081609; PMID:7985761
A:Accession: I47193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-137 <SUN>
A:Cross-references: UNIPARC:UPI00001155E2; EMBL:U15452; NID:G571390; PIDN:AAA67018.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 58; DB 2; Length 137;
Best Local Similarity 78.6%; Pred. No. 0.025;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TSTGGTYHAESVKG 16
|||:||||:|||||
Db 72 TSGGGTYADSVKG 85

RESULT 2

S09382
Ig heavy chain - clawed frog
C:Species: Xenopus sp. (clawed frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S09382
R:Schwager, J.; Buerckert, N.; Courtet, M.; du Pasquier, L.
EMBO J. 8, 2989-3001, 1989
A:Title: Genetic basis of the antibody repertoire in Xenopus: analysis of the VH divers
A:Reference number: S09382; MUID:90059884; PMID:2583090
A:Accession: S09382
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <SCH>
A:Cross-references: UNIPARC:UPI0000176E90
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 53.5; DB 2; Length 115;

Best Local Similarity 70.6%; Pred. No. 0.12;
Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
Qy 1 SITSTGGTYHAESVKG 16
:|||:||||:|||||
Db 67 AITSGGGTYADSVKG 83

RESULT 3

S26885
Ig heavy chain V region (DP-44) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 23-Jul-1999
C:Accession: S26885; S36596
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM1>
A:Cross-references: UNIPARC:UPI0000176E67; EMBL:Z12344
R:Tomlinson, M.
submitted to the EMBL Data Library, June 1992
A:Reference number: S36596
A:Accession: S36596
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5,'Q','7-12,'H','14-97 <TOM2>
A:Cross-references: UNIPARC:UPI000011640F; EMBL:Z12344; NID:G32908; PIDN:CAA78214.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 53; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SITSTGGTYHAESVKG 16
:|||:||||:|||||
Db 50 AITGGGGTYADSVKG 65

RESULT 4

S26886
Ig heavy chain V region (DP-45) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26886
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26886
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: UNIPARC:UPI0000116410; EMBL:Z12345; NID:G32910; PIDN:CAA78215.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 53; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SITSTGGTYHAESVKG 16
:|||:||||:|||||
Db 50 AITGGGGTYADSVKG 65

RESULT 5

S12557
Ig heavy chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S12557
R/Matsuda, F.; Shin, E.K.; Hirabayashi, Y.; Nagaoka, H.; Yoshida, M.C.; Zong, S.Q.; Honji, E.MBO J. 9, 2501-2506, 1990
A/Title: Organization of variable region segments of the human immunoglobulin heavy chains.
A/Reference number: S12557; MUID:90316107; PMID:2114977
A/Accession: S12557
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-116 <MAT>
A/Cross-references: UNIPARC:UPI000013DE0E
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 53; DB 2; Length 116;
Best Local Similarity 62.5%; Pred.No. 0.14;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
:|::|||::|:
Db 69 AIGTGGTYADSVKG 84

RESULT 6
I47183
Ig heavy chain variable VDJ region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47183
R/Sun, J.; Kaczkovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A/Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A/Reference number: I47177; MUID:95081609; PMID:7989761
A/Accession: I47183
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-147 <SUN>
A/Cross-references: UNIPARC:UPI00001155D8; EMBL:UI5436; NID:G571370; PIDN:AAA67008.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 53; DB 2; Length 147;
Best Local Similarity 56.2%; Pred.No. 0.18;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
:|::|||::|:
Db 69 AISTSGSYADSVKG 84

RESULT 7
I47203
Ig heavy chain variable VDJ region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47203
R/Sun, J.; Kaczkovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A/Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A/Reference number: I47177; MUID:95081609; PMID:7989761
A/Accession: I47203
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-145 <SUN>
A/Cross-references: UNIPARC:UPI00001155B8; EMBL:UI5519; NID:G571410; PIDN:AAA67028.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 52; DB 2; Length 145;

J. Immunol. 153, 5618-5627, 1994
A>Title: Expressed swine VH genes belong to a small VH gene family homologous to human A;Reference number: I47177; MUID:95081609; PMID:7989761
A:Accession: I47180
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-148 <SUN>
A:CROSS-references: UNIPARC:UPI00001155D5; EMBL:UI5428; NID:g558854; PIDN:AAA67005.1; PFI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-116/Domains: immunoglobulin homology <IMW>

Query Match 62.2%; Score 51; DB 2; Length 148;
Best Local Similarity 60.0%; Pred. No. 0.39;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16
 : ||:||:||:||||
Db 70 VYSSGTTYADSVKG 84

RESULT 11
MHGWO
Ig heavy chain V region (Moo) - dog (tentative sequence)
C:Species: Canis lupus familiaris (dog)
C>Date: 30-Jun-1980 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C:Accession: A90403; B93131; AG2068
R:Waaserman, R.L.; Capra, J.D.
Biochemistry 16, 3160-3168, 1977
A>Title: Primary structure of the variable regions of two canine immunoglobulin heavy ch
A:Reference number: A90403; MUID:77242268; PMID:407924
A:Accession: A90403
A:Molecule type: protein
A:Residues: 1-112 <WAS>
A:CROSS-references: UNIPROT:P01785; UNIPARC:UPI0000173731
R:McCumber, L.J.; Capra, J.D.
Mol. Immunol. 16, 565-570, 1979
A>Title: The complete amino-acid sequence of a canine mu chain.
A:Reference number: A93131; MUID:80077682; PMID:117299
A:Accession: B93131
A:Molecule type: protein
A:Residues: 113-117 <MCC>
A:CROSS-references: UNIPARC:UPI0000173732
C:Comment: This mu chain was isolated from a myeloma protein.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E;15-97/Domains: immunoglobulin homology <IMW>
F;22-95/Disulfide bonds: #status predicted

Query Match 61.0%; Score 50; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.45;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16
 : ||:||:||:||||
Db 51 ISSSGQTYADAVKG 65

RESULT 12
I47185
Ig heavy chain variable VDJ region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47185
R:Sun, J.; Kaczkovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A>Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A:Reference number: I47177; MUID:95081609; PMID:7989761
A:Accession: I47185
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-145 <SUN>
A:CROSS-references: UNIPARC:UPI00001155DA; EMBL:UI5438; NID:g571374; PMID:AAA67010.1; PFI
C:Superfamily: immunoglobulin V region; immunoglobulin homology

J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:11404388
A;Accession: S26935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <TOM>
A;Cross-references: UNIPARC:UPI000011640E; EMBL:Z12342; NID:G32905; PIDN:CAA78212.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 49; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.54; Mismatches 2; Indels 3; Gaps 0;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYSGGSTYYADSVKG 65

RESULT 16
S46462
Ig heavy chain V region (VAC-5) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S46462
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wir
Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A;Reference number: S46460; MUID:95004581; PMID:7920635
A;Accession: S46462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <COO>
A;Cross-references: UNIPARC:UPI00001165D9; EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 49; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.54; Mismatches 2; Indels 3; Gaps 0;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYSGGSTYYADSVKG 65

RESULT 17
B28966
Ig heavy chain precursor V-region chain 5A - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Aug-1996
C;Accession: B28966; A32782
R;Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 1566-1570, 1988
A;Title: Immunoglobulin heavy chain variable region gene evolution: structure and family
A;Reference number: A28966; MUID:88144476; PMID:3125551
A;Accession: B28966
A;Molecule type: DNA
A;Residues: 1-116 <WIL>
R;Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 3276, 1989
A;Reference number: A32782
A;Contents: annotation; erratum
A;Note: the authors note that this sequence is of higher primate
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 49; DB 2; Length 116;

Best Local Similarity 66.7%; Pred. No. 0.65; Mismatches 2; Indels 3; Gaps 0;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 70 IYSGGSTYYADSVKG 84

RESULT 18
S31110
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31110
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-116 <RAA>
A;Cross-references: UNIPARC:UPI0000176E36; EMBL:X62958
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 49; DB 2; Length 116;
Best Local Similarity 66.7%; Pred. No. 0.65; Mismatches 2; Indels 3; Gaps 0;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 51 IYSGGSTYYADSVKG 65

RESULT 19
I47202
Ig heavy chain variable VDJ region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47202
R;Sun, J.; Kaczkovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A;Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A;Reference number: I47177; MUID:95081609; PMID:7989761
A;Accession: I47202
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-143 <SUN>
A;Cross-references: UNIPARC:UPI00001155E8; EMBL:U15518; NID:G571408; PIDN:AAA67027.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 59.1%; Score 48.5; DB 2; Length 143;
Best Local Similarity 64.7%; Pred. No. 0.98; Mismatches 4; Indels 1; Gaps 1;
Matches 11; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
: | | | | | | | | | | | | | | | | | | | | | |
Db 69 AIYSGGATYYADSVKG 85

RESULT 20
S26788
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26788
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami

A;Reference number: S26786; MUID:92111632; PMID:1730251

A;Accession: S26788

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-86 <MOR>

A;Cross-references: UNIPARC:UPI0000115FC8; EMBL:X61017; NID:g32788; PIDN:CAA43351.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 58.5%; Score 48; DB 2; Length 86;

Best Local Similarity 69.2%; Pred. No. 0.69;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SITGTGTYHAESVKG 16

|||:|:|:|:|

Db 14 STGTSYYADSVKG 26

RESULT 21

S26889

Ig heavy chain V region (DP-47) - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S26889

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26889

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <TOM>

A;Cross-references: UNIPARC:UPI0000031F42; EMBL:Z12347; NID:g32914; PIDN:CAA78217.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 98;

Best Local Similarity 58.8%; Pred. No. 0.96;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16

||:|:|:|:|:|

Db 50 AISGSGGTTYADSVKG 66

RESULT 22

S24259

Ig heavy chain V region (VH26-DK1-JH4) - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S24259

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

A;Accession: S24259

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-99 <STE>

A;Cross-references: UNIPARC:UPI000011608B; EMBL:X67067; NID:g38391; PIDN:CAA47452.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-83/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 99;

Best Local Similarity 58.8%; Pred. No. 0.97;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16

||:|:|:|:|:|

Db 35 AISGSGGTTYADSVKG 51

RESULT 23

S24258

Ig heavy chain V region (VH26-DXP1-JH4) - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S24258

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

A;Accession: S24258

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-100 <STE>

A;Cross-references: UNIPARC:UPI000011608A; EMBL:X67066; NID:g38389; PIDN:CAA47451.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;4-86/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 100;

Best Local Similarity 58.8%; Pred. No. 0.98;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16

||:|:|:|:|:|

Db 38 AISGSGGTTYADSVKG 54

RESULT 24

S24257

Ig heavy chain V region (VH26-DXP1-JH4) - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S24257

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

A;Accession: S24257

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <STE>

A;Cross-references: UNIPARC:UPI0000116089; EMBL:X67065; NID:g38387; PIDN:CAA47450.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;11-93/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 101;

Best Local Similarity 58.8%; Pred. No. 0.99;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16

||:|:|:|:|:|

Db 45 AISGSGGTTYADSVKG 61

RESULT 25

S24260

Ig heavy chain V region (VH26-DA1-JH4) - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C;Accession: S24260

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

A;Accession: S24260

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <STE>

A;Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B5C; EMBL:X67068

C;Superfamily: immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;5-87/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 102;
Best Local Similarity 58.8%; Pred. No. 1;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 39 AISGGGGSTYYADSVKG 55

RESULT 26

S24255

Ig heavy chain V region (VH26-DLR5-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S24255
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
C;Keywords: heterotetramer; immunoglobulin
F;2-84/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 104;
Best Local Similarity 58.8%; Pred. No. 1;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
QY 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 36 AISGGGGSTYYADSVKG 52

RESULT 27

S24249

Ig heavy chain V region (VH26-DNI-DXP1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S24249
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
C;Keywords: heterotetramer; immunoglobulin
F;10-92/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 105;
Best Local Similarity 58.8%; Pred. No. 1;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
QY 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 44 AISGGGGSTYYADSVKG 60

RESULT 28

S24256

Ig heavy chain V region (VH26-DXP4-JH6) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S24256

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

C;Keywords: heterotetramer; immunoglobulin
F;4-86/Domain: immunoglobulin homology <IMM>

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-106 <STE>

A;Cross-references: UNIPARC:UPI0000116088; EMBL:X67064; NID:G38385; PIDN:CAA47449.1; PIR

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;4-86/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 106;

Best Local Similarity 58.8%; Pred. No. 1;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16

:|: :|| ||:|:||||

Db 38 AISGGGGSTYYADSVKG 54

RESULT 29

PH1648

Ig heavy chain V region (clone 2B8) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Accession: PH1648

R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo

A;Reference number: PH1642; MUID:93301610; PMID:8315388

C;Accession: PH1648

A;Molecule type: mRNA

A;Residues: 1-108 <HIL>

A;Cross-references: UNIPARC:UPI0000176BD5

A;Experimental source: B cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 108;

Best Local Similarity 58.8%; Pred. No. 1.1;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16

:|: :|| ||:|:||||

Db 42 AISGGGGSTYYADSVKG 58

RESULT 30

S24254

Ig heavy chain V region (VH26-DXP2-JH4) - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S24254

R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A;Reference number: S24247

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109 <STE>

A;Cross-references: UNIPARC:UPI0000176D51; EMBL:X67062

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 109;

Best Local Similarity 58.8%; Pred. No. 1.1;

Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 49 AISGGSGSTYYADSVKG 65

RESULT 31

PH1653
 Ig heavy chain V region (clone 3G11) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1653
 R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcus aureus

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1653

A:Molecule type: mRNA

A:Residues: 1-109 <HIL>

A:Cross-references: UNIPARC:UPI0000176BDA

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 109;

Best Local Similarity 64.7%; Pred. No. 1.1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 42 AISGGSTYYADSVKG 58

RESULT 32

S24253
 Ig heavy chain V region (VH26-DLR4-JH6) - human

C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S24253
 R: Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24253

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-109 <STE>

A:Cross-references: UNIPARC:UPI0000176D52; EMBL:X67061

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:12-94/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 109;

Best Local Similarity 58.8%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 46 AISGGSGSTYYADSVKG 62

RESULT 33

PH1649

Ig heavy chain V region (clone 2E7) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1649

R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcus aureus

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1649

A:Molecule type: mRNA

A:Residues: 1-109 <HIL>

A:Cross-references: UNIPARC:UPI0000176BDS

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 109;

Best Local Similarity 58.8%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 42 AISGGSGSTYYADSVKG 58

RESULT 34

S24250

Ig heavy chain V region (VH26-DN1-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S24250

R: Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24250

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-110 <STE>

A:Cross-references: UNIPARC:UPI0000176D50; EMBL:X67071

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 110;

Best Local Similarity 58.8%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 49 AISGGSGSTYYADSVKG 65

RESULT 35

S69911

Ig V-D-J region (RM) - human

C:Species: Homo sapiens (man)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S69911

R: Sanota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.

Leukemia 8, 1285-1289, 1994

A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi

A:Reference number: S69909; MUID:94335315; PMID:8057663

A:Accession: S69911

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <SAH>

A:Cross-references: UNIPARC:UPI0000176D55; EMBL:Z33401

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 111;

Best Local Similarity 58.8%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 :|: ||| |||: |||
 Db 50 AISGGSGSTYYADSVKG 66

RESULT 36

PH1647
 Ig heavy chain V region (clone 2D10) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1647
 R:Hilleon, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
 J:Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1647
 A:Molecule type: mRNA
 A:Residues: 1-112 <HIL>
 A:Cross-references: UNIPARC:UPI0000176BD4
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 112;
 Best Local Similarity 58.8%; Pred. No. 1.1;
 Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|: :|| ||:|:||||
 Db 42 AISGGSGSTYYADSVKG 58

RESULT 37
 S24247
 Ig heavy chain V region (VH26-DLR2-JH3) - human
 C:Species: Homo sapiens (man)
 C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S24247
 R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
 submitted to: The EMBL Data Library, June 1992
 A:Description: A single VH gene predominates in the rearranged and expressed human B cell line
 A:Reference number: S24247
 A:Accession: S24247
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-113 <STE>
 A:Cross-references: UNIPARC:UPI0000116084; EMBL:X67060; NID:g38377; PIDN:CAA47445.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 113;
 Best Local Similarity 58.8%; Pred. No. 1.1;
 Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|: :|| ||:|:||||
 Db 49 AISGGSGSTYYADSVKG 65

RESULT 38
 S25571
 Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 20-Jun-2000
 C:Accession: S25571
 R:Adkinson, E.E.; Shackelford, P.G.; Quinn, A.; Carroll, W.L.
 J:Immunol. 147, 1667-1674, 1991
 A:Title: Restricted Ig H chain V gene usage in the human antibody response to Haemophilus influenzae
 A:Reference number: S25571; MUID:91349592; PMID:1908880
 A:Accession: S25571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <ADD>
 A:Cross-references: UNIPARC:UPI0000115EBE; EMBL:X56526; NID:g32985; PIDN:CAA39873.1; PID
 A:Note: the authors translated the codon GCG for residue 105 as Thr
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:23-106/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 113;
 Best Local Similarity 58.8%; Pred. No. 1.1;
 Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|: :|| ||:|:||||
 Db 58 AISGGSGSTYYADSVKG 74

RESULT 39
 A45953
 Ig heavy chain precursor V-III region (VH26) - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: A45953
 R:Chen, P.P.; Liu, M.P.; Sinha, S.; Carson, D.A.
 Arthritis Rheum. 31, 1429-1431, 1988
 A:Title: A 16/6 idiotype-positive anti-DNA antibody is encoded by a conserved V-H gene
 A:Reference number: A45953; MUID:89050363; PMID:3263866
 A:Accession: A45953
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-117 <CHE>
 A:Cross-references: UNIPARC:UPI0000113BD6
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 117;
 Best Local Similarity 58.8%; Pred. No. 1.2;
 Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|: :|| ||:|:||||
 Db 69 AISGGSGSTYYADSVKG 85

RESULT 40
 S31121
 Ig heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S31121
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
 Eur. J. Immunol. 22, 247-251, 1992
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complex
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31121
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-118 <RAA>
 A:Cross-references: UNIPARC:UPI0000176E3B; EMBL:X62971
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 118;
 Best Local Similarity 58.8%; Pred. No. 1.2;
 Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|: :|| ||:|:||||
 Db 50 AISGGSGSTYYADSVKG 66

RESULT 41
 D36005
 Ig heavy chain V region (M43) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 119;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 50 AISGGGGSTYYADSVKG 66

RESULT 44

S31108

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C:Accession: S31108

R:Rasphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31108

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-119 <RAA>

A:Cross-references: UNIPARC:UPI0000176DC8; EMBL:XG2956

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 119;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 50 AISGGGGSTYYADSVKG 66

RESULT 45

S48798

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S48798

R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994

A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797

A:Accession: S48798

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <MAH>

A:Cross-references: UNIPARC:UPI0000116701; EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:PI000000000

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 47.5; DB 2; Length 120;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
:|: :|| ||:|:||||
Db 50 AISGGGGSTYYADSVKG 66

RESULT 46

S31113

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match          57.9%; Score 47.5; DB 2; Length 123;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   : : ||| ||| : |||
Db 50 AISGSGSTYYADSVKG 66

RESULT 49
S72665
Ig V-D-J region (RM) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S72665
R;Zhu, D.
submitted to the EMBL Data Library, May 1994
A;Reference number: S72665
A;Accession: S72665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <ZHU>
A;Cross-references: UNIPARC:UPI0000116643; EMBL:Z233401; NID:g871352; PIDN:CAA83852.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match          57.9%; Score 47.5; DB 2; Length 125;
Best Local Similarity 58.8%; Pred. No. 1.2;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   : : ||| ||| : |||
Db 50 AISGSGHTYYADSVKG 66

RESULT 50
S38489
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38489
R;Marke, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
A;Reference number: S38488
A;Accession: S38489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <MAR>
A;Cross-references: UNIPARC:UPI0000116547; EMBL:Z233028; NID:g414025; PIDN:CAA80563.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match          57.9%; Score 47.5; DB 2; Length 127;
Best Local Similarity 58.8%; Pred. No. 1.3;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   : : ||| ||| : |||
Db 50 AISGSGSTYYADSVKG 66

Search completed: May 11, 2006, 16:37:01
Job time : 48.6066 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 147.934 Seconds
(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82

Sequence: 1 SITSTGGTYHAESVKG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum Match 0%

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.5	66.5	479	Q5PQK9_RAT	Q5PQK9 rattus norv
2	53	64.6	96	Q4SX92_TETNG	Q4SX92 tetraodon n
3	52	63.4	99	Q4TSM5_TETNG	Q4TSM5 tetraodon n
4	52	63.4	724	Q8A8Y9_BACTN	Q8A8Y9 bacteroides
5	51	62.2	97	HV56_MOUSE	P18527 mus musculus
6	50	61.0	117	HV02_CANFA	P01785 canis fami
7	49	59.8	116	HV05_CARAU	P19181 carassius a
8	49	59.8	486	Q91Z07_MOUSE	Q91Z07 mus musculus
9	48.5	59.1	98	Q4TJ56_TETNG	Q4TJ56 tetraodon n
10	48.5	59.1	614	Q6DDQ7_XENLA	Q6DDQ7 xenopus lae
11	48	58.5	632	Q5FHO6_LACAC	Q5FHO6 lactobacill
12	47.5	57.9	118	Q9UL72_HUMAN	Q9UL72 homo sapien
13	47.5	57.9	597	Q96BB9_HUMAN	Q96BB9 homo sapien
14	47	57.3	3200	Q7XP97_ORYSA	Q7XP97 oryza sativ
15	46	56.1	320	Q7VB11_PROMA	P18527 mus musculus
16	46	56.1	676	SPRL1_COTJA	P23499 coturnix co
17	45.5	55.5	367	Q5M8X1_XENTR	Q5M8X1 xenopus tro
18	45	54.9	89	Q7N117_PHOLL	Q7N117 photorhabdu
19	45	54.9	96	Q4T5S4_TETNG	Q4T5S4 tetraodon n
20	45	54.9	121	Q9UL71_HUMAN	Q9UL71 homo sapien
21	45	54.9	225	Q4TRL6_9SPHN	Q4TRL6 erythroba
22	45	54.9	366	Q4FXA9_LEIMA	Q4FXA9 leishmania
23	45	54.9	368	Q4FKP5_9TRYP	Q4FKP5 trypanosoma
24	45	54.9	425	Q9VQ15_DROME	Q9VQ15 drosophila
25	45	54.9	466	Q6IN78_HUMAN	Q6IN78 homo sapien
26	45	54.9	469	Q569F4_HUMAN	Q569F4 homo sapien
27	45	54.9	580	Q8B9B6_NPVRO	Q8B9B6 rachiplusia
28	45	54.9	589	Q5XHD5_XENLA	Q5XHD5 xenopus lae
29	45	54.9	591	Q4QQW0_RAT	Q4QQW0 rattus norv
30	45	54.9	593	Q6INM5_XENLA	Q6INM5 xenopus lae
31	44.5	54.3	475	Q6MZQ6_HUMAN	Q6MZQ6 homo sapien

32	44	53.7	200	Q6MP12_BDEBA	Q6MP12 bdellovibri
33	44	53.7	464	Q6MZU6_HUMAN	Q6MZU6 homo sapien
34	44	53.7	577	Q17794_CAEEL	Q17794 caenorhabdi
35	44	53.7	1413	Q4PCS7_USTMA	Q4PCS7 ustilago ma
36	44	53.7	1944	CHD3_HUMAN	CHD3 homo sapien
37	44	53.7	2000	Q9Y4I0_HUMAN	Q9Y4I0 homo sapien
38	44	53.7	2055	Q5NCG1_MOUSE	Q5NCG1 mus musculus
39	44	53.7	3068	Q8JRG5_PEMV	Q8JRG5 pepper mott
40	43.5	53.0	117	HV3C_HUMAN	P01764 homo sapien
41	43.5	53.0	467	Q4VBH1_RAT	Q4VBH1 rattus norv
42	43	52.4	112	Q5FJZ6_LACAC	Q5FJZ6 lactobacill
43	43	52.4	115	HV3P_HUMAN	P01767 homo sapien
44	43	52.4	174	Q87MNS_VIBPA	Q87MNS vibrio para
45	43	52.4	268	Q4NWX9_ORYSA	Q4NWX9 anaeromyxob
46	43	52.4	398	Q6ESH7_ORYSA	Q6ESH7 oryza sativ
47	43	52.4	403	Q90Y49_AMEME	Q90Y49 ambystoma m
48	43	52.4	494	Q519T8_ENTHI	Q519T8 entamoeba h
49	43	52.4	678	Q929E8_CHLPN	Q929E8 c (pyruvate
50	43	52.4	758	Q8ECD6_SHEON	Q8ECD6 shewanella
51	43	52.4	830	Q6FWJ3_CANGA	Q6FWJ3 candida gla
52	43	52.4	926	Q8LNF3_ORYSA	Q8LNF3 oryza sativ
53	43	52.4	1091	Q5FSC9_GLUOX	Q5FSC9 gluconobact
54	43	52.4	2248	Q4S447_TETNG	Q4S447 tetraodon n
55	42	51.2	96	Q6MI99_BDEBA	Q6MI99 bdellovibri
56	42	51.2	97	Q6B736_RABIT	Q6B736 oryctolagus
57	42	51.2	120	HV3B_HUMAN	P01766 homo sapien
58	42	51.2	206	Q8IG96_DROME	Q8IG96 drosophila
59	42	51.2	235	YHBP_BACSU	P39133 bacillus su
60	42	51.2	351	Q5XQ67_9ARCH	Q5XQ67 uncultured
61	42	51.2	351	Q647Y3_9ARCH	Q647Y3 uncultured
62	42	51.2	371	Q9J8C7_9NUCL	Q9J8C7 spooptera
63	42	51.2	458	Q65ZQ1_HUMAN	Q65ZQ1 homo sapien
64	42	51.2	475	Q6GMW7_HUMAN	Q6GMW7 homo sapien
65	42	51.2	527	Q75FN8_LEPIC	Q75FN8 leptospira
66	42	51.2	527	Q8EXN0_LEPIN	Q8EXN0 leptospira
67	42	51.2	566	Q6LX63_METMP	Q6LX63 methanococc
68	42	51.2	632	Q74H95_LACJO	Q74H95 lactobacill
69	42	51.2	635	Q4QHD8_LEIMA	Q4QHD8 leishmania
70	42	51.2	641	Q883Y5_PSESM	Q883Y5 pseudomonas
71	42	51.2	759	Q73NK9_TREDE	Q73NK9 treponema d
72	42	51.2	820	Q6NN10_DROME	Q6NN10 drosophila
73	42	51.2	920	Q8Y094_DROME	Q8Y094 drosophila
74	42	51.2	993	Q5LH86_BACFN	Q5LH86 bacteroides
75	42	51.2	1060	Q64YL2_BACFR	Q64YL2 bacteroides
76	42	51.2	1859	Q69F85_PHAVU	Q69F85 phaseolus v
77	41.5	50.6	117	HV53_MOUSE	P18524 mus musculus
78	41.5	50.6	255	Q6KB05_MOUSE	Q6KB05 mus musculus
79	41.5	50.6	516	Q6VEF7_9BRYO	Q6VEF7 sphagnum pl
80	41.5	50.6	516	Q6VEF8_9BRYO	Q6VEF8 sphagnum co
81	41.5	50.6	516	Q6VEF9_9BRYO	Q6VEF9 sphagnum de
82	41.5	50.6	516	Q6VEG0_9BRYO	Q6VEG0 sphagnum in
83	41.5	50.6	516	Q6VEG1_9BRYO	Q6VEG1 sphagnum au
84	41.5	50.6	630	Q9LL58_ORYSA	Q9LL58 oryza sativ
85	41	50.0	96	Q4SZG1_TETNG	Q4SZG1 tetraodon n
86	41	50.0	97	Q4SZF9_TETNG	Q4SZF9 tetraodon n
87	41	50.0	105	Q4T1Z2_TETNG	Q4T1Z2 tetraodon n
88	41	50.0	119	HV3L_HUMAN	P01773 homo sapien
89	41	50.0	119	Q5F2I8_MOUSE	Q5F2I8 mus musculus
90	41	50.0	214	MSRA2_SYNY3	P72800 synecocyst
91	41	50.0	216	Q8UJ16_AGR5	Q8UJ16 agrobacteri
92	41	50.0	228	Q7D255_AGR5	Q7D255 agrobacteri
93	41	50.0	228	Q59962_9ACTO	Q59962 streptomyce
94	41	50.0	458	Q5BK05_RAT	Q5BK05 rattus norv
95	41	50.0	468	Q569B4_RAT	Q569B4 rattus norv
96	41	50.0	490	Q5HAC6_9ENTR	Q5HAC6 serratia en
97	41	50.0	580	Q8WPH3_BOMMO	Q8WPH3 bombyx mori
98	41	50.0	614	Q934I6_9SPHI	Q934I6 microscilla
99	41	50.0	662	Q69Z26_MOUSE	Q69Z26 mus musculus
100	41	50.0	689	Q8K2V2_MOUSE	Q8K2V2 mus musculus
101	41	50.0	728	Q8DUT7_STRMU	Q8DUT7 streptococc
102	41	50.0	1059	Q659F1_HUMAN	Q659F1 homo sapien
103	41	50.0	1061	Q659D0_HUMAN	Q659D0 homo sapien
104	41	50.0	1146	ASK10_YEAST	P48361 saccharomyc

105	41	50.0	1195	2	Q5TG86	HUMAN
106	41	50.0	1225	2	Q6Z624	HUMAN
107	41	50.0	1225	2	Q5TG90	HUMAN
108	41	50.0	1254	1	CHD5	HUMAN
109	41	50.0	1954	2	Q5TG89	HUMAN
110	41	50.0	2014	2	Q4SKH0	TETNG
111	41	50.0	2147	2	Q4NUJ3	9DELTA
112	41	50.0	7599	2	Q4IKU3	GIBZE
113	40.5	49.4	479	2	Q1WPF5	MOUSE
114	40.5	49.4	479	2	Q5BK12	RAT
115	40.5	49.4	685	2	Q7SE82	NEUCR
116	40	48.8	117	1	HV58	MOUSE
117	40	48.8	119	2	Q920E7	MOUSE
118	40	48.8	191	2	Q5EM99	STROI
119	40	48.8	192	2	Q5SQ15	CRINE
120	40	48.8	192	2	Q5KDF1	CRINE
121	40	48.8	196	2	Q65Z18	MOUSE
122	40	48.8	200	1	LEUD	VIBCH
123	40	48.8	203	2	Q6N2I0	RHOPA
124	40	48.8	204	2	Q4TSV4	9SPHN
125	40	48.8	243	2	Q5KY56	GROKA
126	40	48.8	261	2	Q6U1V6	9PEZI
127	40	48.8	267	2	Q6UN40	9PEZI
128	40	48.8	284	2	Q89DP1	BRAJA
129	40	48.8	293	2	Q8UEY2	AGRT5
130	40	48.8	305	2	Q6PLD3	MOUSE
131	40	48.8	323	2	Q8XZ00	RALSO
132	40	48.8	329	2	Q9RMH9	STRVD
133	40	48.8	353	2	Q8QS73	9BETA
134	40	48.8	428	2	Q4S2N1	TETNG
135	40	48.8	434	2	Q65GG4	BACLD
136	40	48.8	436	2	Q9BK18	BRAJA
137	40	48.8	447	2	Q6DCF1	XENLA
138	40	48.8	457	2	Q51N22	MAGGR
139	40	48.8	465	2	Q6P6C4	HUMAN
140	40	48.8	514	2	Q5F9X3	NEIMB
141	40	48.8	514	2	Q9K0C4	NEIMB
142	40	48.8	514	2	Q9TVC9	NEIMA
143	40	48.8	516	1	TAF6	YEAST
144	40	48.8	518	2	Q4Q5B0	LEIMA
145	40	48.8	529	2	Q4UBF9	THEAN
146	40	48.8	542	2	Q5AQI9	EMENI
147	40	48.8	550	2	Q5B2H0	EMENI
148	40	48.8	551	2	Q5A908	CANAL
149	40	48.8	576	2	Q624H4	CAEBR
150	40	48.8	582	1	YANB	SCHPO
151	40	48.8	617	2	Q61FT3	CAEBR
152	40	48.8	648	2	Q895B6	CLOTE
153	40	48.8	678	2	Q8AB00	BACTN
154	40	48.8	736	2	Q582D3	9TRYP
155	40	48.8	739	2	Q5F423	CHICK
156	40	48.8	744	2	Q93478	XENLA
157	40	48.8	747	1	KIF3B	MOUSE
158	40	48.8	747	2	Q8BNH4	MOUSE
159	40	48.8	757	2	Q8OU27	MOUSE
160	40	48.8	853	2	Q8AU13	BACTN
161	40	48.8	858	2	Q5LIC9	BACFN
162	40	48.8	858	2	Q64ZE9	BACFR
163	40	48.8	987	1	PMFG	CHLMU
164	40	48.8	1154	2	Q91ZS0	MOUSE
165	40	48.8	1312	1	STRH	STRPN
166	40	48.8	1312	2	Q8DR16	STR6
167	40	48.8	1333	2	Q70JAB	BUTFI
168	40	48.8	1430	2	Q6CTEB	KULFA
169	40	48.8	1748	2	Q4NVB5	9DELTA
170	40	48.8	2238	2	Q91ZS1	MOUSE
171	40	48.8	2780	2	Q91ZS2	MOUSE
172	40	48.8	5290	2	Q57YCS	9TRYP
173	40	48.8	6298	2	Q8VHN7	MOUSE
174	39.5	48.2	112	1	Q9UGP3	HUMAN
175	39.5	48.2	117	1	HV55	MOUSE
176	39.5	48.2	259	2	Q5P516	AZOSE
177	39.5	48.2	296	2	Q51QA0	SHIBO

39.5	48.2	897	2	Q9M671	WHEAT
39	47.6	64	2	Q652K3	ORYSA
39	47.6	162	2	Q7NW40	CHRYO
39	47.6	186	2	Q5DDL3	SCHUA
39	47.6	197	2	Q9WM61	STRPY
39	47.6	208	2	Q72AX8	DESUVH
39	47.6	218	2	Q9XCK5	STRPY
39	47.6	227	2	Q7A7G8	STAAH
39	47.6	227	2	Q99W99	STAAH
39	47.6	235	2	Q9XCK9	STRPY
39	47.6	248	2	Q8L5G4	CICAR
39	47.6	249	2	Q9M515	TRIVS
39	47.6	257	2	Q9SD24	MAROU
39	47.6	259	2	Q4HKV9	CAMLA
39	47.6	259	2	Q4HON8	CAMUP
39	47.6	266	2	Q4IJC4	GIBZE
39	47.6	286	2	Q84N01	MEDTR
39	47.6	293	2	Q5AFB4	CANAL
39	47.6	293	2	Q8D695	VIBVU
39	47.6	294	2	Q92KE0	RHIME
39	47.6	296	2	Q5TI22	ADE09
39	47.6	301	2	Q7PL34	DROME
39	47.6	329	2	Q89EV7	BRAJA
39	47.6	338	2	Q5JH22	PYRKO
39	47.6	341	2	Q6RHU7	9CAUD
39	47.6	342	2	Q7NDS1	GLOVI
39	47.6	370	1	TRPD	METWA
39	47.6	373	2	Q8UK63	AGRT5
39	47.6	377	2	Q5L2C2	GEOKA
39	47.6	378	2	Q8B9B5	NFVRO
39	47.6	379	2	Q75DR8	ASHGO
39	47.6	413	2	Q883B6	PSEGM
39	47.6	419	2	Q5U3F3	BRARE
39	47.6	425	1	VIPA	SALTI
39	47.6	430	2	Q9AP46	CITFR
39	47.6	436	2	Q4SF36	TETNG
39	47.6	436	2	Q6XDM5	PHYIN
39	47.6	436	2	Q6N564	RHOPA
39	47.6	436	2	Q6PFM7	BRARE
39	47.6	437	2	Q6ZF77	STRPY
39	47.6	449	2	Q4NNE0	9DELTA
39	47.6	456	2	Q9L2A0	STRCO
39	47.6	466	2	Q92RF5	RHIME
39	47.6	473	1	UKAC	BACST
39	47.6	476	2	Q5CM44	CRYHO
39	47.6	487	2	Q748T5	GEOSL
39	47.6	493	2	Q7MMV9	PORGI
39	47.6	495	2	Q66PS7	SALET
39	47.6	495	2	Q6V2Y9	9ENTR
39	47.6	495	2	Q6V2Z0	9ENTR
39	47.6	495	2	Q6V2Z2	9ENTR
39	47.6	495	2	Q6V2Z3	9ENTR
39	47.6	522	2	Q815Q4	BACCR
39	47.6	531	2	Q97LM0	CLOAB
39	47.6	565	2	Q73TQ3	MYCPA
39	47.6	569	2	Q4R4B6	NACPA
39	47.6	609	1	UVRC	SHEON
39	47.6	621	2	Q9H9Y1	HUMAN
39	47.6	634	2	Q4NUY5	9DELTA
39	47.6	636	1	GIDA	LACPL
39	47.6	684	2	Q4G0S6	HUMAN
39	47.6	689	2	Q53KJ4	ORYSA
39	47.6	694	2	Q82AF3	STRAW
39	47.6	714	1	PBPF	BACSU
39	47.6	714	2	Q948G7	ORYSA
39	47.6	723	2	Q6K8E9	ORYSA
39	47.6	747	1	KIF3B	HUMAN
39	47.6	753	2	Q6CH75	YARLI
39	47.6	763	2	Q89HZ6	BRAJA
39	47.6	769	2	Q74253	PYCCI
39	47.6	804	2	Q8YTA7	ANASP
39	47.6	806	2	Q89NZ1	BRAJA
39	47.6	818	2	Q5V654	HALMA

Q9m671	tritium ae
Q652k3	oryza sativ
Q7nw40	chromobacte
Q5ddl3	schistosoma
Q9wm61	streptococc
Q72ax8	desulffovibr
Q9xck5	streptococc
Q7a7g8	staphylococ
Q99w99	staphylococ
Q9xck9	streptococc
Q8l5g4	cicer ariet
Q9m515	triphysaria
Q9sd24	marisilea qu
Q4hkV9	campylobact
Q4hON8	campylobact
Q4iJc4	gibberella
Q84n01	medicago tr
Q5afe4	candida alb
Q8d695	vibrio vuln
Q92ke0	rhizobium m
Q5ti22	human adeno
Q7pl34	drosophila
Q89ev7	bradyrhizob
Q5jh22	pyrococcus
Q6rhU7	aeromonas p
Q7nds1	gloeobacter
Q8pt97	methanosarc
Q8uk63	agrobacteri
Q5l2c2	geobacillus
Q8b9b5	rachiplusia
Q75dr8	aahbya goes
Q883b6	pseudomonas
Q5u3f3	brachydanio
Q4972	salmonella
Q9ap46	citrobacter
Q4sf36	tetracodon n
Q6xdm5	phytophthor
Q6n564	rhodopseudo
Q6pfm7	brachydanio
Q6zf77	streptococc
Qanne0	anaeromycob
Q9l2a0	streptomyce
Q92rf5	rhizobium st
Q92fl8	bacillus st
Q5cm44	cryptospori
Q748t5	geobacter s
Q7mmv9	porphyromon
Q66ps7	salmonella
Q6v2y9	salmonella
Q6v2z0	salmonella
Q6v2z2	salmonella
Q6v2z3	salmonella
Q815q4	bacillus ce
Q97lm0	clostridium
Q73tq3	mycobacteri
Q4r4b6	macaca fasc
Q8efv4	shewanella
Q9h9y1	homo sapien
Q4nuY5	anaeromycob
Q89hx6	lactobacill
Q4g0s6	homo sapien
Q53kj4	oryza sativ
Q82af3	streptomyce
P38050	bacillus su
Q948g7	oryza sativ
Q6k8e9	oryza sativ
O15066	homo sapien
O53kj4	varrowia li
Q89hz6	bradyrhizob
O74253	pyncoporus
Q8yta7	anabaena sp
Q89nz1	bradyrhizob
Q5v654	haloarcula

251	39	47.6	873	2	Q954K0_STRPY	Q984K0_streptococc	324	38	46.3	232	2	P93494_PINTA	P93494_pinus taeda
252	39	47.6	885	2	Q57T59_SALCH	Q57T59_salmonella	325	38	46.3	243	2	Q4S9S8_TETNG	Q4S9S8_tetradon n
253	39	47.6	885	2	Q87658_SALTY	Q87658_salmonella	326	38	46.3	249	2	Q93XP1_9ROSA	Q93XP1_prunus cera
254	39	47.6	906	2	Q9RTN7_DEIRA	Q9RTN7_deinococcus	327	38	46.3	253	2	Q8SWY1_PINTA	Q8SWY1_pinus taeda
255	39	47.6	923	2	Q93T12_STRPY	Q93T12_streptococc	328	38	46.3	253	2	Q87SR4_VIBPA	Q87SR4_vibrio para
256	39	47.6	990	2	Q15206_HUMAN	Q15206_homo sapien	329	38	46.3	253	2	Q8DEF2_VIBVU	Q8DEF2_vibrio vuln
257	39	47.6	993	2	Q1474E7_TETNG	Q1474E7_tetradon n	330	38	46.3	253	2	Q7MP63_VIBVU	Q7MP63_vibrio vuln
258	39	47.6	1027	2	Q9BWX2_HUMAN	Q9BWX2_homo sapien	331	38	46.3	256	2	Q8B8C5_SHEON	Q8B8C5_shewanella
259	39	47.6	1027	2	Q86VS3_HUMAN	Q86VS3_homo sapien	332	38	46.3	259	2	Q7TBG9_ADE08	Q7TBG9_human adeno
260	39	47.6	1098	2	Q61304_MOUSE	Q61304_mus musculus	333	38	46.3	260	2	Q9KUM9_VIBCH	Q9KUM9_vibrio chol
261	39	47.6	1136	2	Q9N180_BOVIN	Q9N180_bos taurus	334	38	46.3	261	2	Q6RPF6_CRAPL	Q6RPF6_craterostig
262	39	47.6	1218	2	Q05331_HUMAN	Q05331_homo sapien	335	38	46.3	261	2	Q7SEL5_ADE08	Q7SEL5_human adeno
263	39	47.6	1325	1	Y445_WYCPN	P75334_myocplasma	336	38	46.3	283	2	Q6F9V0_ACTAD	Q6F9V0_acinetobact
264	39	47.6	1369	2	Q4T5L7_TETNG	Q4T5L7_tetradon n	337	38	46.3	301	2	Q7Y0S8_SOLTU	Q7Y0S8_solanum tub
265	39	47.6	1615	2	Q57415_CHICK	Q57415_gallus gall	338	38	46.3	309	2	Q6LGI7_PHOPR	Q6LGI7_photobacter
266	39	47.6	1671	2	Q627R3_ORYSA	Q627R3_oryza sativ	339	38	46.3	309	2	Q9WYX9_THEMEA	Q9WYX9_thermotoga
267	39	47.6	1700	2	Q59EE6_HUMAN	Q59EE6_homo sapien	340	38	46.3	313	2	Q5KVG9_GEOKA	Q5KVG9_geobacillus
268	39	47.6	1719	2	Q13768_HUMAN	Q13768_homo sapien	341	38	46.3	327	2	Q67ME7_SYMBH	Q67ME7_symbiobacte
269	39	47.6	1821	1	LTPB2_HUMAN	Q14767_homo sapien	342	38	46.3	327	2	Q5HP36_STAEBQ	Q5HP36_staphylococ
270	39	47.6	1821	2	Q6AZ94_HUMAN	Q6AZ94_homo sapien	343	38	46.3	327	2	Q8CP44_STAEP	Q8CP44_staphylococ
271	39	47.6	1842	1	LTPB2_BOVIN	Q28019_bos taurus	344	38	46.3	331	1	PLSX_LACLA	Q8CJC7_lactococcus
272	39	47.6	1848	2	Q61302_MOUSE	Q61302_mus musculus	345	38	46.3	333	2	Q6V7C6_HORSP	Q6V7C6_hordeum spo
273	39	47.6	1856	2	Q99407_HUMAN	Q99407_homo sapien	346	38	46.3	333	2	Q6V7B2_HORSP	Q6V7B2_hordeum spo
274	39	47.6	1862	1	ANK1_MOUSE	Q02357_mus musculus	347	38	46.3	333	2	Q6V7B3_HORSP	Q6V7B3_hordeum spo
275	39	47.6	1880	1	ANK1_HUMAN	P16157_homo sapien	348	38	46.3	333	2	Q6V7B6_HORSP	Q6V7B6_hordeum spo
276	39	47.6	1899	2	Q59FP2_HUMAN	Q59FP2_homo sapien	349	38	46.3	333	2	Q6V7B8_HORSP	Q6V7B8_hordeum spo
277	39	47.6	1989	2	Q4SNF1_TETNG	Q4SNF1_tetradon n	350	38	46.3	333	2	Q6V7B9_HORSP	Q6V7B9_hordeum spo
278	39	47.6	2731	2	Q9VJT5_DROME	Q9VJT5_drosophila	351	38	46.3	333	2	Q6V7C0_HORSP	Q6V7C0_hordeum spo
279	39	47.6	3367	2	Q9XZC9_DROME	Q9XZC9_drosophila	352	38	46.3	333	2	Q6V7D6_HORSP	Q6V7D6_hordeum spo
280	39	47.6	3375	2	Q81P51_DROME	Q81P51_drosophila	353	38	46.3	334	2	Q5JE91_PYRKO	Q5JE91_pyrococcus
281	38	46.3	52	2	P71469_LACPL	P71469_lactobacill	354	38	46.3	335	2	Q5CM50_CRYHO	Q5CM50_cryptospori
282	38	46.3	73	2	Q5X8N7_LEGPA	Q5X8N7_legionella	355	38	46.3	335	2	Q6V7C1_HORSP	Q6V7C1_hordeum spo
283	38	46.3	92	2	Q6AJ67_DESPS	Q6AJ67_desulfotale	356	38	46.3	335	2	Q6V7C4_HORSP	Q6V7C4_hordeum spo
284	38	46.3	94	2	Q6HE33_BACHK	Q6HE33_bacillus th	357	38	46.3	335	2	Q6V7D0_HORSP	Q6V7D0_hordeum spo
285	38	46.3	94	2	Q90DH5_9HIV1	Q90DH5_human immun	358	38	46.3	335	2	Q6V7D5_HORSP	Q6V7D5_hordeum spo
286	38	46.3	95	2	Q4NRT1_9DELT	Q4NRT1_anaeromyxob	359	38	46.3	335	2	Q6V7D8_HORSP	Q6V7D8_hordeum spo
287	38	46.3	98	1	HV57_MOUSE	P18528_mus musculus	360	38	46.3	337	2	Q6V7C8_HORSP	Q6V7C8_hordeum spo
288	38	46.3	100	2	Q6B6Z2_RABIT	Q6B6Z2_oryctolagus	361	38	46.3	340	2	Q72MD1_LEPIC	Q72MD1_leptospira
289	38	46.3	100	2	Q6B749_RABIT	Q6B749_oryctolagus	362	38	46.3	340	2	Q8CXR4_LEPIC	Q8CXR4_leptospira
290	38	46.3	105	2	Q6B6Z3_RABIT	Q6B6Z3_oryctolagus	363	38	46.3	344	2	Q4JMK4_9BACT	Q4JMK4_uncultured
291	38	46.3	106	2	Q6B6X9_RABIT	Q6B6X9_oryctolagus	364	38	46.3	344	2	Q8DM49_SYNEL	Q8DM49_synecococc
292	38	46.3	114	2	Q8B5E1_HRSV	Q8B5E1_human respi	365	38	46.3	349	2	Q7UIG5_MYCBO	Q7UIG5_mycobacteri
293	38	46.3	132	2	Q6V7D2_HORSP	Q6V7D2_hordeum spo	366	38	46.3	349	2	P95036_MYCTU	P95036_mycobacteri
294	38	46.3	142	2	Q513Q0_9BACT	Q513Q0_uncultured	367	38	46.3	350	2	Q5A300_CANAL	Q5A300_candida alb
295	38	46.3	143	2	Q6Y878_9GAMA	Q6Y878_macaca mula	368	38	46.3	351	2	Q64D31_9ARCH	Q64D31_uncultured
296	38	46.3	143	2	Q71C60_9GAMA	Q71C60_macaca fusc	369	38	46.3	351	2	Q4PJC6_9BACT	Q4PJC6_uncultured
297	38	46.3	145	2	Q7T7L2_9GAMA	Q7T7L2_gorilla gor	370	38	46.3	361	2	Q63JY9_BURPS	Q63JY9_burkholderi
298	38	46.3	151	2	Q7X9Q4_SAWNI	Q7X9Q4_sambucus ni	371	38	46.3	375	2	Q82FQ7_BURMA	Q82FQ7_burkholderi
299	38	46.3	155	2	Q9SWD1_9CARY	Q9SWD1_rumex patul	372	38	46.3	379	2	Q4LZ64_9BURK	Q4LZ64_burkholderi
300	38	46.3	156	2	Q9SPZ6_PEA	Q9SPZ6_pisum sativ	373	38	46.3	379	2	Q63PI9_BURPS	Q63PI9_burkholderi
301	38	46.3	161	2	Q71C63_9GAMA	Q71C63_macaca fasc	374	38	46.3	388	2	Q96LP7_HUMAN	Q96LP7_homo sapien
302	38	46.3	163	2	Q6TPK1_ACTDE	Q6TPK1_actinidia d	375	38	46.3	389	2	Q7SBE9_NEUCR	Q7SBE9_neurospora
303	38	46.3	172	2	Q8WZ85_HUMAN	Q8WZ85_homo sapien	376	38	46.3	393	2	Q7N4P8_PHOLL	Q7N4P8_photorhabdu
304	38	46.3	174	1	MSRA_PASMU	Q9CN40_pasteurella	377	38	46.3	395	2	Q61E78_PAROL	Q61E78_paralichthy
305	38	46.3	174	2	Q34172_9RHIZ	Q34172_agrobacteri	378	38	46.3	398	2	Q6ZAT5_BURMA	Q6ZAT5_burkholderi
306	38	46.3	177	2	Q4TTS6_NELNU	Q4TTS6_nelumbo nuc	379	38	46.3	399	2	Q7S2Y1_NEUCR	Q7S2Y1_neurospora
307	38	46.3	177	2	Q4TTS7_NELNU	Q4TTS7_nelumbo nuc	380	38	46.3	406	2	Q57VI4_9TRYP	Q57VI4_trypanosoma
308	38	46.3	177	2	Q4TTS8_NELNU	Q4TTS8_nelumbo nuc	381	38	46.3	411	1	P8PT_YERPE	Q8ZFI0_yersinia pe
309	38	46.3	187	2	Q5P2F9_AZOSE	Q5P2F9_azocarcus sp	382	38	46.3	411	2	Q669P7_YRRPS	Q669P7_yersinia pe
310	38	46.3	187	2	Q8UHW5_AGR75	Q8UHW5_agrobacteri	383	38	46.3	412	2	Q50BF4_LACRE	Q50BF4_lactobacill
311	38	46.3	196	2	Q6USQ7_STRPY	Q6USQ7_streptococc	384	38	46.3	421	2	Q8KH61_PSEAE	Q8KH61_pseudomonas
312	38	46.3	197	2	Q6PS81_STRPY	Q6PS81_streptococc	385	38	46.3	430	1	AROA_METWA	Q8PX10_methanosaar
313	38	46.3	197	2	Q6PS91_STRPY	Q6PS91_streptococc	386	38	46.3	431	2	Q98IH0_RHILO	Q98IH0_rhizobium l
314	38	46.3	204	2	Q64SF0_BACFR	Q64SF0_bacteroides	387	38	46.3	435	1	FPRA_RHOCA	P18607_rhodobacter
315	38	46.3	205	2	Q7XC38_ORYSA	Q7XC38_oryza sativ	388	38	46.3	435	2	Q9SVG6_ARATH	Q9SVG6_arabidopsia
316	38	46.3	205	2	Q9AY51_ORYSA	Q9AY51_oryza sativ	389	38	46.3	442	2	Q7SSK1_NEUCR	Q7SSK1_neurospora
317	38	46.3	212	2	Q9F9B9_9BACL	Q9F9B9_paenibacill	390	38	46.3	447	2	Q55JD2_CRYNE	Q55JD2_cryptococcu
318	38	46.3	214	2	Q6TLP3_9BACT	Q6TLP3_uncultured	391	38	46.3	447	2	Q55ZX4_CRYNE	Q55ZX4_cryptococcu
319	38	46.3	218	2	Q9RF14_STRPY	Q9RF14_streptococc	392	38	46.3	447	2	Q5KP83_CRYNE	Q5KP83_cryptococcu
320	38	46.3	231	2	Q4RSV7_TETNG	Q4RSV7_tetradon n	393	38	46.3	447	2	Q5KCC6_CRYNE	Q5KCC6_cryptococcu
321	38	46.3	232	2	Q956M5_CABEL	Q956M5_caenorhabdi	394	38	46.3	464	2	Q5CVL1_CRYPV	Q5CVL1_cryptospori
322	38	46.3	232	2	P93492_PINTA	P93492_pinus taeda	395	38	46.3	464	2	Q8FPF5_MOUSE	Q8FPF5_mus musculu
323	38	46.3	232	2	P93493_PINTA	P93493_pinus taeda	396	38	46.3	475	2	Q55JD3_CRYNE	Q55JD3_cryptococcu

543	37	45.1	250	2	Q56889_9ASCO	Q56889 candida ort	616	37	45.1	395	2	Q6P1K8_HUMAN	Q6P1K8 homo sapien
544	37	45.1	252	2	Q82286_ENTPA	Q82286 enterococcu	617	37	45.1	396	1	TF2H2_MOUSE	TF2H2_MOUSE
545	37	45.1	254	2	Q4J5C7_AZOVI	Q4J5C7 azotobacter	618	37	45.1	396	1	TF2H2_MOUSE	TF2H2_MOUSE
546	37	45.1	255	2	Q8RVK4_MUSAC	Q8RVK4 musa acumin	619	37	45.1	397	2	Q9S874_ARATH	Q9S874 arabidopsis
547	37	45.1	255	2	Q4ZL27_PSSSY	Q4ZL27 pseudomonas	620	37	45.1	397	2	Q91YN8_MOUSE	Q91YN8 mus musculu
548	37	45.1	255	2	Q4K3B2_PSRPF5	Q4K3B2 pseudomonas	621	37	45.1	398	2	Q91YN8_MOUSE	Q91YN8 mus musculu
549	37	45.1	255	2	Q4K3B2_PSRPF5	Q4K3B2 pseudomonas	622	37	45.1	400	2	Q8FJ29_ECOC6	Q8FJ29 escherichia
550	37	45.1	257	2	Q8HT24_PSEBA	Q8HT24 pseudomonas	623	37	45.1	400	2	Q8XAK1_ECOS57	Q8XAK1 escherichia
551	37	45.1	258	2	Q88BX7_PSEPH	Q88BX7 pseudomonas	624	37	45.1	405	2	Q93F41_SHIFL	Q93F41 shigella fl
552	37	45.1	266	2	Q510H6_ENTHI	Q510H6 entamoeba h	625	37	45.1	411	2	Q51620_ENTHI	Q51620 entamoeba h
553	37	45.1	266	2	Q6DGM3_BRARE	Q6DGM3 brachydanio	626	37	45.1	411	2	Q519K8_ENTHI	Q519K8 entamoeba h
554	37	45.1	266	2	Q502T9_BRARE	Q502T9 brachydanio	627	37	45.1	412	2	Q502J4_ENTHI	Q502J4 entamoeba h
555	37	45.1	274	2	Q783D4_NEUCR	Q783D4 neurospora	628	37	45.1	412	2	Q7WM85_BORPA	Q7WM85 bordetella
556	37	45.1	281	2	Q6S9L5_LEPPO	Q6S9L5 leptospira	629	37	45.1	415	2	Q69V55_ORYSA	Q69V55 oryza sativ
557	37	45.1	281	2	Q6S9M2_LEPPO	Q6S9M2 leptospira	630	37	45.1	415	2	Q69V55_ORYSA	Q69V55 oryza sativ
558	37	45.1	282	2	Q60DN1_ORYSA	Q60DN1 oryza sativ	631	37	45.1	429	2	Q9LR72_ARATH	Q9LR72 arabidopsis
559	37	45.1	282	2	Q6S9K5_9LEPT	Q6S9K5 leptospira	632	37	45.1	432	1	TIG_ECOS57	TIG_ECOS57
560	37	45.1	301	2	Q6S9L4_LEPIN	Q6S9L4 leptospira	633	37	45.1	432	1	TIG_ECOS57	TIG_ECOS57
561	37	45.1	301	2	Q582T6_9TRYP	Q582T6 trypanosoma	634	37	45.1	432	1	TIG_ECOS57	TIG_ECOS57
562	37	45.1	302	1	RRM1_DROME	RRM1 drosophila	635	37	45.1	432	1	TIG_PASMU	TIG_PASMU
563	37	45.1	302	2	Q53YH6_DROME	Q53YH6 drosophila	636	37	45.1	432	1	TIG_PASMU	TIG_PASMU
564	37	45.1	302	2	Q6S9L3_LEPIN	Q6S9L3 leptospira	637	37	45.1	432	1	TIG_SALPA	TIG_SALPA
565	37	45.1	303	2	Q6S9K1_9LEPT	Q6S9K1 leptospira	638	37	45.1	432	1	TIG_SALPA	TIG_SALPA
566	37	45.1	303	2	Q6S9L6_LEPIN	Q6S9L6 leptospira	639	37	45.1	432	1	TIG_SALTY	TIG_SALTY
567	37	45.1	305	2	Q98657_HAEIN	Q98657 haemophilus	640	37	45.1	432	1	TIG_SALTY	TIG_SALTY
568	37	45.1	305	2	Q651Y3_BACLD	Q651Y3 bacillus li	641	37	45.1	432	1	TIG_SALTY	TIG_SALTY
569	37	45.1	308	2	Q83G59_TROWH	Q83G59 tropheryma	642	37	45.1	432	1	TIG_VIBVY	TIG_VIBVY
570	37	45.1	317	2	Q83NN9_TROWH	Q83NN9 tropheryma	643	37	45.1	432	2	Q57SB6_SALCH	Q57SB6 salmonella
571	37	45.1	318	2	Q67X80_ORYSA	Q67X80 oryza sativ	644	37	45.1	432	2	Q4QMK6_HAE18	Q4QMK6 haemophilus
572	37	45.1	320	2	Q6GXD3_9LEPT	Q6GXD3 leptospira	645	37	45.1	433	1	TIG_HAE18	TIG_HAE18
573	37	45.1	320	2	Q6GXD4_9LEPT	Q6GXD4 leptospira	646	37	45.1	433	1	TIG_HAE18	TIG_HAE18
574	37	45.1	320	2	Q6GXD5_LEPIN	Q6GXD5 leptospira	647	37	45.1	433	1	TIG_IDILO	TIG_IDILO
575	37	45.1	320	2	Q6GXD6_LEPIN	Q6GXD6 leptospira	648	37	45.1	433	1	TIG_IDILO	TIG_IDILO
576	37	45.1	320	2	Q6GXD7_LEPIN	Q6GXD7 leptospira	649	37	45.1	433	1	TIG_VIBCH	TIG_VIBCH
577	37	45.1	320	2	Q6GXD8_LEPIN	Q6GXD8 leptospira	650	37	45.1	434	1	TIG_ERWCT	TIG_ERWCT
578	37	45.1	320	2	Q6GXD9_LEPIN	Q6GXD9 leptospira	651	37	45.1	434	1	TIG_ERWCT	TIG_ERWCT
579	37	45.1	320	2	Q6GXD9_LEPIN	Q6GXD9 leptospira	652	37	45.1	434	1	TIG_ERWCT	TIG_ERWCT
580	37	45.1	320	2	Q6GXD9_LEPIN	Q6GXD9 leptospira	653	37	45.1	434	1	TIG_ERWCT	TIG_ERWCT
581	37	45.1	320	2	Q91586_LEPIN	Q91586 leptospira	654	37	45.1	434	1	TIG_ERWCT	TIG_ERWCT
582	37	45.1	321	2	Q7NCW6_GLOVI	Q7NCW6 gloeobacter	655	37	45.1	440	2	Q6LN63_VACVI	Q6LN63 vaccinium v
583	37	45.1	327	2	Q4L6L7_STA9J	Q4L6L7 staphylococ	656	37	45.1	447	2	Q6LN63_VACVI	Q6LN63 vaccinium v
584	37	45.1	327	2	Q6G949_STAAS	Q6G949 staphylococ	657	37	45.1	448	2	Q6LN63_VACVI	Q6LN63 vaccinium v
585	37	45.1	327	2	Q5HFQ5_STAAR	Q5HFQ5 staphylococ	658	37	45.1	449	2	Q6LN63_VACVI	Q6LN63 vaccinium v
586	37	45.1	327	2	Q5HFQ5_STAAR	Q5HFQ5 staphylococ	659	37	45.1	460	2	Q6LN63_VACVI	Q6LN63 vaccinium v
587	37	45.1	327	2	Q7A0T8_STAAN	Q7A0T8 staphylococ	660	37	45.1	463	2	Q91LC4_MOUSE	Q91LC4 mus musculu
588	37	45.1	327	2	Q7A5F8_STAAN	Q7A5F8 staphylococ	661	37	45.1	464	2	Q8UEZ2_AGRTE	Q8UEZ2 agrobacteri
589	37	45.1	327	2	Q99TX7_STAAM	Q99TX7 staphylococ	662	37	45.1	464	2	Q8UEZ2_AGRTE	Q8UEZ2 agrobacteri
590	37	45.1	334	2	Q642M9_BRARE	Q642M9 brachydanio	663	37	45.1	470	2	Q6PIP8_MOUSE	Q6PIP8 mus musculu
591	37	45.1	337	2	Q8F1J7_LEPIN	Q8F1J7 leptospira	664	37	45.1	481	2	Q6PIP8_MOUSE	Q6PIP8 mus musculu
592	37	45.1	338	2	Q56265_THEFU	Q56265 thermomonos	665	37	45.1	482	2	Q79VC9_CORGL	Q79VC9 corynebacte
593	37	45.1	338	2	Q56265_THEFU	Q56265 thermomonos	666	37	45.1	482	2	Q79VC9_CORGL	Q79VC9 corynebacte
594	37	45.1	339	2	Q6ZS88_HUMAN	Q6ZS88 homo sapien	667	37	45.1	491	2	Q80Z17_MOUSE	Q80Z17 mus musculu
595	37	45.1	342	2	Q4ZYQ4_PSSSY	Q4ZYQ4 pseudomonas	668	37	45.1	492	2	Q825P6_STRAW	Q825P6 streptomyce
596	37	45.1	342	2	Q889K2_PSSSM	Q889K2 pseudomonas	669	37	45.1	505	2	Q825P6_STRAW	Q825P6 streptomyce
597	37	45.1	344	2	Q8GMV7_9ACTO	Q8GMV7 nonculturae	670	37	45.1	508	1	Q6C4Y5_YARLI	Q6C4Y5 yarrowia li
598	37	45.1	351	2	Q64BV4_9ARCH	Q64BV4 uncultured	671	37	45.1	518	2	Q6C4Y5_YARLI	Q6C4Y5 yarrowia li
599	37	45.1	352	2	Q4N3P9_THERPA	Q4N3P9 theileria p	672	37	45.1	529	2	Q7SEW4_NEUCR	Q7SEW4 neurospora
600	37	45.1	356	1	CHBB2_CHRVO	CHBB2 chromobacte	673	37	45.1	531	2	Q4UAF1_THERC	Q4UAF1 theileria a
601	37	45.1	356	1	CHBB2_SHEON	CHBB2 shewanella	674	37	45.1	534	2	Q4UAF1_THERC	Q4UAF1 theileria a
602	37	45.1	357	2	Q7V9G8_PROMA	Q7V9G8 prochloroco	675	37	45.1	535	2	Q9AB19_CAUCR	Q9AB19 caulobacter
603	37	45.1	358	1	CHBB2_PSESM	CHBB2 pseudomonas	676	37	45.1	538	2	Q83CX6_COXBU	Q83CX6 coxiella bu
604	37	45.1	358	2	Q4ZYD3_PSSSY	Q4ZYD3 pseudomonas	677	37	45.1	538	2	Q4JYJ3_CORJK	Q4JYJ3 corynebacte
605	37	45.1	359	2	Q17830_CABEL	Q17830 caenorhabdi	678	37	45.1	544	2	Q4T8R6_TETNG	Q4T8R6 tetraodon n
606	37	45.1	360	2	Q8NSN0_DROME	Q8NSN0 drosophila	679	37	45.1	558	2	Q5LVA0_SILPO	Q5LVA0 silicibacte
607	37	45.1	368	2	Q55YV8_CRYNE	Q55YV8 cryptococcu	680	37	45.1	560	2	Q88N04_PSEPK	Q88N04 pseudomonas
608	37	45.1	368	2	Q5KN76_CRYNE	Q5KN76 cryptococcu	681	37	45.1	572	2	Q6YZ75_ORYSA	Q6YZ75 oryza sativ
609	37	45.1	372	2	Q59ZHS_CANAL	Q59ZHS candida alb	682	37	45.1	584	1	BCAS1_HUMAN	BCAS1_HUMAN
610	37	45.1	372	2	Q4LG93_9BURK	Q4LG93 burkholderi	683	37	45.1	584	2	Q6INK3_XENIA	Q6INK3 xenopus lae
611	37	45.1	375	2	Q5V616_HALMA	Q5V616 haloarcula	684	37	45.1	604	2	Q6U9F7_9CAUD	Q6U9F7 bacterioph
612	37	45.1	388	2	Q81R08_DROME	Q81R08 drosophila	685	37	45.1	604	2	Q56EL8_9CAUD	Q56EL8 aetionopha
613	37	45.1	388	2	Q5Y521_NOCFA	Q5Y521 nocardia fa	686	37	45.1	605	2	Q6GN83_XENIA	Q6GN83 xenopus lae
614	37	45.1	389	2	Q4WL33_ASPERGILL	Q4WL33 aspergillus	687	37	45.1	616	2	Q5FUC2_GLUOXB	Q5FUC2 gluconobact
615	37	45.1	395	1	TF2H2_HUMAN	TF2H2_HUMAN	688	37	45.1	629	2	Q5WAG4_BACSK	Q5WAG4 bacillus cl

689 37 45.1 632 1 GIDA_BACHD
690 37 45.1 638 2 Q81M54_ORYSA
691 37 45.1 641 2 Q729F6_DESVH
692 37 45.1 643 2 Q61MF3_CABR
693 37 45.1 656 2 Q9F1I3_ARATH
694 37 45.1 660 2 Q681N2_ARATH
695 37 45.1 665 2 Q4SN22_TETNG
696 37 45.1 678 2 Q5L6P6_CHLAB
697 37 45.1 678 2 Q4TM88_9SPHN
698 37 45.1 678 2 Q823T1_CHLCV
699 37 45.1 681 2 Q21046_CABEL
700 37 45.1 700 2 Q8D1M8_YERPE
701 37 45.1 704 2 Q8L849_ARATH
702 37 45.1 704 2 Q3PFA9_ARATH
703 37 45.1 708 2 Q8ZXU4_PYRAE
704 37 45.1 724 2 Q5XBN3_STRP6
705 37 45.1 724 2 Q99ZM4_STRPY
706 37 45.1 724 2 Q8P0J6_STRP8
707 37 45.1 724 2 Q8K742_STRP3
708 37 45.1 726 2 Q4UBJ6_THEAN
709 37 45.1 727 2 Q33T28_STRAG
710 37 45.1 727 2 Q8DYI4_STRAS
711 37 45.1 727 2 Q8E469_STRAS
712 37 45.1 732 2 Q74PH2_YERPE
713 37 45.1 732 2 Q8ZB16_YERPE
714 37 45.1 732 2 Q665A1_YERPS
715 37 45.1 736 2 Q5LXR7_STRT1
716 37 45.1 736 2 Q5M3D1_STRT2
717 37 45.1 739 2 Q664Z5_YERPS
718 37 45.1 764 2 Q9SCY9_ARATH
719 37 45.1 772 2 Q63E41_BACCZ
720 37 45.1 776 2 Q8N9H7_RHOPA
721 37 45.1 786 2 Q8TP44_METAC
722 37 45.1 787 2 Q54C35_DICDI
723 37 45.1 787 2 Q63X79_BURPS
724 37 45.1 787 2 Q62MM5_BURMA
725 37 45.1 800 2 Q8ZB23_YERPE
726 37 45.1 870 2 Q6FC24_ACIAD
727 37 45.1 893 2 Q8I180_DROWI
728 37 45.1 908 1 ACON_BACSU
729 37 45.1 914 2 P33659_BRANA
730 37 45.1 926 2 Q8D4N2_VIBVU
731 37 45.1 926 2 Q7MG80_VIBVY
732 37 45.1 932 2 Q64YL0_BACFN
733 37 45.1 934 2 Q8SZX4_DROME
734 37 45.1 975 2 Q7VUUI_BORPE
735 37 45.1 975 2 Q7W3X4_BORPA
736 37 45.1 975 2 Q7WFA4_BORBR
737 37 45.1 987 2 Q8XVM5_RALSO
738 37 45.1 988 2 P33065_BRANA
739 37 45.1 989 2 Q7K7P3_CABEL
740 37 45.1 999 2 Q8G2T3_BRUSU
741 37 45.1 1000 2 Q8YF07_BRUME
742 37 45.1 1006 2 Q4UIB6_THEAN
743 37 45.1 1011 2 Q5LHN4_BACFN
744 37 45.1 1026 2 Q582H5_9TRYP
745 37 45.1 1057 2 Q9U267_CABEL
746 37 45.1 1057 2 Q5XPS1_CHLRE
747 37 45.1 1143 2 Q7ZT80_ANGAN
748 37 45.1 1157 1 CR8AA_BACUK
749 37 45.1 1169 1 CR8BA_BACUK
750 37 45.1 1177 2 Q6C0B5_YARLI
751 37 45.1 1223 2 Q5YA61_9CAUD
752 37 45.1 1276 2 Q4SI34_TETNG
753 37 45.1 1291 2 Q66JZ8_MOUSE
754 37 45.1 1305 2 Q6CCN3_YARLI
755 37 45.1 1331 1 CNTP2_HUMAN
756 37 45.1 1331 1 CNTP2_PONPY
757 37 45.1 1332 1 CNTP2_MOUSE
758 37 45.1 1343 2 Q4IK63_GIBBEZ
759 37 45.1 1386 2 Q4I3R9_GIBBEZ
760 37 45.1 1608 2 Q56R07_LYCES
761 37 45.1 1734 2 Q4ZE88_MOUSE

762 37 45.1 1765 2 Q6C473_YARLI
763 37 45.1 1837 2 Q9VCZ9_DROME
764 37 45.1 1931 2 Q4Q2X5_LEISHMA
765 37 45.1 2706 2 Q15870_PLAFA
766 37 45.1 2803 2 Q748V3_GEOSL
767 37 45.1 3440 2 Q4QCVO_LEISHMA
768 37 45.1 3672 2 Q7N727_PHOLI
769 37 45.1 3821 2 Q7NU32_CHRVO
770 37 45.1 4610 2 Q8AXB7_BRARE
771 37 45.1 5217 1 H5I1_COCCA
772 36.5 44.5 365 2 Q45135_9MICO
773 36.5 44.5 446 2 Q9Y1X4_9METZ
774 36.5 44.5 473 2 Q6MZV7_HUMAN
775 36.5 44.5 499 2 Q8N5K4_HUMAN
776 36.5 44.5 511 1 C71A6_NEPRA
777 36.5 44.5 568 2 Q9E960_9VIRU
778 36.5 44.5 568 2 Q66149_9VIRU
779 36.5 44.5 568 2 Q89504_9VIRU
780 36.5 44.5 643 2 Q6BX44_DEBHA
781 36.5 44.5 832 2 Q8PUW8_METWA
782 36.5 44.5 892 2 Q52D94_WAGGR
783 36.5 44.5 913 2 Q5L5B3_CHLAB
784 36.5 44.5 1094 2 Q4P6H2_USTWA
785 36.5 44.5 1197 1 TIM_MOUSE
786 36.5 44.5 1205 1 TIM_MOUSE
787 36 43.9 50 2 Q84210_9PARA
788 36 43.9 51 2 Q6FD13_ACIAD
789 36 43.9 75 2 Q663F1_YERPS
790 36 43.9 78 2 Q5V1Q3_HALMA
791 36 43.9 86 2 Q5Z512_ORYSA
792 36 43.9 99 2 Q53N46_ORYSA
793 36 43.9 100 2 Q6B6Z8_RABIT
794 36 43.9 101 2 Q6B6W2_RABIT
795 36 43.9 103 2 Q6B708_RABIT
796 36 43.9 103 2 Q6B713_ORYCTOLAGUS
797 36 43.9 103 2 Q8RCV1_THETN
798 36 43.9 104 2 Q6B710_RABIT
799 36 43.9 105 2 Q6B6X6_RABIT
800 36 43.9 105 2 Q6B6P9_RABIT
801 36 43.9 106 2 Q6B6T3_RABIT
802 36 43.9 106 2 Q6B6Y6_RABIT
803 36 43.9 106 2 Q67RT8_SYMTB
804 36 43.9 109 2 Q6UUE0_ORYSA
805 36 43.9 116 1 HV1A_RABIT
806 36 43.9 120 2 Q648Z3_9ARCH
807 36 43.9 120 2 Q7PA01_RICSI
808 36 43.9 120 2 Q92G63_RICCN
809 36 43.9 125 2 Q9UL95_HUMAN
810 36 43.9 125 2 Q8K4B1_RAT
811 36 43.9 130 2 Q4RCG9_TETNG
812 36 43.9 131 2 Q62532_DROME
813 36 43.9 139 2 Q66G34_YERPS
814 36 43.9 142 2 Q6RI07_CLOBO
815 36 43.9 142 2 Q5I3P7_9BACT
816 36 43.9 143 2 Q5I3P8_9BACT
817 36 43.9 143 2 Q44086_ACIWM
818 36 43.9 143 2 Q5I3P1_9BACT
819 36 43.9 143 2 Q5I3P4_9BACT
820 36 43.9 143 2 Q5I3P6_9BACT
821 36 43.9 144 2 Q52975_CLOBO
822 36 43.9 147 2 Q98UB8_9PERC
823 36 43.9 147 2 Q98UB9_9PERC
824 36 43.9 148 2 Q7T8E2_9GAMA
825 36 43.9 148 2 Q7T8E3_9GAMA
826 36 43.9 148 2 Q7T8E4_9GAMA
827 36 43.9 148 2 Q7T8E5_9GAMA
828 36 43.9 148 2 Q7T8E6_9GAMA
829 36 43.9 152 2 Q92VK5_RHIME
830 36 43.9 153 2 Q66ML8_LEPIN
831 36 43.9 155 2 Q9SPA9_HORVU
832 36 43.9 155 2 Q9ZTR7_HORVU
833 36 43.9 157 2 Q28302_CANFA
834 36 43.9 158 2 Q871X9_NEUCR

Q6C473 yarrowia li
Q9vcz9 drosophila
Q4q2x5 leishmania
Q15870 plasmodium
Q748v3 geobacter s
Q4qcvo leishmania
Q7n727 photorhabdu
Q7nu32 chromobacte
Q8axb7 brachydanio
Q1886 cochliobolu
Q45135 brevbacter
Q9y1x4 ephydatia f
Q6mzv7 homo sapien
Q8n5k4 homo sapien
O4164 nepeta race
Q9e960 cocksfoot m
Q66149 cocksfoot m
Q89504 cocksfoot m
Q6bx44 debaryomyce
Q8puw8 methanosarc
Q52d94 magnaporthe
Q5l5b3 chlamydophi
Q4p6h2 ustilago ma
Q9rix4 mus musculu
Q9z2y1 rattus norv
Q84210 newcastle d
Q6fd13 acinetobact
Q663f1 yersinia ps
Q5viq3 haloarcula
Q5z512 oryza sativ
Q53n46 oryza sativ
Q6b6z8 oryctolagus
Q6b6w2 oryctolagus
Q6b708 oryctolagus
Q6b713 oryctolagus
Q8rcv1 thermoaer
Q6b710 oryctolagus
Q6b6x6 oryctolagus
Q6b6p9 oryctolagus
Q6b6t3 oryctolagus
Q6b6y6 oryctolagus
Q67rt8 symtobacte
Q6ueu0 oryza sativ
P01826 oryctolagus
Q648z3 uncultured
Q7pa01 rickettsia
Q92g63 rickettsia
Q9ul95 homo sapien
Q8k4b1 rattus norv
Q4rcg9 tetraodon n
Q62532 drosophila
Q66g34 yersinia ps
Q6ri07 clostridium
Q5i3p7 uncultured
Q5i3p8 uncultured
Q44086 acinetobact
Q5i3p1 uncultured
Q5i3p4 uncultured
Q5i3p6 uncultured
Q52975 clostridium
Q98ub8 notothenia
Q98ub9 notothenia
Q7t8e2 saginus mi
Q7t8e3 saginus mi
Q7t8e4 saginus mi
Q7t8e5 saginus mi
Q7t8e6 saginus mi
Q92vk5 rhizobium m
Q66ml8 leptospira
Q9spa9 hordeum vul
Q9ztr7 hordeum vul
Q28302 canis faml
Q871x9 neurospora

835	1	161	36	43.9	1	DHN3	HORVU	P12948	bordeum vul	908	36	43.9	259	2	Q8A2G3	BACTN	Q8A2g3	bacteroides
836	2	162	36	43.9	2	Q93XH8	FRAAN	Q93xh8	fragaria an	909	36	43.9	260	2	Q6S9M1	LEPBO	Q6S9m1	leptospiira
837	3	163	36	43.9	3	Q7MY95	PHOLL	Q7my95	photorhabd	910	36	43.9	261	2	Q4NIM3	9MICC	Q4nim3	arthrobacte
838	4	164	36	43.9	4	Q946W4	PRUPE	Q946w4	prunus pers	911	36	43.9	262	2	Q98CG0	RHOLO	Q98cg0	rhizobium l
839	5	165	36	43.9	5	Q93ND5	MYXXA	Q93nd5	myxococcus	912	36	43.9	263	2	Q7QBM0	ANOGA	Q7qbm0	anophelies g
840	6	166	36	43.9	6	Q66ML4	LEPIN	Q66ml4	leptospiira	913	36	43.9	264	2	Q829H4	STRAP	Q829h4	streptomyce
841	7	167	36	43.9	7	Q66V60	PNECA	Q66v60	pneumocysti	914	36	43.9	265	2	Q66MM1	LEPBO	Q66mm1	leptospiira
842	8	168	36	43.9	8	Q7Q4T9	ANOGA	Q7q4t9	anophelies g	915	36	43.9	266	2	Q7QQ43	GLALA	Q7qq43	giardia lam
843	9	169	36	43.9	9	Q66ML5	LEPBO	Q66ml5	leptospiira	916	36	43.9	267	2	Q4G2D2	9TRYP	Q4g2d2	trypanosoma
844	10	170	36	43.9	10	Q66MM2	LEPBO	Q66mm2	leptospiira	917	36	43.9	268	2	Q57NH6	SALCH	Q57nh6	salmonella
845	11	171	36	43.9	11	Q61JQ5	DROME	Q61jq5	drosophila	918	36	43.9	269	2	Q5P178	SALPA	Q5p178	salmonella
846	12	172	36	43.9	12	Q52ZAT	LEGPH	Q52zat	legionella	919	36	43.9	270	2	Q8Z669	SALTI	Q8z669	salmonella
847	13	173	36	43.9	13	Q5XOB6	LEGPL	Q5xob6	legionella	920	36	43.9	271	2	Q8ZNZ9	SALTY	Q8znz9	salmonella
848	14	174	36	43.9	14	Q5X8X5	LEPGA	Q5x8x5	legionella	921	36	43.9	272	2	Q66MK9	9LEPT	Q66mk9	leptospiira
849	15	175	36	43.9	15	Q57S55	ANOGA	Q57s55	anophelies g	922	36	43.9	273	2	Q66MM4	LEPBO	Q66mm4	leptospiira
850	16	176	36	43.9	16	Q9W078	DROME	Q9w078	drosophila	923	36	43.9	274	2	P79792	CHICK	P79792	gallus gall
851	17	177	36	43.9	17	Q8H6C7	9POAL	Q8h6c7	haynaldia v	924	36	43.9	275	2	Q6S9L9	LEPBO	Q6s9l9	leptospiira
852	18	178	36	43.9	18	Q726Y4	DESVH	Q726y4	desulfovibr	925	36	43.9	276	2	Q8S9J3	9LEPT	Q8s9j3	leptospiira
853	19	179	36	43.9	19	Q66ML0	LEPIN	Q66ml0	leptospiira	926	36	43.9	277	2	Q6S9J6	9LEPT	Q6s9j6	leptospiira
854	20	180	36	43.9	20	Q726C1	DESVH	Q726c1	desulfovibr	927	36	43.9	278	2	Q6S9K9	LEPIN	Q6s9k9	leptospiira
855	21	181	36	43.9	21	Q62KV1	BURMA	Q62kv1	burkholderi	928	36	43.9	279	2	Q6S9J2	9LEPT	Q6s9j2	leptospiira
856	22	182	36	43.9	22	Q63TK1	BURPS	Q63tk1	burkholderi	929	36	43.9	280	2	Q6S9K2	9LEPT	Q6s9k2	leptospiira
857	23	183	36	43.9	23	HIS1	LEPIC	P62382	leptospiira	930	36	43.9	281	2	Q6S9K3	9LEPT	Q6s9k3	leptospiira
858	24	184	36	43.9	24	HIS1	LEPIN	Q8fep1	leptospiira	931	36	43.9	282	2	Q6S9L7	LEPIN	Q6s9l7	leptospiira
859	25	185	36	43.9	25	Q68KH3	PNEJI	Q68kh3	pneumocysti	932	36	43.9	283	2	Q6S9I9	9LEPT	Q6s9i9	leptospiira
860	26	186	36	43.9	26	Q68KG9	PNEJI	Q68kg9	pneumocysti	933	36	43.9	284	2	Q6S9J5	9LEPT	Q6s9j5	leptospiira
861	27	187	36	43.9	27	Q68KH0	PNEJI	Q68kh0	pneumocysti	934	36	43.9	285	2	Q6S9M3	LEPBO	Q6s9m3	leptospiira
862	28	188	36	43.9	28	Q68KH1	PNEJI	Q68kh1	pneumocysti	935	36	43.9	286	2	Q6S9M6	LEPBO	Q6s9m6	leptospiira
863	29	189	36	43.9	29	Q68KH2	PNEJI	Q68kh2	pneumocysti	936	36	43.9	287	2	Q7EY69	ORVSA	Q7ey69	oryza sativ
864	30	190	36	43.9	30	Q68KH3	PNEJI	Q68kh3	pneumocysti	937	36	43.9	288	2	Q6F9P3	ACTAD	Q6f9p3	acinetobact
865	31	191	36	43.9	31	Q68KH6	PNEJI	Q68kh6	pneumocysti	938	36	43.9	289	2	Q4FP30	9RICK	Q4fp30	canidatus
866	32	192	36	43.9	32	Q68KH7	PNEJI	Q68kh7	pneumocysti	939	36	43.9	290	2	Q7VVK3	PROMA	Q7vdk3	prochloroco
867	33	193	36	43.9	33	Q68KH9	PNEJI	Q68kh9	pneumocysti	940	36	43.9	291	2	Q64ZY3	BACFR	Q64zy3	bacteroides
868	34	194	36	43.9	34	Q68K11	PNEJI	Q68k11	pneumocysti	941	36	43.9	292	1	RL5	MOUSE	P47962	mus musculu
869	35	195	36	43.9	35	Q68K12	PNEJI	Q68k12	pneumocysti	942	36	43.9	293	2	Q6S9J7	9LEPT	Q6s9j7	leptospiira
870	36	196	36	43.9	36	Q6B327	PNEJI	Q6b327	pneumocysti	943	36	43.9	294	2	Q5NFI9	FRATT	Q5nfi9	franciella
871	37	197	36	43.9	37	Q90UP5	PNEJI	Q90up5	pneumocysti	944	36	43.9	295	2	CD20	HUMAN	P11836	homo sapien
872	38	198	36	43.9	38	Q4F8K1	EUCGL	Q4f8k1	eucalyptus	945	36	43.9	296	2	Q4KGD2	PSEF5	Q4kgd2	pseudomonas
873	39	199	36	43.9	39	Q55T05	CRVNE	Q55t05	cryptococc	946	36	43.9	297	2	Q89GH7	BRAJA	Q89gh7	bradyrhizob
874	40	200	36	43.9	40	Q5KH07	CRVNE	Q5kh07	cryptococc	947	36	43.9	298	2	Q913S2	PSEAE	Q913s2	pseudomonas
875	41	201	36	43.9	41	Q70261	CANFA	Q70261	canis famil	948	36	43.9	299	2	Q88EE3	PSEPK	Q88ee3	pseudomonas
876	42	202	36	43.9	42	Q70293	CANFA	Q70293	canis famil	949	36	43.9	300	2	Q58EUC	MOUSE	Q58euc	mus musculu
877	43	203	36	43.9	43	Q5D635	HORSP	Q5d635	hordeum spo	950	36	43.9	301	2	Q6S9M5	LEPBO	Q6s9m5	leptospiira
878	44	204	36	43.9	44	Q5D636	HORSP	Q5d636	hordeum spo	951	36	43.9	302	2	Q87IB3	VIBPA	Q87ib3	vibriio para
879	45	205	36	43.9	45	Q9HFH0	PENFN	Q9hfh0	penicillium	952	36	43.9	303	2	P74164	SYNY3	P74164	synecocyst
880	46	206	36	43.9	46	Q61VU6	TRITU	Q61vu6	triticum tu	953	36	43.9	304	2	Q55VY9	CRVNE	Q55vy9	cryptococc
881	47	207	36	43.9	47	Q5NZM4	AZOSE	Q5nzm4	azococcus sp	954	36	43.9	305	2	Q5KKA2	CRVNE	Q5kka2	cryptococc
882	48	208	36	43.9	48	HIS1	AGRT5	Q8unh1	agrobacteri	955	36	43.9	306	2	Q48703	ARATH	Q48703	arabidopsis
883	49	209	36	43.9	49	HIS1	RHIME	Q92rr6	rhizobium m	956	36	43.9	307	2	Q6S9J0	9LEPT	Q6s9j0	leptospiira
884	50	210	36	43.9	50	Q41579	WHEAT	Q41579	tritium ae	957	36	43.9	308	2	Q6S9J1	9LEPT	Q6s9j1	leptospiira
885	51	211	36	43.9	51	Q8YD10	BRUME	Q8ydl0	brucella me	958	36	43.9	309	2	Q6S9J8	9LEPT	Q6s9j8	leptospiira
886	52	212	36	43.9	52	Q9HFA4	ASPOR	Q9hfa4	aspergillus	959	36	43.9	310	2	Q6S9K7	9LEPT	Q6s9k7	leptospiira
887	53	213	36	43.9	53	Q4MIK9	BACEC	Q4mik9	bacillus ce	960	36	43.9	311	2	Q6S9L8	LEPIN	Q6s9l8	leptospiira
888	54	214	36	43.9	54	Q5LIT9	BACFN	Q5lit9	bacteroides	961	36	43.9	312	2	Q6S9M0	LEPBO	Q6s9m0	leptospiira
889	55	215	36	43.9	55	Q5YVK3	NOCPA	Q5yvk3	nocardia fa	962	36	43.9	313	2	Q6S9K6	9LEPT	Q6s9k6	leptospiira
890	56	216	36	43.9	56	Q6JPB3	9NUCL	Q6jpb3	neodiprion	963	36	43.9	314	2	Q4TH58	TETNG	Q4th58	tetraodon n
891	57	217	36	43.9	57	Q4LQW6	9BURK	Q4lqw6	burkholderi	964	36	43.9	315	2	Q8LB34	ARATH	Q8lb34	arabidopsis
892	58	218	36	43.9	58	Q4FTV4	9GAMM	Q4ftv4	psychrobact	965	36	43.9	316	2	Q9ZPE7	ARATH	Q9zpe7	arabidopsis
893	59	219	36	43.9	59	Q6HGD4	BACHK	Q6hgd4	bacillus th	966	36	43.9	317	2	Q48546	9LEPT	Q48546	leptospiira
894	60	220	36	43.9	60	Q9ZP36	TOBAC	Q9zp36	nicotiana t	967	36	43.9	318	2	Q6GXC9	LEPBO	Q6gxc9	leptospiira
895	61	221	36	43.9	61	Q6XD96	9REOV	Q6xd96	human rotav	968	36	43.9	319	2	Q6GXD0	LEPBO	Q6gxd0	leptospiira
896	62	222	36	43.9	62	Q9B8I9	9REOV	Q9b8i9	human rotav	969	36	43.9	320	2	Q6GXD1	LEPBO	Q6gxd1	leptospiira
897	63	223	36	43.9	63	Q4HY72	GIBZE	Q4hy72	gibberella	970	36	43.9	321	2	Q6GXD2	LEPBO	Q6gxd2	leptospiira
898	64	224	36	43.9	64	Q6MJ08	BDEBA	Q6mj08	bdellovibri	971	36	43.9	322	2	Q6GXE1	LEPIN	Q6gxe1	leptospiira
899	65	225	36	43.9	65	Q84UK5	PRUPE	Q84uk5	prunus pers	972	36	43.9	323	2	Q6GXE2	LEPIN	Q6gxe2	leptospiira
900	66	226	36	43.9	66	Q8VWV8	9ROSA	Q8vwv8	prunus cera	973	36	43.9	324	2	Q6GXE3	LEPIN	Q6gxe3	leptospiira
901	67	227	36	43.9	67	Q9FUM2	PRUAV	Q9fum2	prunus aviu	974	36	43.9	325	2	Q6S9K4	9LEPT	Q6s9k4	leptospiira
902	68	228	36	43.9	68	Q89ZU6	BACTN	Q89zu6	bacteroides	975	36	43.9	326	2	Q6S9L0	LEPIN	Q6s9l0	leptospiira
903	69	229	36	43.9	69	Q84L77	PYRGO	Q84l77	pyrus commu	976	36	43.9	327	2	Q6S9L2	LEPIN	Q6s9l2	leptospiira
904	70	230	36	43.9	70	Q6E3K9	9ACTO	Q6e3k9	propionibac	977	36	43.9	328	2	Q72TP4	LEPIC	Q72tp4	leptospiira
905	71	231	36	43.9	71	Q6S9J4	9LEPT	Q6s9j4	leptospiira	978	36	43.9	329	2	Q52G64	MAGGR	Q52g64	magnaporthe
906	72	232	36	43.9	72	Q45683	CAEEL	Q45683	caenorhabdi	979	36	43.9	330	2	Q8D5D5	VIBVU	Q8d5d5	vibriio vuln
907	73	233	36	43.9	73	Q89ZT8	BACTN	Q89zt8	bacteroides	980	36	43.9	331	2	Q73W37	MYCPA	Q73w37	mycobacteri

981 36 43.9 335 1 XYNB_STRLI
 982 36 43.9 335 2 O9RK6_STRCO
 983 36 43.9 336 2 O87J0_VIBPA
 984 36 43.9 336 2 QMCB0_VIBVY
 985 36 43.9 338 2 Q7VLA5_HAEDU
 986 36 43.9 338 2 Q4SVB8_TETNG
 987 36 43.9 343 2 Q4N996_THEPA
 988 36 43.9 344 2 Q512V7_ENTHI
 989 36 43.9 346 2 Q74D31_GEOSL
 990 36 43.9 347 2 Q70S25_NEIME
 991 36 43.9 350 1 Y2185_FYRAE
 992 36 43.9 351 2 Q8IQV7_DROME
 993 36 43.9 351 2 Q8MR04_DROME
 994 36 43.9 351 2 Q8KN22_VIBCH
 995 36 43.9 352 1 CHEB2_XANAC
 996 36 43.9 352 1 CHEB2_XANCP
 997 36 43.9 352 2 Q5DWS6_9DINO
 998 36 43.9 352 2 Q5DWS7_KARBR
 999 36 43.9 352 2 Q4UTU6_XANCP
 1000 36 43.9 354 2 Q5FP49_GLUOX

P26515 streptomyce
 O9rk6 streptomyce
 O87j0 vibrio para
 Qmcb0 vibrio vuln
 Q7vla5 haemophilus
 Q4svb8 tetraodon n
 Q4n996 theileria p
 Q512v7 entamoeba h
 Q74d31 geobacter s
 Q70s25 neisseria m
 Q8zvp4 pyrobaculum
 Q8iqv7 drosophila
 Q8mr04 drosophila
 Q9kn22 vibrio chol
 Q9pm5 xanthomonas
 Q9p7a6 xanthomonas
 Q5dws6 karenia mik
 Q5dws7 karenia bre
 Q4utu6 xanthomonas
 Q5fp49 gluconobact

ALIGNMENTS

RESULT 1
 Q5PQK9 RAT PRELIMINARY; PRT; 479 AA.

ID Q5PQK9 RAT PRELIMINARY; PRT; 479 AA.
 AC Q5PQK9;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Igha protein.
 GN Name=Igha;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAUBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]

NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC NIH MGC Project;
 RG Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC087137; AA087137.1; -, mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 479 AA; 52354 MW; 1692EP3457BE686E CRC64;

Query Match 66.5%; Score 54.5; DB 2; Length 479;
 Best Local Similarity 70.6%; Pred. No. 1.6;
 Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
 |||:|||||:|:|:|
 Db 69 SITNTGGKTYPDSVKG 85

RESULT 2

Q4SX92 TETNG
 ID Q4SX92 TETNG PRELIMINARY; PRT; 96 AA.
 AC Q4SX92;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF12787, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00011060001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN NUCLEOTIDE SEQUENCE.
 RP JAILLON O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Kellis M., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957 (2004).
 RL [2]

NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAAE01012787; CAF94740.1; -; Genomic_DNA.

FT NON TER 1 1
 FT NON TER 96 96
 SQ SEQUENCE 96 AA; 10590 MW; 85BED888AAEE7486 CRC64;

Query Match 64.6%; Score 53; DB 2; Length 96;
 Best Local Similarity 62.5%; Pred. No. 0.51;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
 :||:|||||:|:|:|
 Db 47 AISGGSTYISVKG 62

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RESULT 3
ID Q4TSM5_TETNG PRELIMINARY; PRT; 99 AA.
AC Q4TSM5;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCF9197, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0006732001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segrens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Athouart V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Contanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Voif J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01009197; CAF91807.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10975 MW; 1EC40587BED4BAF5 CRC64;

Query Match 63.4%; Score 52; DB 2; Length 99;
Best Local Similarity 70.6%; Pred. No. 0.79;
Matches 12; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 ITSTGG--TYHAESVKG 16
Db ||||| :||:|||||
48 IISTGGSSTYSSEVKG 64

RESULT 4
Q8A8Y9_BACTN PRELIMINARY; PRT; 724 AA.
AC Q8A8Y9;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Putative outer membrane protein, probably involved in nutrient
DE binding.
GN OrderedLocusNames=BT1028;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AB016930; AA076135.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 724 AA; 80254 MW; A88F53638F53BB8A CRC64;

Query Match 63.4%; Score 52; DB 2; Length 724;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVK 15
Db ||||| :||:|||||
495 SACGAGGTYHAEGVK 509

RESULT 5
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/GJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -! MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -! SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; JT0504; HVMS91.
DR HSP; P01783; IIGC.
DR SMR; P18527; 1-97.
DR Ensembl; ENSMUSG00000062386; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region.
FT DOMAIN 1 >97
FT NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 62.2%; Score 51; DB 1; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
Db ||||| :||:|||||
50 SISSGGSTYPSVKG 65

RESULT 6
HV02_CANPA
ID HV02_CANPA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)

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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH 11;
RC TISSUE=Mammary tumor metastasized to lung, MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -; mRNA.
DR HSSP; P01789; IMCP.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 486 AA; 52682 MW; 4FF835125DA870B CRC64;

Query Match 59.8%; Score 49; DB 2; Length 486;
Best Local Similarity 56.2%; Pred. No. 14; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 4;

QY 1 SITSTGGTYHARSVKG 16
Db 69 AITSGTYTPDNVKG 84

RESULT 9
Q4TJ56 TETNG
ID Q4TJ56 TETNG PRELIMINARY; PRT; 98 AA.
AC Q4TJ56
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAF649, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00004372001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellini V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CD EMBL; CAAE01000649; CAF87076.1; -; Genomic_DNA.
FT NON_TER 1
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SQ SEQUENCE 98 AA; 10882 MW; 0EB7F34D9BC4648D CRC64;

Query Match 59.1%; Score 48.5; DB 2; Length 98;
Best Local Similarity 64.7%; Pred. No. 3.1;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHARSVKG 16
Db 47 SISSSGSYTYSESVKG 63

RESULT 10
Q8DDQ7 XENLA
ID Q8DDQ7 XENLA PRELIMINARY; PRT; 614 AA.
AC Q8DDQ7
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MGC69086 protein.
GN Name=MGC69086;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077477; AAH77477.1; -; mRNA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR001680; WD40.
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DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
SQ SEQUENCE 614 AA; 68254 MW; 2631B7CF955270C0 CRC64;

Query Match
Best Local Similarity 59.1%; Score 48.5; DB 2; Length 614;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 2 ITSTGG-TYHAESVKG 16
| : | : | : | : | : |
Db 68 ISSDGGSTYYADSVKG 83

RESULT 11
QSFPQ6 LACAC Q5FHO6 LACAC PRELIMINARY; PRT; 632 AA.

ID QSFPQ6;
AC QSFPQ6;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DE Glucose inhibited division protein A.
GN Name=gIdA; OrderedLocusNames=LBA1975;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
ON NCBI_TaxID=1579;
RX NCBII_TaxID=1579;
RP NUCLEOTIDE SEQUENCE.
RC STPAIN-NCFM;
RC PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R., Buck B.L., McAuliffe O., Southern N., Dobson A., Duong T., Callanan M., Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium Lactobacillus acidophilus NCFM.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
CC -I- FUNCTION: Not known (By similarity).
DR GO; GO:0015036; AAV43768.1; -: Genomic DNA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPRO01327; FAD_pyr_redox.
DR InterPro; IPRO02218; GIDA.
DR InterPro; IPRO04416; GIDA_sub.
DR Pfam; PF01134; GIDA; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
DR PRODOM; PD003738; GIDA; 1.
DR TIGRFAMs; TIGR00136; gIdA; 1.
DR PROSITE; PS01280; GIDA_1; 1.
DR PROSITE; PS01281; GIDA_2; 1.
KW Complete proteome.
SQ SEQUENCE 632 AA; 70478 MW; 7394E66AAD38BC02 CRC64;

Query Match
Best Local Similarity 58.5%; Score 48; DB 2; Length 632;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESV 14
| : | : | : | : | : |
Db 142 ITNTGAKYHAKSV 154

RESULT 12
Q9UL72_HUMAN Q9UL72 HUMAN PRELIMINARY; PRT; 118 AA.

AC Q9UL72;
DT 01-MAY-2000 (TRENBLrel. 13, Created)

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Goughman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Trimmick J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells."
RL Nucleic Acids Res. 17:4385-0(1989).
DR EMBL: BC015760; AAL15760.1; -; mRNA.
DR F1R: S05271; S05271.
DR P1R: S24260; S24260.
DR HSP: P01861; IADQ.
DR Ensembl: ENSG00000130076; Homo sapiens.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 57.9%; Score 47.5; DB 2; Length 597;
Best Local Similarity 58.8%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYRAESVKG 16
:|: ||| |||: |||
Db 69 AISGSGGTYYADSVKG 85

RESULT 14
Q7XP97_ORYSA PRELIMINARY; PRT; 3200 AA.
AC Q7XP97;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE OSUNBa0060B20.14 protein. 26, Last annotation update)
GN Name=OSJNba0060B20.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Yang K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun X., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,

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RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4."
RL Nature 420:316-320(2002).
DR EMBL: AL662948; CAE03706.1; -; Genomic_DNA.
DR Gramene; Q7XP97;
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro: IPR000953; Chromo.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR005162; Retrotrans_gag.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTse.
DR Pfam: PF00385; Chromo; 1.
DR Pfam: PF03732; Retrotrans_gag; 1.
DR Pfam: PF00665; RVE; 1.
DR Pfam: PF00078; RVT; 1.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 3200 AA; 359905 MW; 1217DBC0984DFE27 CRC64;

Query Match 57.3%; Score 47; DB 2; Length 3200;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
||||| |||: |||: |||
Db 3128 TSTGGTYHAESVKG 3141

RESULT 15
Q7VB11_PROMA PRELIMINARY; PRT; 320 AA.
ID Q7VB11_PROMA PRELIMINARY;
AC Q7VB11;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted protein family PW-13.
GN OrderedLocustNames=Pro1290;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=12119;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SARG / CMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztaas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxypotrophic genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR EMBL: AE017164; AAQ00334.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 320 AA; 34466 MW; CSB1B23425AF3D4F CRC64;

Query Match 56.1%; Score 46; DB 2; Length 320;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
|||: |||: |||: |||
Db 183 SYTTTNGTYHSQBPQ 198

RESULT 16
SPRL1_COTJA STANDARD; PRT; 676 AA.
ID SPRL1_COTJA

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QY 2 ITSTGG-TYHAEVSKG 16
DB 70 ISSDGGSTYADSVRG 85

RESULT 18
Q7N117_PHOLL
ID Q7N117_PHOLL PRELIMINARY; PRT; 89 AA.
AC Q7N117;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Similarities with unknown protein of Photorhabdus.
GN Ordered locus names=plu3685;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Rude C., Chandler M., Charles J.-F.,
RA Dassa E., Derosé R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Médigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouline M., Glaser P., Boemare N., Danchin A., Kunst P.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313 (2003).
RL EMBL; BX571871; CAB16058.1; -; Genomic_DNA.
DR PhotoList; plu3685; -.
KW Complete proteome.
SQ SEQUENCE 89 AA; 9580 MW; 64D467E63E8192A3 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 89;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 STTSGGTTHAEVSKG 16
DB 36 TLVNTGGTYLGSVKVG 51

RESULT 19
Q4T5S4_TETNG
ID Q4T5S4_TETNG PRELIMINARY; PRT; 96 AA.
AC Q4T5S4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 3 SCAP9141, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG000665001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bienmont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01009141; CAF91758.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10733 MW; 473C4C407BB3E1F0 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 96;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 4 STGGTY--HAESVKG 16
DB 49 STGGSYTDSVSKG 63

RESULT 20
Q9UL71_HUMAN
ID Q9UL71_HUMAN PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035043; AAD56279.1; -; mRNA.
DR HSSP; P01852; INFD.
DR SMR; Q9UL71; 1-121.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCPA5D50736 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 121;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGTTHAEVSKG 16
DB 56 GSTTYADSVKG 66

RESULT 21
Q4TRL6_9SPHN
ID Q4TRL6_9SPHN PRELIMINARY; PRT; 225 AA.
AC Q4TRL6;
DT 13-SEP-2005 (TREMBlrel. 31, Created)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Peptide methionine sulfoxide reductase.
 GN ORFNames=ELI0510;
 OS Erythrobacter litoralis HTCC2594.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Erythrobacter.
 OX NCBI_TaxID=314225;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTCC2594;
 RA Giovannoni S.J., Cho J.-C., Ferreira S., Johnson J., Kravitz S.,
 RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
 RA Friedman R., Venter J.C.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGG01000001; EAL76704.1; -; Genomic DNA.
 SQ SEQUENCE 225 AA; 24952 MW; 7DD5362F3713F098 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 225;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVK 15

Db 85 SITVSGVTDHAESVK 99

RESULT 22

ID Q4FXA9_LEIMA PRELIMINARY; PRT; 366 AA.
 AC Q4FXA9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE 2-oxoisovalerate dehydrogenase beta subunit, mitochondrial, putative
 DE (EC 1.2.4.4).
 GN ORFNames=LMJ_0939;
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Friedlin;
 RX PubMed=16020728; DOI=10.1126/science.1112680;
 RA Ivins A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
 RA Beriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
 RA Apostolou Z., Atipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
 RA Blanchettin G., Borzym K., Boche G., Bruschi C.V., Collins M.,
 RA Cadag E., Ciaroni L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
 RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoet A.,
 RA Fazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
 RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
 RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
 RA Lord A., Louie I., Marra M., Masuy D., Matthews K., Michaeli S.,
 RA Mottram J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
 RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,
 RA Quail M.A., Rabinovitch E., Reinhardt R., Rieger M., Rinta J.,
 RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
 RA Schafer M., Schein J., Schwartz D.C., Seger K., Seyler A., Sharp S.,
 RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
 RA Voickert G., Wamburt G., Warren T., Wedler H., Woodward J., Zhou S.,
 RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
 RA Myler P.J.;
 RT "The Genome of the Kinetoplastid Parasite, Leishmania major.";
 RL Science 309:436-442(2005).
 DR EMBL; CP000081; AA214234.1; -; Genomic_DNA.
 KW Oxidoreductase.

SQ SEQUENCE 366 AA; 39949 MW; 78A943FDCB72EB4E CRC64;

Query Match 54.9%; Score 45; DB 2; Length 366;

Best Local Similarity 50.0%; Pred. No. 50;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 SITSTGGTYHAESVK 16
 Db 163 SAVGHGGIYHSQSVEG 178

RESULT 23

ID Q4FKP5_9TRYP PRELIMINARY; PRT; 368 AA.
 AC Q4FKP5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Branched-chain alpha-keto acid dehydrogenase ei-beta subunit,
 DE putative.
 GN ORFNames=Tb10.v4.0043;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=927/4 GUTat10.1;
 RA Lennard N., Barron A., Clark L., Corton C., Harris B., Line A.,
 RA Berriman M., Hertz-Fowler C., Renauld H., Bohme U., Arrowsmith C.,
 RA Cronin C., Davies R., Doggett J., Fraser A., Johnson D., Larke N.,
 RA Leech V., Lord A., MacLeod A., Norbertczak H., Ormand D., Quail M.,
 RA Rabinovitch E., Rajandream M., Reitter C., Sharp S., Woodward J.,
 RA Hall N., Melville S. and Barrell B.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT009752; CAJ16754.1; -; Genomic DNA.
 SQ SEQUENCE 368 AA; 40222 MW; D106F741C2748AC5 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 368;
 Best Local Similarity 50.0%; Pred. No. 51;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVK 16

Db 165 SAVGHGGIYHSQSVEG 180

RESULT 24

ID Q9VQI5_DROME PRELIMINARY; PRT; 425 AA.
 AC Q9VQI5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG31694-PA (LP04564p).
 GN Name=CG3098; ORFNames=CG31694;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Galbart W.M., Glasser K.,
RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatin genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomes perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.

RC STRAIN-Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE003581; AAF51186.2; -; Genomic_DNA.
DR EMBL; AY119016; AAM50876.1; -; mRNA.
DR Ensembl; CG31694; Drosophila melanogaster.
DR FlyBase; FBgn0051694; CG31694.
DR InterPro; IPR007701; IFRD.
DR InterPro; IPR006921; IFRD_C.
DR Pfam; PF05004; IFRD; 1.
DR Pfam; PF04836; IFRD_C; 1.
SQ SEQUENCE 425 AA; 47327 MW; B7AEC2AAB7B81DF2 CRC64;
Query Match 54.9%; Score 45; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 STTSTGGTVHAESV 14
DB 201 SVTAEAGTFHAEL 214
RESULT 25
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.


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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCED81076E CRC64;

Query Match 54.9%; Score 45; DB 2; Length 466;
Best Local Similarity 72.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGTYYAHSVKG 16
| | | | |
Db 74 GATYYADSVKG 84

RESULT 26
Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.
ID Q569F4
AC Q569F4
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 54.9%; Score 45; DB 2; Length 469;
Best Local Similarity 72.7%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGTYYAHSVKG 16
| | | | |

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Db 75 GSTYYADSVKG 85

RESULT 27
Q8B9B6 NPVRO PRELIMINARY; PRT; 580 AA.
ID Q8B9B6
AC Q8B9B6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE IE-1.
OS Rachiplusia ou multiple nucleopolyhedrovirus (RomNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=80366;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22695336; PubMed=12810877; DOI=10.1099/vir.0.19146-0;
RA Harrison R.L., Bonning B.C.;
RT "Comparative analysis of the genomes of Rachiplusia ou and Autographa
RT californica multiple nucleopolyhedroviruses.";
RL J. Gen. Virol. 84:1827-1842(2003).
DR EMBL; AY145471; AAN28024.1; -; Genomic_DNA.
DR InterPro; IPR005092; TATR.
DR Pfam; PF03430; TATR; 1.
SQ SEQUENCE 580 AA; 66691 MW; 59E1241CB3A3B6AF CRC64;

Query Match 54.9%; Score 45; DB 2; Length 580;
Best Local Similarity 69.2%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
| | | | |
Db 109 STSSTYHAESDVG 121

RESULT 28
Q5XHD5 XENLA PRELIMINARY; PRT; 589 AA.
ID Q5XHD5
AC Q5XHD5
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072253; AAH72253.1; -, mRNA.
DR HSSP; P01842; IADQ.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR001680; WD40.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD-REPEATS_1; UNKNOWN 1.
SQ SEQUENCE 593 AA; 65875 MW; BE314FF9211E12FC CRC64;

Query Match 54.9%; Score 45; DB 2; Length 593;
Best Local Similarity 72.7%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGTTHAESVKG 16
DB 73 GSTYVADSVKG 83

RESULT 31
Q6MZQ6_HUMAN Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 54.3%; Score 44.5; DB 2; Length 475;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 10; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

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QY 2 ITSTG-GTYHAESVKG 16
DB 70 ISSGVNTYYADSVKG 85

RESULT 32
Q6MPI2_BDEBA Q6MPI2_BDEBA PRELIMINARY; PRT; 200 AA.
AC Q6MPI2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MsrA protein precursor (EC 1.8.4.6).
DE Name=msrA; OrderedLocNames=Bdl058;
GN Bdellovibrio bacteriovorus.
OS Bacteri; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692 (2004).
DR EMBL; BX842648; CAE78986.1; -, Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008113; F:protein-methionine-S-oxide reductase activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR002569; MsrA.
DR Pfam; PF01625; PMSR; 1.
DR PRODOM; PD003489; PMSR; 1.
DR TIGRFAMs; TIGR00401; msrA; 1.
KW Complete proteome; Oxidoreductase; Signal.
FT SIGNAL 1 9 Potential.
SQ SEQUENCE 200 AA; 22656 MW; BEE1B67642F2F21D CRC64;

Query Match 53.7%; Score 44; DB 2; Length 200;
Best Local Similarity 60.0%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SITSTGTYHAESVKG 15
DB 77 NIVKTGTTNHAETVK 91

RESULT 33
Q6MZU6_HUMAN Q6MZU6_HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -, mRNA.
DR HSSP; P01861; IADQ.

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DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGL1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C6E8EA0ABC CRC64;

Query Match 53.7%; Score 44; DB 2; Length 464;
 Best Local Similarity 55.6%; Pred. No. 96;
 Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
 QY 1 SITSTGGT--YHAEVSKG 16
 | : | | | : | : | | |
 DB 69 SFSSRRGGSYEYVADSVKG 86

RESULT 34

Q17794_CAEEL
 ID Q17794_CAEEL PRELIMINARY; PRT; 577 AA.

AC Q17794;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DT Pctaire class cell cycle kinase protein 1, isoform a (Pct-1).
 GN Name=pct-1; ORFNames=C07G1.3;
 GN Caenorhabditis elegans.
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RC Boxem M., Srinivasan D.G., van den Heuvel S.;
 RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Bristol N2;
 RA Boxem M., Srinivasan D.G., van den Heuvel S.;
 RT "The Caenorhabditis elegans gene ncc-1 encodes a cdc2-related kinase
 RT required for M phase in meiotic and mitotic cell divisions, but not
 RT for S phase.";
 RL Development 0:0-0(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; U58751; AAB00656.1; -; Genomic DNA.
 DR EMBL; AF129110; RAD37120.1; -; mRNA.
 DR PIR; T15445; T15445.
 DR HSSP; P24941; 1010.
 DR Ensemble; C07G1.3; Caenorhabditis elegans.
 DR WormBase; WBGene0003961; pct-1.
 DR WormPep; C07G1.3a; C06779.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot.kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Complete proteome; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 577 AA; 65483 MW; 70DB3A0F435A0ACF CRC64;
 Query Match 53.7%; Score 44; DB 2; Length 577;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SITSTGGTTHAEVSKG 16
 | | | | | : | | : |
 DB 21 SITSSGGSYDSDCRG 36

RESULT 35

Q4PCS7_USTMA

ID Q4PCS7_USTMA PRELIMINARY; PRT; 1413 AA.
 AC Q4PCS7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=UM02086.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RP STRAIN=521;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Bittshateyn B., Bloom T., Blye J., Boguslavsky L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshateang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Buffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gniese A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabelli R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond P.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougne C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataravan V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.;
 RT "The genome sequence of Ustilago maydis.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACF01000077; EAK83070.1; -; Genomic DNA.
 KW Hypothetical protein.

```
SQ SEQUENCE 1413 AA; 151731 MW; 2DB6FEBB7917FBA0 CRC64;
Query Match 53.7%; Score 44; DB 2; Length 1413;
Best Local Similarity 46.7%; Pred. No. 3.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SITSTGGTYHAESVK 15
:: ||||| :||| :|
Db 1396 TVASTGGVGFHAPMLK 1410

RESULT 36
CHD3 HUMAN STANDARD; PRT; 1944 AA.
AC Q12873;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chromodomain helicase-DNA-binding protein 3 (CHD-3) (Mi-2 autoantigen
DE 240 kDa protein) (M12-alpha).
GN Name=CHD3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal;
RX MEDLINE=97470991; PubMed=9326634; DOI=10.1073/pnas.94.21.11472;
RA Woodage T., Basrai M.A., Baxevanis A.D., Hieter P., Collins F.S.;
RT "Characterization of the CHD family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 121-654.
RC TISSUE=Thymus;
RX MEDLINE=96013633; PubMed=7560064;
RA Ge Q., Nilasena D.S., O'Brien C.A., Frank M.B., Targoff I.N.;
RT "Molecular analysis of a major antigenic region of the 240 kD protein
RT of Mi-2 autoantigen.";
RL J. Clin. Invest. 96:1730-1737(1995).
RN [3]
RP INTERACTION WITH TRIM28.
RX PubMed=1230151; DOI=10.1101/gad.869501;
RA Schultz D.C., Friedman J.R., Rauscher F.J. III;
RT "Targeting histone deacetylase complexes via KRAB-zinc finger
RT proteins: the PHD and bromodomains of KAP-1 form a cooperative unit
RT that recruits a novel isoform of the Mi-2alpha subunit of NuRD.";
RL Genes Dev. 15:428-443(2001).
RN [4]
RP INTERACTION WITH PAIRBP1.
RX PubMed=12505151; DOI=10.1016/S0014-5793(02)03737-7;
RA Lenos T.A., Passos D.O., Nery F.C., Kobarg J.;
RT "Characterization of a new family of proteins that interact with the
RT C-terminal region of the chromatin-remodeling factor CHD-3.";
RL FEBS Lett. 533:14-20(2003).
RN [5]
RP PHOSPHORYLATION SITES SER-713 AND SER-1601.
RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
RA Beaulieu S.A., Jedrychowski M., Schwartz D., Elias J.E., Willen J.,
RA Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
RT "Large-scale characterization of HeLa cell nuclear phosphoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
CC -!- FUNCTION: Probable transcription regulator.
CC -!- SUBUNIT: Central component of the nucleosome remodelling and
CC histone deacetylase (NuRD) repressive complex. Interacts with
CC TRIM28 and PAIRBP1.
CC -!- INTERACTION:
CC Q8NC53:PAI-RBP1; NbExp=4; IntAct=EBI-523590, EBI-523558;
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: One of the main antigens reacting with anti-MI-2 positive
CC sera of dermatomyositis.
CC -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
```

```
CC CC -!- SIMILARITY: Contains 2 chromo domains.
CC CC -!- SIMILARITY: Contains 2 PHD-type zinc fingers.
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC CC EMBL; AF006515; AAB87383.1; -; mRNA.
CC DR EMBL; U08379; AAC50228.1; -; mRNA.
CC DR HSSP; Q14839; 1MM2.
CC DR SMR; Q12873; 453-508.
CC DR IntAct; Q12873; -.
CC DR Ensembl; ENSG00000170004; Homo sapiens.
CC DR HGNC; HGNC:1918; CHD3.
CC DR MIM; 602120; -.
CC DR GO; GO:0004003; F:ATP-dependent DNA helicase activity; TAS.
CC DR GO; GO:0003677; F:DNA binding; TAS.
CC DR GO; GO:0008270; F:zinc ion binding; TAS.
CC DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .); TAS.
CC DR GO; GO:0006357; P:regulation of transcription from RNA polyme. .; TAS.
CC DR InterPro; IPR012957; CHDC12.
CC DR InterPro; IPR012958; CHDNT.
CC DR InterPro; IPR000953; Chromo.
CC DR InterPro; IPR011545; DEAD/DEAH_N.
CC DR InterPro; IPR002464; DEAH_box_.
CC DR InterPro; IPR009462; DUF1086.
CC DR InterPro; IPR009463; DUF1087.
CC DR InterPro; IPR001650; Helicase_C.
CC DR InterPro; IPR000330; SNF2_N_.
CC DR InterPro; IPR001965; Znf_PHD.
CC DR InterPro; IPR001841; Znf_RING.
CC DR Pfam; PF08074; CHDCT2; 1.
CC DR Pfam; PF08073; CHDNT; 1.
CC DR Pfam; PF00385; Chromo; 1.
CC DR Pfam; PF06461; DUF1086; 1.
CC DR Pfam; PF06465; DUF1087; 1.
CC DR Pfam; PF00271; Helicase_C; 1.
CC DR Pfam; PF00628; PHD; 2.
CC DR Pfam; PF00176; SNF2_N; 1.
CC DR SMART; SM00298; CHROMO; 2.
CC DR SMART; SM00487; DEXDC; 1.
CC DR SMART; SM00490; HELICC; 1.
CC DR SMART; SM00249; PHD; 2.
CC DR SMART; SM00184; RING; 2.
CC DR PROSITE; PS00598; CHROMO_1; 1.
CC DR PROSITE; PS50013; CHROMO_2; 2.
CC DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
CC DR PROSITE; PS01359; ZF_PHD_1; 2.
CC DR PROSITE; PS00016; ZF_PHD_2; 2.
CC KW Antigen; ATP-binding; Chromatin regulator; DNA-binding; Helicase;
KW Hydrolase; Metal-binding; Nuclear protein; Nucleotide-binding;
KW Phosphorylation; Repeat; transcription; transcription regulation;
KW Zinc; zinc-finger.
FT DOMAIN 494 594 Chromo 1.
FT DOMAIN 631 673 Chromo 2.
FT ZN_FING 379 426 PHD-type 1.
FT ZN_FING 456 503 PHD-type 2.
FT NP_BIND 761 768 ATP (potential).
FT MOTIF 883 886 DEAH box.
FT COMPBIAS 206 221 DEAH box.
FT COMPBIAS 243 246 Poly-Ala.
FT COMPBIAS 355 358 Poly-Pro.
FT COMPBIAS 434 446 Poly-Lys.
FT COMPBIAS 697 703 Poly-Glu.
FT MOD_RES 713 713 Poly-Lys.
FT MOD_RES 1601 1601 Phosphoserine.
FT CONFLICT 121 126 GEGDGG -> PHFOCK (in Ref. 2).
FT CONFLICT 309 312 Missing (in Ref. 2).
FT CONFLICT 653 653 W -> G (in Ref. 2).
FT SEQUENCE 1944 AA; 220692 MW; 0712E6FIDSf7D335 CRC64;
```

Query Match 53.7%; Score 44; DB 1; Length 1944;
 Best Local Similarity 53.3%; Pred. No. 4.5e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
 ||:||||| :||
 Db 729 ITATGTLHMYQLEG 743

RESULT 37
 Q9Y410 HUMAN
 ID Q9Y410_HUMAN PRELIMINARY; PRT; 2000 AA.
 AC Q9Y410;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Zinc-finger helicase.
 GN Name=hZFH;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Aubry F., Mattei M.G., Galibert F.;
 RT "Identification of a human 17p-located cDNA encoding a protein of the
 RL Eur. J. Biochem. 254:558-564 (1998).
 CC -I- INTERACTION;
 CC Q99728:BAARD1; NbExp=1; IntAct=EBI-473114, EBI-473181;
 CC Q75400:FNBP3; NbExp=1; IntAct=EBI-473114, EBI-473291;
 CC Q9Y2X7:GIT1; NbExp=1; IntAct=EBI-473114, EBI-466061;
 CC P42858:HD; NbExp=1; IntAct=EBI-473114, EBI-466029;
 CC EMBL; U91543; AAC39923.1; -; mRNA.
 DR HSSP; Q14839; IMM2.
 DR SMR; Q9Y410; 453-508.
 DR IntAct; Q9Y410; -.
 DR Ensembl; ENSG00000170004; Homo sapiens.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0004386; F:helicase activity; NAS.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR000953; Chromo.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR002464; DEAD box.
 DR InterPro; IPR009462; DUF1086.
 DR InterPro; IPR009463; DUF1087.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000330; SNF2_N.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF00385; Chromo; 1.
 DR Pfam; PF06461; DUF1086; 1.
 DR Pfam; PF06465; DUF1087; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00628; PHD; 2.
 DR Pfam; PF00176; SNF2_N; 1.
 DR SMART; SM00298; CHROMO; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR SMART; SM00249; PHD; 2.
 DR SMART; SM00184; RING; 2.
 DR PROSITE; PS00598; CHROMO_1; 1.
 DR PROSITE; PS50013; CHROMO_2; 2.
 DR PROSITE; PS00690; DEAD ATP HELICASE; UNKNOWN_1.
 DR PROSITE; PS50016; ZF_PHD_2; 2.
 KW Helicase; Zinc-finger.
 SQ SEQUENCE 2000 AA; 226576 MW; B085A42A5AC7971F CRC64;

Query Match 53.7%; Score 44; DB 2; Length 2000;
 Best Local Similarity 53.3%; Pred. No. 4.6e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ITSTGGTYHAESVKG 16
 ||:||||| :||
 Db 729 ITATGTLHMYQLEG 743

RESULT 38
 Q5NCG1 MOUSE
 ID Q5NCG1_MOUSE PRELIMINARY; PRT; 2055 AA.
 AC Q5NCG1;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Chromodomain helicase DNA binding protein 3.
 GN Name=Chd3; ORFNames=RP23-26L6.13-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bird C.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Wallis J.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL645527; CAI35246.1; -; Genomic_DNA.
 DR EMBL; AL596125; CAI35991.1; -; Genomic_DNA.
 DR EMBL; AL596125; CAI35246.1; JOINED; Genomic_DNA.
 DR EMBL; AL645527; CAI35991.1; JOINED; Genomic_DNA.
 DR SMR; Q5NCG1; 505-560.
 DR GO; GO:0000785; C:chromatin; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003682; F:chromatin binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0006333; P:chromatin assembly or disassembly; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000953; Chromo.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR002464; DEAD box.
 DR InterPro; IPR009462; DUF1086.
 DR InterPro; IPR009463; DUF1087.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000330; SNF2_N.
 DR Pfam; PF00385; Chromo; 1.
 DR Pfam; PF06461; DUF1086; 1.
 DR Pfam; PF06465; DUF1087; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00628; PHD; 2.
 DR Pfam; PF00176; SNF2_N; 1.
 DR SMART; SM00298; CHROMO; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR SMART; SM00249; PHD; 2.
 DR PROSITE; PS00598; CHROMO_1; UNKNOWN_1.
 DR PROSITE; PS50013; CHROMO_2; 2.
 DR PROSITE; PS00690; DEAD ATP HELICASE; UNKNOWN_1.
 DR PROSITE; PS50016; ZF_PHD_2; 2.
 KW Helicase.
 SQ SEQUENCE 2055 AA; 232744 MW; ECFEE5D2D9B1875F CRC64;

Query Match 53.7%; Score 44; DB 2; Length 2055;
 Best Local Similarity 53.3%; Pred. No. 4.8e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
 ||:||||| :||
 Db 781 ITATGTLHMYQLEG 795

```

RESULT 39
Q8URQ5_PEMV PRELIMINARY; PRT; 3068 AA.
ID Q8URQ5_PEMV
AC Q8URQ5;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Pepper mottle virus (PEMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12209;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Florida;
RA Warren C.E., Murphy J.F.;
RT "The complete nucleotide sequence of Pepper mottle virus-Florida
RNA.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF501591; AAM74061.1; -; Genomic_RNA.
DR HSSP; P04517; ILVM.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR001730; Peptidase_C4.
DR InterPro; IPR001456; Peptidase_C6.
DR InterPro; IPR002540; Pept_S30_Poty_P1.
DR InterPro; IPR001592; Poty_coat_PS.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_F3D.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF01577; Poty_P1; 1.
DR Pfam; PF00680; RDRP_1; 1.
DR PRINTS; PR00966; NIAPOTYPASE.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICe; 1.
KW Polyprotein.
FT CHAIN 288 743 helper component proteinase.
FT CHAIN 744 1104 p3 protein.
FT CHAIN 1105 1156 6K1
FT CHAIN 1157 1790 cylindrical inclusion protein.
FT CHAIN 1791 1842 6K2.
FT CHAIN 1843 2276 nuclear inclusion A.
FT CHAIN 2277 2795 nuclear inclusion B.
FT CHAIN 2796 3068 coat protein.
SQ SEQUENCE 3068 AA; 347949 MW; 3913AF2E8BBD3FF3 CRC64;

Query Match 53.7%; Score 44; DB 2; Length 3068;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGTYHAESVK 15
:::|:|:|:|:|
Db 221 VSTWGSTHAESLK 234

RESULT 40
Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
ID Q4VBH1_RAT
HV3C HUMAN
ID HV3C HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565 (1980).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 20-117.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Tsapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human
monoclonal IgM with an antibody activity to myelin-associated
glycoprotein.";
RL Eur. J. Immunol. 23:846-851 (1993).
RN [3]
RP 3D-STRUCTURE MODELING OF 20-117.
RX MEDLINE=86094276; PubMed=3866244;
RA Toyonaga B., Yoshikai Y., Vadasz V., Chin B., Mak T.W.;
RT "Organization and sequences of the diversity, joining, and constant
region genes of the human T-cell receptor beta chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628 (1985)
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; J00236; AAA53516.1; -; Unassigned DNA.
DR EMBL; M35415; AAA58735.1; -; Genomic DNA.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; Model, H-20-117.
DR HGNC; HGNC:5545; IGHV@.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V-III region VH26.
FT DOMAIN 20 >117 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 53.0%; Score 43.5; DB 1; Length 117;
Best Local Similarity 52.9%; Pred. No. 27;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVK 16
:::|:|:|:|:|
Db 69 AISGGSGSTYYGDSVK 85

RESULT 41
Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
ID Q4VBH1_RAT
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AC Q4VBH1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE LOC299354 protein.
GN Name=LOC299354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC095846; AAH95846.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG-v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 467 AA; 51651 MW; 1PF0328F50160BD3 CRC64;

Query Match 53.0%; Score 43.5; DB 2; Length 467;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
Db 69 SINTDGGSTYPPDSVKG 85

RESULT 42
Q5FJZ6 LACAC
ID Q5FJZ6 LACAC PRELIMINARY; PRT; 112 AA.
AC Q5FJZ6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative acyl carrier protein phosphodiesterase.

GN Name=acPD; OrderedLocusNames=LBA1137;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAlliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
Lactobacillus acidophilus NCFM.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3905-3912(2005).
DR EMBL; CP000033; AAV42978.1; -; Genomic_DNA.
DR InterPro; IPR003680; NADHdh_2.
DR Pfam; PF02525; Flavodoxin_2; 1.
KW Complete proteome.
SQ SEQUENCE 112 AA; 12480 MW; 4BE4CEF2F91CC1C5 CRC64;

Query Match 52.4%; Score 43; DB 2; Length 112;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVK 15
Db 43 IQAGGLYHGEGIK 56

RESULT 43
HV3F HUMAN
ID HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: The sequence of the alpha-2, A2m(2) allotype, C
region of this myeloma protein is also given.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A02050; A2HUBU.
CC HSSP; P01783; IIGC.
CC SMR; P01767; 1-115.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
FT Immunoglobulin V region.
DOMAIN 1 111
FT DOMAIN 1 111

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FT  NON TER      115      115
SQ  SEQUENCE     115 AA;  12379 MW;  208876A7DF52DCF4 CRC64;

Query Match      52.4%; Score 43; DB 1; Length 115;
Best Local Similarity 72.7%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  6 GGTGTHAESVKG 16
    | | | | |
Db  55 GTTYADSVKG 65

RESULT 44
Q87MN5_VIBPA PRELIMINARY; PRT; 174 AA.
ID  Q87MN5_VIBPA PRELIMINARY; PRT; 174 AA.
AC  Q87MN5;
DT  01-JUN-2003 (TrEMBLrel. 24, Created)
DT  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Hypothetical protein VP2197.
DE  OrderedLocustNames=VP2197;
GN  Vibrio parahaemolyticus.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC  Vibrionaceae; Vibrio.
OX  NCBI_TaxID=670;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=RIMD 2210633 / Serotype O3:H6;
RX  MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA  Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA  Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA  Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT  "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT  distinct from that of V. cholerae.";
RL  Lancet 361:743-749 (2003).
DR  EMBL; BA000031; BAC60459.1; -; Genomic_DNA.
DR  InterPro; IPR005025; FNM_red.
DR  Pfam; PF03358; FNM_red; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 174 AA; 18652 MW; EF07E18F54116C3E CRC64;

Query Match      52.4%; Score 43; DB 2; Length 174;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 SITSTGGTYHAESVKG 16
    | | | | |
Db  14 SINKTLATYAAEQVKG 29

RESULT 45
Q4NMW9_9DELTA PRELIMINARY; PRT; 268 AA.
ID  Q4NMW9_9DELTA PRELIMINARY; PRT; 268 AA.
AC  Q4NMW9;
DT  13-SEP-2005 (TrEMBLrel. 31, Created)
DT  13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT  13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE  Hypothetical protein.
GN  ORFNames=AdhDRAFT_2825;
OS  Anaeromyxobacter dehalogenans 2CP-C.
OC  Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC  Cytophacterrinae; Myxococcaceae; Anaeromyxobacter.
OX  NCBI_TaxID=290397;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=2CP-C;
RG  US DOE Joint Genome Institute (JGI-PGF);
RA  Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA  Hamon N., Israni S., Pittluck S., Richardson P.;
RT  "Sequencing of the draft genome assembly of Anaeromyxobacter
RT  dehalogenans 2CP-C.";
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN  [2]

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RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=2CP-C;
RG  US DOE Joint Genome Institute (JGI-ORNL);
RA  Larimer F., Land M.;
RT  "Annotation of the draft genome assembly of Anaeromyxobacter
RT  dehalogenans 2CP-C.";
RL  Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AHHD01000007; EAL79977.1; -; Genomic_DNA.
KW  Hypothetical protein.
SQ  SEQUENCE 268 AA; 29625 MW; 73CDD72FB1ADEEBB CRC64;

Query Match      52.4%; Score 43; DB 2; Length 268;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  3 TSTGGTYHAESV 14
    | | | | |
Db  38 TSLGTYNAVSV 49

RESULT 46
Q6ESH7_ORYSA PRELIMINARY; PRT; 398 AA.
ID  Q6ESH7_ORYSA PRELIMINARY; PRT; 398 AA.
AC  Q6ESH7;
DT  25-OCT-2004 (TrEMBLrel. 28, Created)
DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT  10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE  Protein kinase-like.
GN  Name=P0461B08.19; Synonyms=OJ1486 E07.4;
OS  Oryza sativa (japonica cultivar-group).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzaceae; Oryza.
OX  NCBI_TaxID=39947;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Sasaki T., Matsumoto T., Katayose Y.;
RL  Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
RT  clone:OJ1486_E07.";
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC  -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR  EMBL; AP005108; BAD28393.1; -; Genomic_DNA.
DR  EMBL; AP004139; BAD27770.1; -; Genomic_DNA.
DR  Gramene; Q6ESH7; -.
DR  GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR  GO; GO:0005524; F:ATP binding; IEA.
DR  GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR  GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR  GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR  GO; GO:0016567; P:protein ubiquitination; IEA.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  InterPro; IPR001245; Tyr_pkinase.
DR  InterPro; IPR003613; Ubox.
DR  Pfam; PF00069; Pkinase; 1.
DR  Pfam; PF04564; U-box; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKc_1.
DR  SMART; SM00219; TyrKc; 1.
DR  SMART; SM00504; Ubox; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

```

KW ATP-binding; Kinase; Nucleotide-binding;
 SQ Serine/threonine-protein kinase; Transferase.
 SW SEQUENCE 398 AA; 44267 MW; F7D74AD626044E7F CRC64;

Query Match 52.4%; Score 43; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 1.2e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVK 16
 :|||:|:|:|:
 DB 333 IAADGFTYEAIAIK 347

RESULT 47
 Q90Y49 AMME PRELIMINARY; PRT; 403 AA.
 AC Q90Y49;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE POU domain transcription factor brn-1.
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=21541044; PubMed=11685581; DOI=10.1007/s004270100171;
 RA Masi T., Johnson A.D.;
 RT "Axbrn-1: a maternal transcript encodes a POU transcription factor that is later expressed in the developing central nervous system of axolotl embryos."
 RL Dev. Genes Evol. 211:449-452(2001).
 CC EMBL; AF276075; RAL27274.1; -; mRNA.
 DR HSP; F14859; IOCT.
 DR SMR; Q90Y49; 223-369.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeodomain-rel.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR000327; POU.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF00157; POU; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000583; POU; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00352; POU; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00035; POU 1; 1.
 DR PROSITE; PS00465; POU 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 403 AA; 43368 MW; D3C56DC9649447E CRC64;

Query Match 52.4%; Score 43; DB 2; Length 403;
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 VTSVSGVHPSPVK 42
 :|||:|:|:|:
 DB 29 VTSVSGVHPSPVK 42

RESULT 48
 Q519T8 ENTHI PRELIMINARY; PRT; 494 AA.
 ID Q519T8 ENTHI
 AC Q519T8;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=39,t00007;
 OS Entamoeba histolytica HM-1.IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1;IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Almark U.C., Samuelson J., Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T., Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M., Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A., Chillingworth T., Church C., Hance Z., Harris B., Harris D., Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S., Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., Fraser C.M., Hall N.;
 RT "The genome of the protist parasite Entamoeba histolytica."
 RL Nature 433:863-868(2005).
 CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 DR EMBL; AAFB01000160; EAL49615.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 494 AA; 56149 MW; A3500CD0D4213EAB CRC64;

Query Match 52.4%; Score 43; DB 2; Length 494;
 Best Local Similarity 53.3%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVK 16
 :|||:|:|:|:
 DB 86 LTSTGGTKHRVMIAG 100

RESULT 49
 Q929E8 CHLPN PRELIMINARY; PRT; 678 AA.
 ID Q929E8 CHLPN PRELIMINARY;
 AC Q929E8; Q7AJF9; Q7BXV4; Q7DEA8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE (Pyruvate) Oxoisovalerate dehydrogenase Alpha & Beta Fusion (2-oxoisovalerate dehydrogenase, E1 component, alpha and beta subunit)
 DE (2-oxoisovalerate dehydrogenase alpha and beta subunit) ((Pyruvate) oxoisovalerate dehydrogenase alpha and beta fusion).
 GN Name=pdhA/pdhB; Synonyms=pdhA_pdhB;
 GN OrderedLocusNames=CF0743; Cpn0033;
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;
 RA Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.P., White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J., Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C., Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.P.,

RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL pneumoniae A339."; 28:1397-1406 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehlendorfer I., Benesch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J1138;
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314 (2000).
DR EMBL; AE001588; AAD18186.1; -; Genomic DNA.
DR EMBL; AE002233; AAF38548.1; -; Genomic DNA.
DR EMBL; AE017157; AAP97970.1; -; Genomic DNA.
DR EMBL; BA000008; BAA98245.1; -; Genomic DNA.
DR PIR; C86495; C86495.
DR PIR; H72128; H72128.
DR HSSP; Q8ZUR7; 11K6.
DR TIGR; CP0743; -.
DR GO; GO:0016624; F:oxidoreductase activity, acting on the alde. .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR InterPro; IPR005476; Transketo_C.
DR InterPro; IPR005475; Transketo_Cen_R.
DR InterPro; IPR009014; Transketo_C_like.
DR Pfam; PF00676; El_dh; 1.
DR Pfam; PF02780; Transketolase_C; 1.
DR Pfam; PF02779; Transket_pyr; 1.
DR Complete proteome; Pyruvate.
KW COMPLETE PROTEOME; Pyruvate.
SQ SEQUENCE 678 AA; 74175 MW; 8F28EBD45EB3FD8 CRC64;

Query Match 52.4%; Score 43; DB 2; Length 678;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGTTHAESVKG 16
|||:|:|:
Db 474 GGPYHSQSIEG 484

RESULT 50
Q8ECD6 SHEON PRELIMINARY; PRT; 758 AA.
ID Q8ECD6;
AC Q8ECD6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Chemotaxis protein.
GN OrderedLocNames=SQ3207;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprial M.,

RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RL Shewanella oneidensis";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015758; AAN56206.1; -; Genomic DNA.
DR HSSP; Q56310; 1159.
DR TIGR; SO3207; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR002545; CHEW.
DR InterPro; IPR004105; H-kinase dim.
DR InterPro; IPR004358; His_kin_like_C.
DR InterPro; IPR008207; Hpt.
DR Pfam; PF01584; CHEW; 1.
DR Pfam; PF02895; H-kinase dim; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01627; Hpt; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR PRODOM; PD003142; Hpt_N; 1.
DR SMART; SM00260; CHEW; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00073; HPT; 1.
DR PROSITE; PS50851; CHEW; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
KW Complete proteome.
SQ SEQUENCE 758 AA; 80821 MW; 968489F630DA2496 CRC64;

Query Match 52.4%; Score 43; DB 2; Length 758;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ITSTGGTVHAESVKG 16
|||:|:|:
Db 589 ITQLNGTVHIDSMKG 603

Search completed: May 11, 2006, 16:35:39
Job time : 186.934 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:37 ; Search time 36.9836 Seconds
(without alignments)
35.767 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82

Sequence: 1 SITSTGGTYHAESVKG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCUTS_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	16	2	US-09-155-106-2
2	71.5	87.2	122	2	US-09-155-106-18
3	71.5	87.2	122	2	US-09-155-106-19
4	71.5	87.2	122	2	US-09-155-106-20
5	71.5	87.2	122	2	US-09-155-106-26
6	71.5	87.2	122	2	US-09-155-106-32
7	53	64.6	97	2	US-10-194-975-48
8	53	64.6	97	2	US-09-534-717-617
9	53	64.6	97	2	US-09-534-717-618
10	52.5	64.0	118	1	US-08-958-201-2
11	52.5	64.0	118	1	US-08-958-201-4
12	51	62.2	88	2	US-09-840-459-51
13	51	62.2	88	2	US-09-497-625A-51
14	51	62.2	131	1	US-08-259-372A-4
15	51	62.2	131	1	US-08-468-671-4
16	50.5	61.6	17	1	US-08-264-093-22
17	50.5	61.6	17	2	US-09-424-840B-72
18	50.5	61.6	17	2	US-09-424-840B-88
19	50.5	61.6	98	2	US-09-534-717-620
20	50.5	61.6	98	2	US-09-534-717-621
21	50.5	61.6	98	2	US-09-534-717-633
22	50.5	61.6	98	2	US-09-534-717-634
23	50.5	61.6	118	1	US-08-652-816A-11
24	50.5	61.6	120	1	US-08-428-193-14
25	50.5	61.6	121	2	US-09-424-840B-26
26	50.5	61.6	126	1	US-08-276-852-145
27	50.5	61.6	126	1	US-08-899-575-145

28	50.5	61.6	126	1	US-08-899-575-145	Sequence 145, App
29	50.5	61.6	126	4	PCT-US95-08743-145	Sequence 145, App
30	50.5	61.6	268	2	US-09-976-118-1	Sequence 1, Appli
31	50	61.0	102	1	US-08-273-146-65	Sequence 65, Appl
32	49	59.8	95	2	US-09-043-514-2	Sequence 2, Appli
33	49	59.8	97	2	US-10-194-975-29	Sequence 29, Appl
34	49	59.8	97	2	US-10-194-975-31	Sequence 31, Appl
35	49	59.8	97	2	US-09-534-717-616	Sequence 616, App
36	49	59.8	116	2	US-08-545-809A-135	Sequence 135, App
37	49	59.8	116	2	US-09-515-697-135	Sequence 135, App
38	48.5	59.1	98	2	US-09-534-717-622	Sequence 622, App
39	48.5	59.1	118	2	US-08-545-809A-145	Sequence 145, App
40	48.5	59.1	118	2	US-09-515-697-145	Sequence 145, App
41	48	58.5	129	2	US-09-563-222C-51	Sequence 51, Appl
42	48	58.5	127	2	US-09-840-459-87	Sequence 87, Appl
43	48	58.5	135	2	US-09-497-625A-87	Sequence 87, Appl
44	48	58.5	135	2	US-08-579-378A-16	Sequence 16, Appl
45	48	58.5	135	2	US-08-579-378A-20	Sequence 20, Appl
46	48	58.5	263	2	US-09-069-821-3	Sequence 3, Appli
47	48	58.5	263	2	US-09-956-086-3	Sequence 3, Appli
48	48	58.5	263	2	US-09-956-087-3	Sequence 3, Appli
49	48	58.5	283	2	US-09-420-592A-6	Sequence 6, Appli
50	48	58.5	283	2	US-09-985-442-6	Sequence 6, Appli
51	48	58.5	283	2	US-09-983-580-6	Sequence 6, Appli
52	48	58.5	443	4	PCT-US96-13152-4	Sequence 4, Appli
53	48	58.5	533	2	US-10-104-047-3224	Sequence 3224, Ap
54	47.5	57.9	17	2	US-09-192-854-10	Sequence 10, Appl
55	47.5	57.9	17	2	US-09-424-840B-107	Sequence 107, App
56	47.5	57.9	17	2	US-09-511-939-14	Sequence 14, Appl
57	47.5	57.9	17	2	US-09-511-939-38	Sequence 38, Appl
58	47.5	57.9	17	2	US-09-511-939-68	Sequence 68, Appl
59	47.5	57.9	17	2	US-09-511-939-74	Sequence 74, Appl
60	47.5	57.9	17	2	US-09-511-939-80	Sequence 80, Appl
61	47.5	57.9	17	2	US-09-511-939-86	Sequence 86, Appl
62	47.5	57.9	17	2	US-09-511-939-92	Sequence 92, Appl
63	47.5	57.9	17	2	US-09-511-939-122	Sequence 122, App
64	47.5	57.9	17	2	US-09-511-939-128	Sequence 128, App
65	47.5	57.9	17	2	US-09-511-939-134	Sequence 134, App
66	47.5	57.9	17	2	US-09-511-939-140	Sequence 140, App
67	47.5	57.9	17	2	US-09-511-939-146	Sequence 146, App
68	47.5	57.9	17	2	US-09-511-939-188	Sequence 188, App
69	47.5	57.9	17	2	US-09-511-939-194	Sequence 194, App
70	47.5	57.9	17	2	US-09-511-939-212	Sequence 212, App
71	47.5	57.9	17	2	US-09-511-939-218	Sequence 218, App
72	47.5	57.9	17	2	US-09-511-939-236	Sequence 236, App
73	47.5	57.9	17	2	US-09-511-939-260	Sequence 260, App
74	47.5	57.9	17	2	US-09-511-939-266	Sequence 266, App
75	47.5	57.9	17	2	US-09-511-939-272	Sequence 272, App
76	47.5	57.9	17	2	US-09-511-939-284	Sequence 284, App
77	47.5	57.9	17	2	US-09-511-939-296	Sequence 296, App
78	47.5	57.9	17	2	US-09-511-939-308	Sequence 308, App
79	47.5	57.9	17	2	US-09-511-939-314	Sequence 314, App
80	47.5	57.9	98	2	US-10-194-975-22	Sequence 22, Appl
81	47.5	57.9	98	2	US-09-534-717-619	Sequence 619, App
82	47.5	57.9	98	2	US-08-896-535-74	Sequence 74, Appl
83	47.5	57.9	116	1	US-08-428-197-2	Sequence 2, Appli
84	47.5	57.9	116	2	US-08-983-607-36	Sequence 36, Appl
85	47.5	57.9	116	2	US-09-840-459-80	Sequence 80, Appl
86	47.5	57.9	116	2	US-09-497-625A-80	Sequence 80, Appl
87	47.5	57.9	116	4	PCT-US93-10555-2	Sequence 2, Appli
88	47.5	57.9	117	2	US-08-545-809A-109	Sequence 109, App
89	47.5	57.9	117	2	US-08-983-607-46	Sequence 46, Appl
90	47.5	57.9	117	2	US-09-840-459-83	Sequence 83, Appl
91	47.5	57.9	117	2	US-09-497-625A-83	Sequence 83, Appl
92	47.5	57.9	118	1	US-09-515-697-109	Sequence 109, Appl
93	47.5	57.9	120	1	US-08-652-816A-12	Sequence 12, Appl
94	47.5	57.9	120	1	US-08-428-197-20	Sequence 20, Appl
95	47.5	57.9	120	1	US-08-428-197-22	Sequence 22, Appl
96	47.5	57.9	120	1	US-08-428-197-24	Sequence 24, Appl
97	47.5	57.9	120	1	US-08-428-197-26	Sequence 26, Appl
98	47.5	57.9	120	1	US-08-428-197-28	Sequence 28, Appl
99	47.5	57.9	120	1	US-08-428-197-30	Sequence 30, Appl
100	47.5	57.9	120	1	US-08-428-197-32	Sequence 32, Appl

101	47.5	57.9	120	1	US-08-428-197-34	Sequence 34, Appl	174	46	56.1	119	2	US-09-266-119-18	Sequence 18, Appl
102	47.5	57.9	120	1	US-08-428-197-40	Sequence 40, Appl	175	46	56.1	119	2	US-09-266-119-19	Sequence 19, Appl
103	47.5	57.9	120	1	US-09-025-769B-38	Sequence 38, Appl	176	46	56.1	119	2	US-09-266-119-20	Sequence 20, Appl
104	47.5	57.9	120	2	US-09-025-769B-63	Sequence 63, Appl	177	46	56.1	119	2	US-09-266-119-21	Sequence 21, Appl
105	47.5	57.9	120	2	US-09-490-070A-38	Sequence 38, Appl	178	46	56.1	119	2	US-09-266-119-22	Sequence 22, Appl
106	47.5	57.9	120	2	US-09-490-070A-63	Sequence 63, Appl	179	46	56.1	119	2	US-09-266-119-28	Sequence 28, Appl
107	47.5	57.9	120	2	US-09-840-459-85	Sequence 85, Appl	180	46	56.1	119	2	US-09-602-709-18	Sequence 18, Appl
108	47.5	57.9	120	2	US-09-490-153-38	Sequence 38, Appl	181	46	56.1	119	2	US-09-602-709-19	Sequence 19, Appl
109	47.5	57.9	120	2	US-09-490-153-63	Sequence 63, Appl	182	46	56.1	119	2	US-09-602-709-20	Sequence 20, Appl
110	47.5	57.9	120	2	US-09-497-625A-85	Sequence 85, Appl	183	46	56.1	119	2	US-09-602-709-21	Sequence 21, Appl
111	47.5	57.9	120	2	US-09-490-324-38	Sequence 38, Appl	184	46	56.1	119	2	US-09-602-709-22	Sequence 22, Appl
112	47.5	57.9	120	2	US-09-490-324-63	Sequence 63, Appl	185	46	56.1	119	2	US-09-602-709-28	Sequence 28, Appl
113	47.5	57.9	120	4	PCT-US93-10555-20	Sequence 20, Appl	186	46	56.1	121	1	US-08-887-352B-3	Sequence 3, Appl
114	47.5	57.9	120	4	PCT-US93-10555-22	Sequence 22, Appl	187	46	56.1	121	1	US-09-109-207C-3	Sequence 3, Appl
115	47.5	57.9	120	4	PCT-US93-10555-24	Sequence 24, Appl	188	46	56.1	121	2	US-09-296-005-3	Sequence 3, Appl
116	47.5	57.9	120	4	PCT-US93-10555-26	Sequence 26, Appl	189	46	56.1	121	2	US-09-920-171-3	Sequence 3, Appl
117	47.5	57.9	120	4	PCT-US93-10555-28	Sequence 28, Appl	190	46	56.1	121	2	US-09-716-028-3	Sequence 3, Appl
118	47.5	57.9	120	4	PCT-US93-10555-30	Sequence 30, Appl	191	46	56.1	121	2	US-10-113-996-3	Sequence 3, Appl
119	47.5	57.9	120	4	PCT-US93-10555-32	Sequence 32, Appl	192	46	56.1	373	2	US-09-828-995B-35	Sequence 35, Appl
120	47.5	57.9	120	4	PCT-US93-10555-34	Sequence 34, Appl	193	46	56.1	453	2	US-08-466-151-8	Sequence 8, Appl
121	47.5	57.9	120	4	PCT-US93-10555-40	Sequence 40, Appl	194	46	56.1	453	2	US-08-466-163B-8	Sequence 8, Appl
122	47.5	57.9	121	2	US-09-840-459-92	Sequence 92, Appl	195	46	56.1	453	2	US-09-802-096-8	Sequence 8, Appl
123	47.5	57.9	121	2	US-09-497-625A-62	Sequence 62, Appl	196	46	56.1	453	2	US-09-802-077-8	Sequence 8, Appl
124	47.5	57.9	122	1	US-08-958-201-6	Sequence 6, Appl	197	46	56.1	470	2	US-09-925-179-8	Sequence 8, Appl
125	47.5	57.9	123	1	US-08-428-197-38	Sequence 38, Appl	198	46	56.1	470	2	US-09-828-995B-11	Sequence 11, Appl
126	47.5	57.9	124	2	PCT-US93-10555-38	Sequence 38, Appl	199	45.5	55.5	17	2	US-09-424-840B-76	Sequence 76, Appl
127	47.5	57.9	124	2	US-08-983-607-51	Sequence 51, Appl	200	45.5	55.5	116	2	US-09-184-658-48	Sequence 48, Appl
128	47.5	57.9	124	2	US-09-840-459-89	Sequence 89, Appl	201	45.5	55.5	116	2	US-03-504-262D-48	Sequence 48, Appl
129	47.5	57.9	124	2	US-09-497-625A-89	Sequence 89, Appl	202	45.5	55.5	117	1	US-07-942-245-34	Sequence 34, Appl
130	47.5	57.9	125	1	US-08-478-039-99	Sequence 99, Appl	203	45.5	55.5	123	2	US-08-537-871A-24	Sequence 24, Appl
131	47.5	57.9	125	1	US-08-476-349A-99	Sequence 99, Appl	204	45.5	55.5	289	2	US-09-184-658-63	Sequence 63, Appl
132	47.5	57.9	125	1	US-08-428-197-1	Sequence 1, Appl	205	45.5	55.5	289	2	US-09-504-262D-63	Sequence 63, Appl
133	47.5	57.9	125	2	US-09-840-459-76	Sequence 76, Appl	206	45	54.9	17	1	US-07-988-925-2	Sequence 2, Appl
134	47.5	57.9	125	2	US-09-840-459-84	Sequence 84, Appl	207	45	54.9	17	1	US-08-362-780-2	Sequence 2, Appl
135	47.5	57.9	125	2	US-09-497-625A-76	Sequence 76, Appl	208	45	54.9	17	2	US-08-478-684G-2	Sequence 2, Appl
136	47.5	57.9	125	2	US-09-497-625A-64	Sequence 64, Appl	209	45	54.9	98	2	US-09-534-717-600	Sequence 600, App
137	47.5	57.9	125	4	PCT-US93-10555-1	Sequence 1, Appl	210	45	54.9	98	2	US-08-896-535-75	Sequence 75, Appl
138	47.5	57.9	128	2	US-09-840-459-77	Sequence 77, Appl	211	45	54.9	99	2	US-10-194-975-27	Sequence 27, Appl
139	47.5	57.9	128	2	US-09-840-459-79	Sequence 79, Appl	212	45	54.9	111	2	US-09-899-896-7	Sequence 7, Appl
140	47.5	57.9	128	2	US-09-497-625A-77	Sequence 77, Appl	213	45	54.9	113	2	US-08-974-896-6	Sequence 6, Appl
141	47.5	57.9	128	2	US-09-497-625A-79	Sequence 79, Appl	214	45	54.9	113	2	US-09-795-798-6	Sequence 6, Appl
142	47.5	57.9	131	2	US-08-983-607-28	Sequence 28, Appl	215	45	54.9	113	2	US-08-908-469-11	Sequence 11, Appl
143	47.5	57.9	140	2	US-08-983-607-32	Sequence 32, Appl	216	45	54.9	117	2	US-09-157-370-1	Sequence 1, Appl
144	47.5	57.9	144	1	US-08-026-320A-2	Sequence 2, Appl	217	45	54.9	117	2	US-09-025-769B-24	Sequence 24, Appl
145	47.5	57.9	236	2	US-09-458-090A-64	Sequence 64, Appl	218	45	54.9	117	2	US-09-490-070A-24	Sequence 24, Appl
146	47.5	57.9	236	2	US-09-458-090A-104	Sequence 104, App	219	45	54.9	117	2	US-09-490-153-24	Sequence 24, Appl
147	47.5	57.9	236	2	US-09-453-234-64	Sequence 64, App	220	45	54.9	117	2	US-09-490-324-24	Sequence 24, Appl
148	47.5	57.9	236	2	US-09-453-234-104	Sequence 104, App	221	45	54.9	118	2	US-08-545-809A-125	Sequence 125, App
149	47.5	57.9	240	2	US-09-193-854-2	Sequence 2, Appl	222	45	54.9	118	2	US-09-515-697-125	Sequence 125, App
150	47.5	57.9	240	2	US-09-511-939-2	Sequence 2, Appl	223	45	54.9	119	1	US-07-988-925-11	Sequence 11, Appl
151	47.5	57.9	281	2	US-09-025-769B-178	Sequence 178, App	224	45	54.9	119	1	US-08-362-780-11	Sequence 11, Appl
152	47.5	57.9	281	2	US-09-490-070A-178	Sequence 178, App	225	45	54.9	119	1	US-08-362-780-25	Sequence 25, Appl
153	47.5	57.9	281	2	US-09-490-153-178	Sequence 178, App	226	45	54.9	119	2	US-09-648-067A-15	Sequence 15, Appl
154	47.5	57.9	281	2	US-09-490-324-178	Sequence 178, App	227	45	54.9	119	2	US-08-478-684G-11	Sequence 11, Appl
155	47.5	57.9	288	2	US-09-818-247-22	Sequence 22, Appl	228	45	54.9	119	2	US-09-602-812A-6	Sequence 6, Appl
156	47	57.3	288	2	US-09-840-459-78	Sequence 78, Appl	229	45	54.9	122	1	US-07-934-373C-21	Sequence 21, Appl
157	47	57.3	128	2	US-09-497-625A-78	Sequence 78, Appl	230	45	54.9	122	2	US-08-437-642B-21	Sequence 21, Appl
158	47	57.3	131	2	US-08-537-871A-14	Sequence 14, Appl	231	45	54.9	122	2	US-08-146-206C-21	Sequence 21, Appl
159	46.5	56.7	98	2	US-10-194-975-30	Sequence 30, Appl	232	45	54.9	122	2	US-09-705-686-21	Sequence 21, Appl
160	46.5	56.7	126	2	US-08-983-607-26	Sequence 26, Appl	233	45	54.9	122	2	US-09-705-392A-21	Sequence 21, Appl
161	46	56.1	16	2	US-09-170-769A-11	Sequence 11, Appl	234	45	54.9	122	2	US-09-705-398-21	Sequence 21, Appl
162	46	56.1	119	1	US-08-207-996-18	Sequence 18, Appl	235	45	54.9	122	4	PCT-US93-07832-21	Sequence 21, Appl
163	46	56.1	119	1	US-08-207-996-19	Sequence 19, Appl	236	45	54.9	124	2	US-09-530-139-58	Sequence 58, Appl
164	46	56.1	119	1	US-08-207-996-20	Sequence 20, Appl	237	45	54.9	125	2	US-09-266-805-7	Sequence 7, Appl
165	46	56.1	119	1	US-08-207-996-21	Sequence 21, Appl	238	45	54.9	125	2	US-09-554-765-9	Sequence 9, Appl
166	46	56.1	119	1	US-08-207-996-22	Sequence 22, Appl	239	45	54.9	126	2	US-09-554-765-7	Sequence 7, Appl
167	46	56.1	119	1	US-08-207-996-27	Sequence 27, Appl	240	45	54.9	146	2	US-09-554-765-11	Sequence 11, Appl
168	46	56.1	119	1	US-08-760-840A-18	Sequence 18, Appl	241	45	54.9	147	2	US-09-554-765-10	Sequence 10, Appl
169	46	56.1	119	1	US-08-760-840A-19	Sequence 19, Appl	242	45	54.9	408	2	US-09-554-765-15	Sequence 15, Appl
170	46	56.1	119	1	US-08-760-840A-20	Sequence 20, Appl	243	45	54.9	409	2	US-09-554-765-14	Sequence 14, Appl
171	46	56.1	119	1	US-08-760-840A-21	Sequence 21, Appl	244	44.5	54.3	22	2	US-08-918-148-16	Sequence 16, Appl
172	46	56.1	119	1	US-08-760-840A-22	Sequence 22, Appl	245	44.5	54.3	22	2	US-09-138-091A-16	Sequence 16, Appl
173	46	56.1	119	1	US-08-760-840A-28	Sequence 28, Appl	246	44.5	54.3	89	2	US-09-840-459-48	Sequence 48, Appl

247	44.5	54.3	89	2	US-09-497-625A-48	Sequence 48, Appl	320	41.5	50.6	110	2	US-08-545-809A-129	Sequence 129, App
248	44.5	54.3	98	1	US-08-665-202-31	Sequence 31, Appl	321	41.5	50.6	110	2	US-09-515-697-129	Sequence 129, App
249	44.5	54.3	98	2	US-09-315-574-31	Sequence 31, Appl	322	41.5	50.6	158	1	US-08-653-402B-6	Sequence 6, Appl
250	44.5	54.3	98	2	US-10-194-975-17	Sequence 17, Appl	323	41.5	50.6	158	1	US-08-653-402B-10	Sequence 10, Appl
251	44.5	54.3	98	2	US-09-534-717-601	Sequence 601, Appl	324	41	50.0	114	2	US-10-014-012-215	Sequence 215, App
252	44.5	54.3	98	2	US-09-534-717-639	Sequence 639, Appl	325	41	50.0	115	1	US-08-379-057-31	Sequence 31, Appl
253	44.5	54.3	112	1	US-08-211-202-133	Sequence 133, Appl	326	41	50.0	115	2	US-08-545-809A-122	Sequence 122, App
254	44.5	54.3	117	1	US-08-428-197-36	Sequence 36, Appl	327	41	50.0	115	2	US-09-515-697-122	Sequence 122, App
255	44.5	54.3	117	2	US-08-545-809A-99	Sequence 99, Appl	328	41	50.0	138	1	US-08-379-057-14	Sequence 14, Appl
256	44.5	54.3	117	2	US-09-515-697-99	Sequence 99, Appl	329	41	50.0	641	1	US-09-107-532A-6094	Sequence 6094, Ap
257	44.5	54.3	117	4	PCT-US93-10555-36	Sequence 36, Appl	330	41	50.0	979	2	US-10-104-047-2446	Sequence 2446, Ap
258	44.5	54.3	122	1	US-08-276-852-80	Sequence 80, Appl	331	40.5	49.4	17	2	US-09-192-854-37	Sequence 37, Appl
259	44.5	54.3	122	1	US-08-899-575-80	Sequence 80, Appl	332	40.5	49.4	17	2	US-09-192-854-96	Sequence 96, Appl
260	44.5	54.3	122	1	US-08-899-575-80	Sequence 80, Appl	333	40.5	49.4	17	2	US-09-511-933-56	Sequence 56, Appl
261	44.5	54.3	122	4	PCT-US95-08743-80	Sequence 80, Appl	334	40.5	49.4	17	2	US-09-511-933-170	Sequence 170, App
262	44.5	54.3	123	1	US-08-665-202-30	Sequence 30, Appl	335	40.5	49.4	120	2	US-09-232-290-38	Sequence 38, Appl
263	44.5	54.3	123	2	US-09-315-574-30	Sequence 30, Appl	336	40.5	49.4	120	2	US-09-232-290-42	Sequence 42, Appl
264	44.5	54.3	130	2	US-09-225-322B-8	Sequence 8, Appl	337	40.5	49.4	124	2	US-09-518-737-2	Sequence 2, Appl
265	44.5	54.3	130	2	US-09-225-322B-18	Sequence 18, Appl	338	40.5	49.4	456	2	US-09-493-880A-11	Sequence 11, Appl
266	44.5	54.3	130	2	US-09-764-304-8	Sequence 8, Appl	339	40	48.8	50	2	US-09-270-767-35904	Sequence 35904, A
267	44.5	54.3	130	2	US-09-764-304-18	Sequence 18, Appl	340	40	48.8	50	2	US-09-270-767-51121	Sequence 51121, A
268	44.5	54.3	245	2	US-08-918-148-75	Sequence 75, Appl	341	40	48.8	89	2	US-09-840-459-49	Sequence 49, Appl
269	44.5	54.3	245	1	US-09-138-091A-73	Sequence 73, Appl	342	40	48.8	89	2	US-09-497-625A-49	Sequence 49, Appl
270	44	53.7	51	1	US-08-765-179B-3	Sequence 3, Appl	343	40	48.8	98	2	US-09-840-459-38	Sequence 38, Appl
271	44	53.7	97	2	US-09-534-717-658	Sequence 658, App	344	40	48.8	98	2	US-09-840-459-39	Sequence 39, Appl
272	44	53.7	109	1	US-08-379-057-32	Sequence 2, Appl	345	40	48.8	98	2	US-09-497-625A-38	Sequence 38, Appl
273	44	53.7	121	1	US-08-339-582-2	Sequence 32, Appl	346	40	48.8	98	2	US-09-497-625A-39	Sequence 39, Appl
274	44	53.7	1935	2	US-09-949-016-10970	Sequence 10970, A	347	40	48.8	109	1	US-08-793-490-6	Sequence 6, Appl
275	43.5	53.0	98	1	US-08-428-197-48	Sequence 48, Appl	348	40	48.8	110	2	US-09-899-896-5	Sequence 5, Appl
276	43.5	53.0	98	2	US-09-840-459-44	Sequence 44, Appl	349	40	48.8	112	2	US-08-537-871A-31	Sequence 31, Appl
277	43.5	53.0	98	2	US-09-497-625A-44	Sequence 44, Appl	350	40	48.8	115	2	US-08-545-809A-144	Sequence 144, App
278	43.5	53.0	98	2	US-09-534-717-623	Sequence 623, App	351	40	48.8	115	2	US-09-515-697-144	Sequence 144, App
279	43.5	53.0	98	4	PCT-US93-10555-48	Sequence 48, Appl	352	40	48.8	116	1	US-08-888-366-10	Sequence 10, Appl
280	43.5	53.0	119	1	US-08-475-000-16	Sequence 16, Appl	353	40	48.8	116	1	US-08-888-366-12	Sequence 12, Appl
281	43.5	53.0	119	1	US-08-483-199-16	Sequence 16, Appl	354	40	48.8	116	2	US-08-537-871A-18	Sequence 18, Appl
282	43.5	53.0	119	1	US-08-484-508-16	Sequence 16, Appl	355	40	48.8	117	1	US-07-942-245-38	Sequence 38, Appl
283	43.5	53.0	119	2	US-08-983-607-22	Sequence 22, Appl	356	40	48.8	117	2	US-08-752-693A-3	Sequence 3, Appl
284	43.5	53.0	123	2	US-08-537-871A-17	Sequence 17, Appl	357	40	48.8	117	2	US-08-326-362-2	Sequence 2, Appl
285	43.5	53.0	144	2	US-08-537-871A-35	Sequence 35, Appl	358	40	48.8	118	1	US-08-326-362-2	Sequence 2, Appl
286	43	52.4	111	4	PCT-US94-07659-6	Sequence 6, Appl	359	40	48.8	118	2	US-08-379-057-30	Sequence 30, Appl
287	43	52.4	119	4	PCT-US94-07659-6	Sequence 6, Appl	360	40	48.8	118	2	US-09-269-332-45	Sequence 45, Appl
288	43	52.4	124	2	US-08-983-607-47	Sequence 47, Appl	361	40	48.8	118	2	US-09-269-332-56	Sequence 56, Appl
289	43	52.4	124	2	US-09-840-459-81	Sequence 81, Appl	362	40	48.8	118	2	US-09-269-332-88	Sequence 88, Appl
290	43	52.4	124	2	US-09-497-625A-81	Sequence 81, Appl	363	40	48.8	118	2	US-09-269-332-90	Sequence 90, Appl
291	43	52.4	125	2	US-08-537-871A-27	Sequence 27, Appl	364	40	48.8	119	1	US-08-442-542-45	Sequence 45, Appl
292	43	52.4	198	2	US-09-328-352-6436	Sequence 6436, Ap	365	40	48.8	119	2	US-08-765-469-45	Sequence 45, Appl
293	43	52.4	247	4	PCT-US94-07659-2	Sequence 2, Appl	366	40	48.8	120	1	US-07-934-373C-4	Sequence 4, Appl
294	43	52.4	259	2	US-09-742-693-33	Sequence 33, Appl	367	40	48.8	120	2	US-08-437-642B-4	Sequence 4, Appl
295	43	52.4	260	2	US-09-742-693-31	Sequence 31, Appl	368	40	48.8	120	2	US-08-146-206C-4	Sequence 4, Appl
296	43	52.4	260	2	US-09-742-693-32	Sequence 32, Appl	369	40	48.8	120	2	US-09-705-686-4	Sequence 4, Appl
297	43	52.4	410	2	US-09-198-452A-50	Sequence 50, Appl	370	40	48.8	120	2	US-09-705-392A-4	Sequence 4, Appl
298	43	52.4	681	2	US-09-438-185A-35	Sequence 35, Appl	371	40	48.8	128	2	US-09-705-398-4	Sequence 4, Appl
299	42.5	51.8	117	1	US-08-476-349A-97	Sequence 97, Appl	372	40	48.8	128	2	US-09-905-243-69	Sequence 69, Appl
300	42.5	51.8	117	1	US-08-476-349A-97	Sequence 97, Appl	373	40	48.8	131	2	US-10-148-737A-3	Sequence 3, Appl
301	42	51.2	64	2	US-09-479-614-17	Sequence 17, Appl	374	40	48.8	136	1	US-08-253-877C-57	Sequence 57, Appl
302	42	51.2	121	1	US-08-887-352B-4	Sequence 4, Appl	375	40	48.8	136	1	US-08-452-164A-57	Sequence 57, Appl
303	42	51.2	121	2	US-09-109-207C-4	Sequence 4, Appl	376	40	48.8	136	2	US-08-976-183A-31	Sequence 31, Appl
304	42	51.2	121	2	US-09-296-005-4	Sequence 4, Appl	377	40	48.8	136	2	US-08-976-183A-32	Sequence 32, Appl
305	42	51.2	121	2	US-09-920-171-4	Sequence 4, Appl	378	40	48.8	136	2	US-08-976-183A-33	Sequence 33, Appl
306	42	51.2	121	2	US-09-716-028-4	Sequence 4, Appl	379	40	48.8	136	2	US-08-976-183A-34	Sequence 34, Appl
307	42	51.2	121	2	US-10-113-996-4	Sequence 4, Appl	380	40	48.8	137	1	US-08-331-398A-61	Sequence 61, Appl
308	42	51.2	227	1	US-08-681-432-2	Sequence 2, Appl	381	40	48.8	137	1	US-08-331-397B-61	Sequence 61, Appl
309	42	51.2	232	1	US-08-437-642B-26	Sequence 26, Appl	382	40	48.8	137	1	US-08-759-804A-60	Sequence 60, Appl
310	42	51.2	232	2	US-08-437-642B-26	Sequence 26, Appl	383	40	48.8	137	2	US-09-269-332-76	Sequence 76, Appl
311	42	51.2	232	4	PCT-US93-07832-26	Sequence 26, Appl	384	40	48.8	137	2	US-09-269-332-77	Sequence 77, Appl
312	42	51.2	364	2	US-09-270-767-42122	Sequence 42122, A	385	40	48.8	142	2	US-09-069-628-24	Sequence 24, Appl
313	42	51.2	470	2	US-09-291-299A-1	Sequence 1, Appl	386	40	48.8	143	2	US-09-069-628-23	Sequence 23, Appl
314	42	51.2	476	2	US-09-291-299A-3	Sequence 3, Appl	387	40	48.8	145	2	US-09-069-628-26	Sequence 26, Appl
315	42	51.2	496	2	US-09-479-614-2	Sequence 2, Appl	388	40	48.8	150	2	US-08-976-183A-55	Sequence 55, Appl
316	42	51.2	496	2	US-09-479-614-29	Sequence 29, Appl	389	40	48.8	237	1	US-08-224-591-16	Sequence 16, Appl
317	41.5	50.6	17	2	US-09-192-854-164	Sequence 164, App	390	40	48.8	237	1	US-08-926-789-16	Sequence 16, Appl
318	41.5	50.6	17	2	US-09-511-933-290	Sequence 290, App	391	40	48.8	241	1	US-08-224-591-18	Sequence 18, Appl
319	41.5	50.6	97	2	US-09-534-717-661	Sequence 661, App	392	40	48.8	241	1	US-08-926-789-18	Sequence 18, Appl

393	40	48.8	245	2	US-09-069-821-5	Sequence 5, Appli	466	39	47.6	760	2	US-09-949-016-10413	Sequence 10413, A
394	40	48.8	245	2	US-09-956-086-5	Sequence 5, Appli	467	39	47.6	1656	2	US-09-949-016-7247	Sequence 7247, Ap
395	40	48.8	245	2	US-09-956-087-5	Sequence 5, Appli	468	39	47.6	1719	2	US-09-949-016-6966	Sequence 6966, Ap
396	40	48.8	251	2	US-09-902-540-13852	Sequence 13852, A	469	39	47.6	1821	2	US-09-949-016-5938	Sequence 5938, Ap
397	40	48.8	261	2	US-08-768-373-2	Sequence 2, Appli	470	39	47.6	1856	2	US-09-949-016-6964	Sequence 6964, Ap
398	40	48.8	261	2	US-09-849-242A-2	Sequence 2, Appli	471	39	47.6	1880	2	US-09-949-016-5876	Sequence 5876, Ap
399	40	48.8	265	2	US-09-420-592A-5	Sequence 5, Appli	472	39	47.6	1881	2	US-09-949-016-6965	Sequence 6965, Ap
400	40	48.8	265	2	US-09-985-442-5	Sequence 5, Appli	473	39	47.6	1883	2	US-09-949-016-9010	Sequence 9010, Ap
401	40	48.8	265	2	US-09-983-580-5	Sequence 5, Appli	474	39	47.6	1883	2	US-09-949-016-9011	Sequence 9011, Ap
402	40	48.8	516	2	US-09-538-092-236	Sequence 296, App	475	39	47.6	1883	2	US-09-949-016-9012	Sequence 9012, Ap
403	40	48.8	554	2	US-09-248-796A-19033	Sequence 19033, A	476	39	47.6	1883	2	US-09-949-016-9013	Sequence 9013, Ap
404	40	48.8	1290	2	US-09-107-433-4399	Sequence 4399, Ap	477	39	47.6	1883	2	US-09-949-016-9014	Sequence 9014, Ap
405	40	48.8	1303	2	US-09-583-110-5037	Sequence 5037, Ap	478	39	47.6	1883	2	US-09-949-016-9015	Sequence 9015, Ap
406	40	48.8	2780	2	US-10-220-587-2	Sequence 2, Appli	479	39	47.6	1883	2	US-09-949-016-9016	Sequence 9016, Ap
407	39.5	48.2	17	2	US-09-383-667-28	Sequence 28, Appli	480	39	47.6	1883	2	US-09-949-016-9017	Sequence 9017, Ap
408	39.5	48.2	17	2	US-09-192-854-134	Sequence 124, App	481	39.5	47.0	98	1	US-08-211-202-116	Sequence 116, App
409	39.5	48.2	17	2	US-09-511-939-224	Sequence 224, App	482	38.5	47.0	98	2	US-09-840-459-45	Sequence 45, Appli
410	39.5	48.2	110	2	US-10-014-012-217	Sequence 217, App	483	38.5	47.0	98	2	US-09-497-625A-45	Sequence 45, Appli
411	39.5	48.2	123	2	US-09-840-459-82	Sequence 82, Appli	484	38.5	47.0	98	2	US-10-194-975-28	Sequence 28, Appli
412	39.5	48.2	123	2	US-09-497-625A-82	Sequence 82, Appli	485	38.5	47.0	98	2	US-09-534-717-656	Sequence 656, App
413	39.5	48.2	124	1	US-08-276-852-146	Sequence 146, App	486	38.5	47.0	98	2	US-09-534-717-660	Sequence 660, App
414	39.5	48.2	124	1	US-08-899-575-146	Sequence 146, App	487	38.5	47.0	110	1	US-08-211-202-117	Sequence 117, App
415	39.5	48.2	124	1	US-08-899-575-146	Sequence 146, App	488	38.5	47.0	111	1	US-08-211-202-134	Sequence 134, App
416	39.5	48.2	124	4	PCT-US95-08743-146	Sequence 146, App	489	38.5	47.0	113	1	US-07-789-344A-10	Sequence 10, Appli
417	39	47.6	17	2	US-09-192-854-29	Sequence 29, Appli	490	38.5	47.0	117	2	US-08-545-809A-130	Sequence 130, App
418	39	47.6	17	2	US-09-192-854-93	Sequence 93, Appli	491	38.5	47.0	117	2	US-09-515-697-130	Sequence 130, App
419	39	47.6	17	2	US-09-192-854-139	Sequence 139, App	492	38.5	47.0	126	2	US-08-983-607-48	Sequence 48, Appli
420	39	47.6	17	2	US-09-511-939-44	Sequence 44, Appli	493	38.5	47.0	137	2	US-09-019-441A-8	Sequence 8, Appli
421	39	47.6	17	2	US-09-511-939-164	Sequence 164, App	494	38	46.3	17	2	US-09-406-532-16	Sequence 16, Appli
422	39	47.6	17	2	US-09-511-939-248	Sequence 248, App	495	38	46.3	17	2	US-09-534-717-380	Sequence 380, App
423	39	47.6	17	2	US-09-534-717-399	Sequence 389, App	496	38	46.3	28	2	US-09-099-041A-19	Sequence 19, Appli
424	39	47.6	19	1	US-08-737-085A-4	Sequence 4, Appli	497	38	46.3	28	2	US-09-245-281-19	Sequence 19, Appli
425	39	47.6	19	2	US-09-246-258-4	Sequence 4, Appli	498	38	46.3	28	2	US-09-207-359B-19	Sequence 19, Appli
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431	39	47.6	27	2	US-09-532-106-21	Sequence 21, Appli	504	38	46.3	118	2	US-09-406-532-21	Sequence 21, Appli
432	39	47.6	27	2	US-09-839-666-21	Sequence 21, Appli	505	38	46.3	119	1	US-08-192-102-5	Sequence 5, Appli
433	39	47.6	27	2	US-10-372-735-126	Sequence 126, App	506	38	46.3	119	1	US-08-324-799-5	Sequence 5, Appli
434	39	47.6	97	2	US-10-194-975-18	Sequence 18, Appli	507	38	46.3	119	1	US-08-192-861A-5	Sequence 5, Appli
435	39	47.6	97	2	US-09-534-717-638	Sequence 638, App	508	38	46.3	119	2	US-09-133-119-5	Sequence 5, Appli
436	39	47.6	111	2	US-08-537-871A-30	Sequence 30, Appli	509	38	46.3	119	2	US-08-192-093A-5	Sequence 5, Appli
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438	39	47.6	119	2	US-08-767-128-26	Sequence 26, Appli	511	38	46.3	119	2	US-09-756-388B-5	Sequence 5, Appli
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441	39	47.6	123	2	US-09-553-949-1	Sequence 73, Appli	514	38	46.3	123	2	US-09-344-587-13	Sequence 13, Appli
442	39	47.6	128	1	US-08-478-039-73	Sequence 102, App	515	38	46.3	211	1	US-08-575-964-1	Sequence 1, Appli
443	39	47.6	128	1	US-08-478-039-102	Sequence 73, Appli	516	38	46.3	211	1	US-08-963-500-1	Sequence 1, Appli
444	39	47.6	128	1	US-08-476-349A-73	Sequence 73, Appli	517	38	46.3	225	2	US-09-456-093A-68	Sequence 68, Appli
445	39	47.6	128	1	US-08-476-349A-102	Sequence 102, App	518	38	46.3	225	2	US-09-453-234-68	Sequence 68, Appli
446	39	47.6	128	1	US-09-530-139-16	Sequence 16, Appli	519	38	46.3	225	2	US-08-661-052-4	Sequence 4, Appli
447	39	47.6	130	1	US-08-478-039-70	Sequence 70, Appli	520	38	46.3	300	1	US-08-188-082-4	Sequence 4, Appli
448	39	47.6	130	1	US-08-478-039-93	Sequence 93, Appli	521	38	46.3	300	2	US-09-188-082-4	Sequence 4, Appli
449	39	47.6	130	1	US-08-478-349A-70	Sequence 70, Appli	522	38	46.3	300	2	US-09-364-088-4	Sequence 4, Appli
450	39	47.6	130	1	US-08-476-349A-93	Sequence 93, Appli	523	38	46.3	300	2	US-09-102-716-4	Sequence 4, Appli
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452	39	47.6	217	4	PCT-US94-14106-59	Sequence 59, Appli	525	38	46.3	301	2	US-09-188-082-14	Sequence 14, Appli
453	39	47.6	236	2	US-09-530-139-46	Sequence 46, Appli	526	38	46.3	301	2	US-09-364-088-14	Sequence 14, Appli
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455	39	47.6	239	2	US-09-530-139-40	Sequence 40, Appli	528	38	46.3	314	2	US-09-248-796A-18901	Sequence 18901, A
456	39	47.6	250	2	US-09-530-139-44	Sequence 44, Appli	529	38	46.3	317	2	US-09-134-001C-3207	Sequence 3207, Ap
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461	39	47.6	348	2	US-09-646-028-51	Sequence 51, Appli	534	38	46.3	420	2	US-09-543-681A-7921	Sequence 7921, Ap
462	39	47.6	470	2	US-09-859-053-32	Sequence 32, Appli	535	38	46.3	452	2	US-09-252-931A-30368	Sequence 30368, A
463	39	47.6	470	2	US-09-859-053-36	Sequence 36, Appli	536	38	46.3	508	2	US-10-104-047-3233	Sequence 3233, Ap
464	39	47.6	517	2	US-09-107-532A-6058	Sequence 6058, Ap	537	38	46.3	553	1	US-08-494-168-8	Sequence 8, Appli
465	39	47.6	747	2	US-09-949-016-6552	Sequence 6552, Ap	538	38	46.3	553	1	US-08-661-052-16	Sequence 16, Appli

539	38	46.3	553	2	US-09-188-082-16	Sequence 16, Appl	612	37	45.1	119	1	US-08-491-845-2	Sequence 2, Appl
540	38	46.3	553	2	US-09-364-088-16	Sequence 16, Appl	613	37	45.1	119	1	US-08-491-845-10	Sequence 10, Appl
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542	38	46.3	641	2	US-09-134-000C-5865	Sequence 5865, Ap	615	37	45.1	122	2	US-08-483-749A-2	Sequence 2, Appl
543	38	46.3	900	2	US-09-328-352-8072	Sequence 8072, Ap	616	37	45.1	123	1	US-08-478-039-71	Sequence 71, Appl
544	38	46.3	953	2	US-09-099-041A-8	Sequence 8, Appl	617	37	45.1	123	1	US-08-478-039-104	Sequence 104, App
545	38	46.3	953	2	US-09-245-281-8	Sequence 8, Appl	618	37	45.1	123	1	US-08-476-349A-71	Sequence 71, Appl
546	38	46.3	953	2	US-09-207-359B-8	Sequence 8, Appl	619	37	45.1	123	1	US-08-476-349A-104	Sequence 104, App
547	38	46.3	953	2	US-09-340-620A-8	Sequence 8, Appl	620	37	45.1	123	1	US-08-356-272-3	Sequence 3, Appl
548	38	46.3	953	2	US-09-365-364-8	Sequence 8, Appl	621	37	45.1	123	1	US-09-424-840B-10	Sequence 10, Appl
549	38	46.3	953	2	US-09-728-721-8	Sequence 8, Appl	622	37	45.1	125	1	US-08-331-398A-65	Sequence 65, Appl
550	38	46.3	953	2	US-09-949-002-387	Sequence 387, App	623	37	45.1	125	1	US-08-331-397B-65	Sequence 65, Appl
551	38	46.3	953	2	US-10-183-770A-4	Sequence 4, Appl	624	37	45.1	125	1	US-08-759-804A-64	Sequence 64, Appl
552	38	46.3	953	2	US-09-949-002-524	Sequence 524, App	625	37	45.1	128	2	US-09-919-497-69	Sequence 69, Appl
553	38	46.3	966	2	US-09-207-359B-47	Sequence 47, Appl	626	37	45.1	128	2	US-09-949-016-6172	Sequence 6172, Ap
554	38	46.3	966	2	US-09-865-364-47	Sequence 9, Appl	627	37	45.1	129	2	US-09-530-139-24	Sequence 24, Appl
555	38	46.3	1712	2	US-09-961-403-9	Sequence 9, Appl	628	37	45.1	151	2	US-09-564-329A-15	Sequence 15, Appl
556	38	46.3	2471	1	US-08-185-432-16	Sequence 16, Appl	629	37	45.1	151	2	US-09-963-620-15	Sequence 15, Appl
557	38	46.3	2471	1	US-08-083-590A-19	Sequence 19, Appl	630	37	45.1	151	2	US-09-855-632-15	Sequence 15, Appl
558	38	46.3	2471	2	US-08-532-384-19	Sequence 19, Appl	631	37	45.1	151	2	US-09-934-773-15	Sequence 15, Appl
559	38	46.3	2471	2	US-08-899-232-1	Sequence 1, Appl	632	37	45.1	151	2	US-09-855-153-15	Sequence 15, Appl
560	38	46.3	2471	2	US-09-121-457-1	Sequence 1, Appl	633	37	45.1	151	2	US-10-224-720-15	Sequence 15, Appl
561	37.5	45.7	17	2	US-09-192-854-135	Sequence 135, App	634	37	45.1	157	2	US-09-668-097A-12	Sequence 12, Appl
562	37.5	45.7	17	2	US-09-511-939-242	Sequence 242, App	635	37	45.1	163	2	US-09-472-087-13	Sequence 13, Appl
563	37.5	45.7	114	1	US-08-652-558-52	Sequence 52, Appl	636	37	45.1	163	2	US-09-472-087-84	Sequence 84, Appl
564	37.5	45.7	115	4	PCT-US93-10555-42	Sequence 42, Appl	637	37	45.1	175	2	US-09-949-016-11403	Sequence 11403, A
565	37.5	45.7	115	4	US-08-428-197-42	Sequence 42, Appl	638	37	45.1	189	1	US-08-709-912-13	Sequence 13, Appl
566	37.5	45.7	123	2	US-10-083-424-18	Sequence 18, Appl	639	37	45.1	189	1	US-09-047-370-13	Sequence 13, Appl
567	37.5	45.7	375	2	US-09-444-412-2	Sequence 2, Appl	640	37	45.1	191	1	US-08-044-621D-35	Sequence 35, Appl
568	37.5	45.7	375	2	US-09-660-742-12	Sequence 12, Appl	641	37	45.1	191	1	US-08-709-912-11	Sequence 11, Appl
569	37.5	45.7	375	2	US-09-825-414-36	Sequence 36, Appl	642	37	45.1	191	1	US-09-047-370-11	Sequence 11, Appl
570	37.5	45.7	375	2	US-09-825-414-62	Sequence 62, Appl	643	37	45.1	200	1	US-07-744-570B-2	Sequence 2, Appl
571	37.5	45.7	474	2	US-09-848-832-3	Sequence 3, Appl	644	37	45.1	216	1	US-08-315-695-20	Sequence 20, Appl
572	37.5	45.1	17	2	US-09-497-997C-31	Sequence 31, Appl	645	37	45.1	225	2	US-09-071-035-376	Sequence 376, App
573	37	45.1	17	2	US-09-424-840B-63	Sequence 63, Appl	646	37	45.1	225	2	US-10-206-576-376	Sequence 376, App
574	37	45.1	17	2	US-09-424-840B-74	Sequence 74, Appl	647	37	45.1	229	1	US-08-887-352B-20	Sequence 20, Appl
575	37	45.1	21	2	US-09-497-997C-19	Sequence 19, Appl	648	37	45.1	229	2	US-09-109-207C-20	Sequence 20, Appl
576	37	45.1	22	2	US-09-497-997C-4	Sequence 4, Appl	649	37	45.1	229	2	US-09-296-005-20	Sequence 20, Appl
577	37	45.1	22	2	US-09-497-997C-20	Sequence 20, Appl	650	37	45.1	229	2	US-09-920-171-20	Sequence 20, Appl
578	37	45.1	30	2	US-09-336-093-4	Sequence 4, Appl	651	37	45.1	229	2	US-09-716-028-20	Sequence 20, Appl
579	37	45.1	30	2	US-09-557-465D-4	Sequence 4, Appl	652	37	45.1	229	2	US-10-113-996-20	Sequence 20, Appl
580	37	45.1	30	2	US-09-497-997C-7	Sequence 7, Appl	653	37	45.1	233	1	US-08-887-352B-25	Sequence 25, Appl
581	37	45.1	30	2	US-09-720-003C-5	Sequence 5, Appl	654	37	45.1	233	2	US-09-109-207C-25	Sequence 25, Appl
582	37	45.1	30	2	US-10-144-549-21	Sequence 21, Appl	655	37	45.1	233	2	US-09-296-005-25	Sequence 25, Appl
583	37	45.1	31	2	US-09-497-997C-9	Sequence 9, Appl	656	37	45.1	233	2	US-09-920-171-25	Sequence 25, Appl
584	37	45.1	33	2	US-09-497-997C-23	Sequence 23, Appl	657	37	45.1	233	2	US-09-716-028-25	Sequence 25, Appl
585	37	45.1	49	2	US-09-497-997C-10	Sequence 10, Appl	658	37	45.1	233	2	US-10-113-996-25	Sequence 25, Appl
586	37	45.1	87	2	US-09-840-459-53	Sequence 53, Appl	659	37	45.1	240	2	US-09-570-858B-16	Sequence 16, Appl
587	37	45.1	87	2	US-09-497-625A-53	Sequence 53, Appl	660	37	45.1	248	1	US-08-887-352B-22	Sequence 22, Appl
588	37	45.1	98	2	US-09-840-459-41	Sequence 41, Appl	661	37	45.1	248	2	US-09-109-207C-22	Sequence 22, Appl
589	37	45.1	98	2	US-09-497-625A-41	Sequence 41, Appl	662	37	45.1	248	2	US-09-296-005-22	Sequence 22, Appl
590	37	45.1	100	2	US-09-840-459-36	Sequence 36, Appl	663	37	45.1	248	2	US-09-920-171-22	Sequence 22, Appl
591	37	45.1	100	2	US-09-497-625A-36	Sequence 36, Appl	664	37	45.1	248	2	US-09-716-028-22	Sequence 22, Appl
592	37	45.1	107	2	US-09-497-997C-26	Sequence 26, Appl	665	37	45.1	248	2	US-10-113-996-22	Sequence 22, Appl
593	37	45.1	109	2	US-09-949-016-6916	Sequence 6916, Ap	666	37	45.1	252	2	US-09-071-035-374	Sequence 374, App
594	37	45.1	110	2	US-10-014-012-21	Sequence 210, App	667	37	45.1	252	2	US-10-206-576-374	Sequence 374, App
595	37	45.1	110	2	US-10-014-012-21	Sequence 211, App	668	37	45.1	257	2	US-09-252-991A-19163	Sequence 19163, A
596	37	45.1	111	2	US-10-014-012-226	Sequence 226, App	669	37	45.1	267	2	US-09-902-540-12438	Sequence 12438, A
597	37	45.1	112	2	US-10-014-012-212	Sequence 212, App	670	37	45.1	285	2	US-09-318-661-4	Sequence 4, Appl
598	37	45.1	114	1	US-08-887-352B-12	Sequence 12, Appl	671	37	45.1	285	2	US-09-883-758-4	Sequence 4, Appl
599	37	45.1	114	2	US-08-483-749A-10	Sequence 10, Appl	672	37	45.1	298	2	US-09-318-661-2	Sequence 2, Appl
600	37	45.1	114	2	US-09-109-207C-12	Sequence 12, Appl	673	37	45.1	298	2	US-09-883-758-2	Sequence 2, Appl
601	37	45.1	114	2	US-09-296-005-12	Sequence 12, Appl	674	37	45.1	299	2	US-09-540-236-21335	Sequence 2135, Ap
602	37	45.1	114	2	US-09-920-171-12	Sequence 12, Appl	675	37	45.1	309	2	US-09-270-767-46351	Sequence 46351, A
603	37	45.1	114	2	US-09-716-028-12	Sequence 12, Appl	676	37	45.1	322	2	US-09-248-796A-17975	Sequence 17975, A
604	37	45.1	114	2	US-10-113-996-12	Sequence 12, Appl	677	37	45.1	344	1	US-08-468-812-2	Sequence 2, Appl
605	37	45.1	115	1	US-08-468-661-1	Sequence 1, Appl	678	37	45.1	344	2	US-08-590-563-2	Sequence 2, Appl
606	37	45.1	115	1	US-08-466-272A-1	Sequence 1, Appl	679	37	45.1	344	2	US-09-770-621-2	Sequence 2, Appl
607	37	45.1	115	1	US-08-478-857-1	Sequence 1, Appl	680	37	45.1	344	2	US-09-235-832-2	Sequence 2, Appl
608	37	45.1	115	1	US-08-471-771-1	Sequence 1, Appl	681	37	45.1	380	2	US-09-668-097A-26	Sequence 26, Appl
609	37	45.1	115	2	US-09-130-783-1	Sequence 1, Appl	682	37	45.1	395	2	US-09-949-016-8564	Sequence 8564, Ap
610	37	45.1	117	2	US-07-942-245-32	Sequence 32, Appl	683	37	45.1	432	2	US-09-075-087-2	Sequence 2, Appl
611	37	45.1	117	2	US-08-537-871A-26	Sequence 26, Appl	684	37	45.1	432	2	US-09-472-971-1	Sequence 1, Appl

685	37	45.1	433	2	US-09-809-665A-161	Sequence 161, App	758	36	43.9	120	2	US-10-014-012-230	Sequence 230, App
686	37	45.1	435	2	US-09-489-039A-13510	Sequence 13510, A	759	36	43.9	122	1	US-08-276-852-143	Sequence 143, App
687	37	45.1	437	2	US-09-543-681A-6277	Sequence 6277, Ap	760	36	43.9	122	1	US-08-899-575-143	Sequence 143, App
688	37	45.1	451	1	US-08-887-352B-14	Sequence 14, Appl	761	36	43.9	122	1	US-08-899-575-143	Sequence 143, App
689	37	45.1	451	1	US-08-887-352B-16	Sequence 16, Appl	762	36	43.9	122	4	PCT-US95-08743-143	Sequence 143, App
690	37	45.1	451	2	US-08-466-151-65	Sequence 65, Appl	763	36	43.9	134	1	US-07-977-696C-13	Sequence 13, Appl
691	37	45.1	451	2	US-09-109-207C-14	Sequence 14, Appl	764	36	43.9	134	1	US-08-129-930B-13	Sequence 13, Appl
692	37	45.1	451	2	US-09-109-207C-16	Sequence 16, Appl	765	36	43.9	134	1	US-08-976-288A-13	Sequence 13, Appl
693	37	45.1	451	2	US-09-296-005-14	Sequence 14, Appl	766	36	43.9	134	2	US-09-947-839B-13	Sequence 13, Appl
694	37	45.1	451	2	US-09-296-005-16	Sequence 16, Appl	767	36	43.9	141	2	US-09-069-628-25	Sequence 25, Appl
695	37	45.1	451	2	US-09-920-171-14	Sequence 14, Appl	768	36	43.9	144	2	US-09-546-136-5	Sequence 5, Appl
696	37	45.1	451	2	US-09-920-171-16	Sequence 16, Appl	769	36	43.9	191	1	US-08-709-912-10	Sequence 10, Appl
697	37	45.1	451	2	US-09-716-028-14	Sequence 14, Appl	770	36	43.9	191	1	US-09-047-370-10	Sequence 10, Appl
698	37	45.1	451	2	US-09-716-028-16	Sequence 16, Appl	771	36	43.9	196	2	US-09-107-532A-5809	Sequence 5809, Ap
699	37	45.1	451	2	US-10-113-986-14	Sequence 14, Appl	772	36	43.9	206	1	US-08-315-695-19	Sequence 19, Appl
700	37	45.1	451	2	US-10-113-986-16	Sequence 16, Appl	773	36	43.9	215	1	US-08-044-621D-34	Sequence 34, Appl
701	37	45.1	451	2	US-09-925-179-65	Sequence 65, Appl	774	36	43.9	221	2	US-09-252-919A-21282	Sequence 21282, A
702	37	45.1	451	2	US-09-925-179-68	Sequence 68, Appl	775	36	43.9	223	2	US-09-462-246-2	Sequence 2, Appl
703	37	45.1	478	2	US-10-104-047-3812	Sequence 3812, Ap	776	36	43.9	234	2	US-09-436-983-6	Sequence 6, Appl
704	37	45.1	481	2	US-09-603-208A-2	Sequence 2, Appl	777	36	43.9	242	1	US-08-224-591-14	Sequence 14, Appl
705	37	45.1	525	2	US-09-540-236-2855	Sequence 2855, Ap	778	36	43.9	242	1	US-08-392-338A-23	Sequence 23, Appl
706	37	45.1	584	2	US-09-949-016-6402	Sequence 6402, Ap	779	36	43.9	242	1	US-08-926-789-14	Sequence 14, Appl
707	37	45.1	594	2	US-09-949-016-10179	Sequence 10179, A	780	36	43.9	242	2	US-09-166-750-23	Sequence 23, Appl
708	37	45.1	903	2	US-09-252-991A-28775	Sequence 28775, A	781	36	43.9	242	2	US-09-166-093-23	Sequence 23, Appl
709	37	45.1	1157	1	US-07-876-280-30	Sequence 30, Appl	782	36	43.9	242	2	US-09-172-019-23	Sequence 23, Appl
710	37	45.1	1157	1	US-07-812-180A-2	Sequence 2, Appl	783	36	43.9	242	2	US-09-166-094-23	Sequence 23, Appl
711	37	45.1	1157	1	US-08-315-468-2	Sequence 2, Appl	784	36	43.9	242	2	US-09-443-213-23	Sequence 23, Appl
712	37	45.1	1157	2	US-07-941-650A-2	Sequence 2, Appl	785	36	43.9	242	6	5455030-17	Patent No. 5455030
713	37	45.1	1169	1	US-08-315-468-4	Sequence 4, Appl	786	36	43.9	244	1	US-08-392-338A-13	Sequence 13, Appl
714	37	45.1	1331	2	US-09-949-016-6861	Sequence 6861, Ap	787	36	43.9	244	2	US-09-166-750-13	Sequence 13, Appl
715	37	45.1	1935	2	US-09-949-016-10403	Sequence 10403, A	788	36	43.9	244	2	US-09-166-093-13	Sequence 13, Appl
716	36.5	44.5	17	2	US-09-192-854-128	Sequence 128, App	789	36	43.9	244	2	US-09-172-019-13	Sequence 13, Appl
717	36.5	44.5	17	2	US-09-511-939-230	Sequence 230, App	790	36	43.9	244	2	US-09-166-094-13	Sequence 13, Appl
718	36.5	44.5	22	2	US-08-918-148-39	Sequence 39, Appl	791	36	43.9	244	4	PCT-US93-11138-14	Sequence 14, Appl
719	36.5	44.5	22	2	US-09-138-091A-39	Sequence 39, Appl	792	36	43.9	245	2	US-09-342-084-4	Sequence 4, Appl
720	36.5	44.5	98	2	US-10-194-975-21	Sequence 21, Appl	793	36	43.9	250	1	US-08-392-338A-15	Sequence 15, Appl
721	36.5	44.5	98	2	US-09-534-717-657	Sequence 657, App	794	36	43.9	250	2	US-09-166-750-15	Sequence 15, Appl
722	36.5	44.5	98	2	US-09-534-717-659	Sequence 659, App	795	36	43.9	250	2	US-09-166-093-15	Sequence 15, Appl
723	36.5	44.5	117	2	US-08-545-809A-107	Sequence 107, App	796	36	43.9	250	2	US-09-172-019-15	Sequence 15, Appl
724	36.5	44.5	117	2	US-09-515-697-107	Sequence 107, App	797	36	43.9	250	2	US-09-166-094-15	Sequence 15, Appl
725	36.5	44.5	120	4	PCT-US93-07832-4	Sequence 4, Appl	798	36	43.9	250	2	US-09-166-094-15	Sequence 15, Appl
726	36.5	44.5	122	2	US-08-537-871A-22	Sequence 22, Appl	799	36	43.9	250	2	US-09-443-213-15	Sequence 15, Appl
727	36.5	44.5	129	2	US-09-240-274-143	Sequence 143, App	800	36	43.9	253	1	US-08-392-338A-17	Sequence 17, Appl
728	36.5	44.5	129	2	US-09-848-798-143	Sequence 143, App	801	36	43.9	253	2	US-09-166-750-17	Sequence 17, Appl
729	36.5	44.5	136	2	US-08-284-516C-36	Sequence 56, Appl	802	36	43.9	253	2	US-09-166-093-17	Sequence 17, Appl
730	36.5	44.5	136	2	US-09-537-911A-56	Sequence 56, Appl	803	36	43.9	253	2	US-09-172-019-17	Sequence 17, Appl
731	36.5	44.5	144	2	US-09-069-628-13	Sequence 13, Appl	804	36	43.9	253	2	US-09-166-094-17	Sequence 17, Appl
732	36.5	44.5	179	2	US-08-862-124-2	Sequence 2, Appl	805	36	43.9	253	2	US-09-443-213-17	Sequence 17, Appl
733	36.5	44.5	245	2	US-08-918-148-78	Sequence 78, Appl	806	36	43.9	299	2	US-09-270-767-45708	Sequence 45708, A
734	36.5	44.5	245	2	US-09-138-091A-76	Sequence 76, Appl	807	36	43.9	320	1	US-08-362-739-2	Sequence 2, Appl
735	36.5	44.5	287	2	US-08-862-124-17	Sequence 17, Appl	808	36	43.9	320	2	US-08-914-350A-2	Sequence 2, Appl
736	36.5	44.5	304	2	US-08-862-124-14	Sequence 14, Appl	809	36	43.9	335	2	US-09-570-856B-15	Sequence 15, Appl
737	36.5	44.5	1197	2	US-09-618-425-2	Sequence 2, Appl	810	36	43.9	357	2	US-09-270-767-45129	Sequence 45129, A
738	36	43.9	19	1	US-07-977-696C-78	Sequence 78, Appl	811	36	43.9	358	2	US-09-543-681A-7578	Sequence 17956, A
739	36	43.9	19	1	US-08-129-930B-78	Sequence 78, Appl	812	36	43.9	372	2	US-09-252-991A-17956	Sequence 3, Appl
740	36	43.9	19	2	US-08-976-288A-78	Sequence 78, Appl	813	36	43.9	374	2	US-09-436-983-3	Sequence 3, Appl
741	36	43.9	19	2	US-09-947-839B-78	Sequence 78, Appl	814	36	43.9	377	2	US-09-248-796A-14772	Sequence 14772, A
742	36	43.9	35	2	US-08-525-539A-33	Sequence 33, Appl	815	36	43.9	405	2	US-09-252-991A-27573	Sequence 27573, A
743	36	43.9	83	2	US-10-014-012-223	Sequence 22, App	816	36	43.9	418	2	US-09-328-352-5700	Sequence 5700, Ap
744	36	43.9	97	2	US-09-534-717-615	Sequence 615, Appl	817	36	43.9	461	2	US-09-252-991A-24456	Sequence 24456, A
745	36	43.9	98	2	US-09-627-896B-32	Sequence 32, Appl	818	36	43.9	508	2	US-09-489-039A-13575	Sequence 13575, A
746	36	43.9	100	2	US-09-840-459-35	Sequence 35, Appl	819	36	43.9	509	2	US-09-833-745-34	Sequence 34, Appl
747	36	43.9	100	2	US-09-497-625A-35	Sequence 35, Appl	820	36	43.9	511	2	US-09-833-745-35	Sequence 35, Appl
748	36	43.9	109	1	US-07-942-245-21	Sequence 21, Appl	821	36	43.9	513	2	US-09-833-745-47	Sequence 47, Appl
749	36	43.9	110	2	US-09-471-276-868	Sequence 868, App	822	36	43.9	513	2	US-09-833-745-48	Sequence 48, Appl
750	36	43.9	115	2	US-10-014-012-222	Sequence 22, App	823	36	43.9	513	2	US-09-833-745-51	Sequence 51, Appl
751	36	43.9	116	2	US-08-545-809A-101	Sequence 101, App	824	36	43.9	513	2	US-09-833-745-53	Sequence 53, Appl
752	36	43.9	116	2	US-09-515-697-101	Sequence 101, App	825	36	43.9	513	2	US-09-833-745-54	Sequence 54, Appl
753	36	43.9	118	1	US-08-652-816A-13	Sequence 13, Appl	826	36	43.9	513	2	US-09-252-991A-33046	Sequence 33046, A
754	36	43.9	118	2	US-09-232-290-58	Sequence 58, Appl	827	36	43.9	515	2	US-09-328-352-5090	Sequence 5090, Ap
755	36	43.9	119	2	US-08-875-674A-1	Sequence 1, Appl	828	36	43.9	525	2	US-09-107-532A-5095	Sequence 5095, Ap
756	36	43.9	119	2	US-08-875-674A-3	Sequence 3, Appl	829	36	43.9	525	2	US-09-252-991A-26876	Sequence 26876, A
757	36	43.9	120	2	US-10-194-975-114	Sequence 114, App	830	36	43.9	577	2		

831	724	2	US-09-121-964-1	Sequence 1, Appli	904	35	42.7	292	2	US-09-328-352-7538	Sequence 7538, Ap
832	741	2	US-09-302-540-15369	Sequence 15369, A	905	35	42.7	309	2	US-09-079-029-9	Sequence 9, Appli
833	844	2	US-09-252-991A-27184	Sequence 27184, A	906	35	42.7	316	1	US-08-038-932B-1	Sequence 1, Appli
834	879	2	US-09-543-681A-6067	Sequence 6067, Ap	907	35	42.7	316	1	US-08-656-349-1	Sequence 1, Appli
835	901	2	US-09-134-001C-5351	Sequence 5351, Ap	908	35	42.7	316	1	US-08-682-643-4	Sequence 4, Appli
836	951	2	US-09-924-097A-15	Sequence 15, Appl	909	35	42.7	316	2	US-09-104-623A-5	Sequence 5, Appli
837	951	2	US-09-252-991A-32439	Sequence 32439, A	910	35	42.7	316	2	US-09-019-532-5	Sequence 5, Appli
838	1118	2	US-08-479-722B-2	Sequence 2, Appli	911	35	42.7	316	2	US-09-338-746-5	Sequence 5, Appli
839	1833	2	US-09-592-685-2	Sequence 2, Appli	912	35	42.7	333	2	US-09-902-540-10638	Sequence 10638, A
840	1833	4	PCT-US95-02251-18	Sequence 18, Appl	913	35	42.7	333	2	US-09-393-627B-28	Sequence 28, Appl
841	1912	2	US-08-913-832A-2	Sequence 2, Appli	914	35	42.7	373	2	US-09-489-039A-11774	Sequence 11774, A
842	1912	2	US-09-249-181A-2	Sequence 2, Appli	915	35	42.7	381	2	US-09-216-295-22	Sequence 22, Appl
843	1912	2	US-09-158-707-2	Sequence 2, Appli	916	35	42.7	381	2	US-09-632-570-22	Sequence 22, Appl
844	5179	2	US-09-538-092-1258	Sequence 1258, Ap	917	35	42.7	381	2	US-09-632-575-52	Sequence 52, Appl
845	35.5	43.3	US-09-192-854-103	Sequence 103, App	918	35	42.7	430	2	US-09-513-151A-2	Sequence 2, Appli
846	35.5	43.3	US-09-511-939-182	Sequence 182, App	919	35	42.7	476	2	US-09-252-991A-28457	Sequence 28457, A
847	35.5	43.3	US-09-534-717-352	Sequence 352, App	920	35	42.7	479	2	US-09-902-540-15979	Sequence 15979, A
848	35.5	43.3	US-09-534-717-366	Sequence 366, App	921	35	42.7	483	2	US-09-904-615-154	Sequence 154, App
849	35.5	43.3	US-08-749-816-14	Sequence 14, Appl	922	35	42.7	483	2	US-10-054-988-154	Sequence 154, App
850	35.5	43.3	US-09-144-914-18	Sequence 18, Appl	923	35	42.7	501	2	US-09-270-767-42045	Sequence 42045, A
851	35.5	43.3	US-08-398-613A-22	Sequence 22, Appl	924	35	42.7	521	2	US-09-248-796A-19002	Sequence 19002, A
852	35.5	43.3	US-08-398-612A-22	Sequence 22, Appl	925	35	42.7	529	2	US-09-328-352-5049	Sequence 5049, Ap
853	35.5	43.3	US-08-398-611A-22	Sequence 22, Appl	926	35	42.7	585	2	US-09-134-000C-5945	Sequence 5945, Ap
854	35.5	43.3	US-08-491-334A-22	Sequence 22, Appl	927	35	42.7	650	2	US-09-107-532A-5521	Sequence 5521, Ap
855	35.5	43.3	US-09-027-449-19	Sequence 19, Appl	928	35	42.7	795	2	US-09-198-452A-314	Sequence 314, App
856	35.5	43.3	US-08-804-444A-19	Sequence 19, Appl	929	35	42.7	795	2	US-09-438-185A-302	Sequence 302, App
857	35.5	43.3	US-09-026-985-19	Sequence 19, Appl	930	35	42.7	795	2	US-09-198-452A-500	Sequence 500, App
858	35.5	43.3	US-09-121-952A-19	Sequence 19, Appl	931	35	42.7	940	2	US-09-438-185A-468	Sequence 468, App
859	35.5	43.3	US-09-234-340A-19	Sequence 19, Appl	932	35	42.7	1048	2	US-09-252-991A-29368	Sequence 29368, A
860	35.5	43.3	US-09-355-014-19	Sequence 19, Appl	933	35	42.7	2777	2	US-10-220-587-4	Sequence 4, Appli
861	35.5	43.3	US-09-489-039A-13912	Sequence 13912, A	934	34.5	42.1	17	2	US-09-339-922A-102	Sequence 102, App
862	35.5	43.3	US-09-328-352-4304	Sequence 4304, Ap	935	34.5	42.1	17	2	US-09-339-922A-104	Sequence 104, App
863	35.5	43.3	US-08-398-612A-30	Sequence 30, Appl	936	34.5	42.1	17	2	US-09-497-997C-32	Sequence 32, Appl
864	35.5	43.3	US-08-398-611A-30	Sequence 30, Appl	937	34.5	42.1	17	2	US-09-192-854-64	Sequence 64, Appl
865	35.5	43.3	US-08-491-334A-30	Sequence 30, Appl	938	34.5	42.1	17	2	US-09-511-939-104	Sequence 104, App
866	35.5	43.3	US-09-027-449-27	Sequence 27, Appl	939	34.5	42.1	17	2	US-09-534-717-388	Sequence 388, App
867	35.5	43.3	US-08-804-444A-27	Sequence 27, Appl	940	34.5	42.1	23	2	US-09-497-997C-6	Sequence 6, Appli
868	35.5	43.3	US-09-026-985-27	Sequence 27, Appl	941	34.5	42.1	23	2	US-09-497-997C-22	Sequence 22, Appl
869	35.5	43.3	US-09-121-952A-27	Sequence 27, Appl	942	34.5	42.1	110	2	US-09-497-997C-22	Sequence 22, Appl
870	35.5	43.3	US-09-234-340A-27	Sequence 27, Appl	943	34.5	42.1	117	2	US-09-339-922A-2	Sequence 2, Appli
871	35.5	43.3	US-09-355-014-27	Sequence 27, Appl	944	34.5	42.1	117	2	US-09-339-922A-6	Sequence 6, Appli
872	35.5	43.3	US-08-398-613A-30	Sequence 30, Appl	945	34.5	42.1	117	2	US-08-791-391A-2	Sequence 2, Appli
873	35	42.7	US-09-424-840B-64	Sequence 64, Appl	946	34.5	42.1	117	2	US-08-791-391A-6	Sequence 6, Appli
874	35	42.7	US-10-226-795-34	Sequence 34, Appl	947	34.5	42.1	117	2	US-09-016-061-2	Sequence 2, Appli
875	35	42.7	US-09-534-717-360	Sequence 360, App	948	34.5	42.1	117	2	US-09-016-061-6	Sequence 6, Appli
876	35	42.7	US-09-252-991A-29912	Sequence 29912, A	949	34.5	42.1	142	1	US-08-860-174A-7	Sequence 7, Appli
877	35	42.7	US-10-194-975-20	Sequence 20, Appl	950	34.5	42.1	225	2	US-09-456-090A-56	Sequence 56, Appl
878	35	42.7	US-09-534-717-599	Sequence 599, App	951	34.5	42.1	225	2	US-09-456-090A-60	Sequence 60, Appl
879	35	42.7	US-09-534-717-611	Sequence 611, App	952	34.5	42.1	225	2	US-09-456-090A-92	Sequence 92, Appl
880	35	42.7	US-08-652-816A-14	Sequence 14, Appl	953	34.5	42.1	225	2	US-09-456-090A-100	Sequence 100, App
881	35	42.7	US-08-545-809A-106	Sequence 106, App	954	34.5	42.1	225	2	US-09-456-090A-106	Sequence 106, App
882	35	42.7	US-09-515-697-106	Sequence 106, App	955	34.5	42.1	225	2	US-09-453-234-56	Sequence 56, Appl
883	35	42.7	US-08-487-761-15	Sequence 15, Appl	956	34.5	42.1	225	2	US-09-453-234-60	Sequence 60, Appl
884	35	42.7	US-08-442-542-14	Sequence 14, Appl	957	34.5	42.1	225	2	US-09-453-234-92	Sequence 92, Appl
885	35	42.7	US-08-765-469-14	Sequence 14, Appl	958	34.5	42.1	225	2	US-09-453-234-100	Sequence 100, App
886	35	42.7	US-08-652-558-39	Sequence 39, Appl	959	34.5	42.1	225	2	US-09-453-234-106	Sequence 106, App
887	35	42.7	US-09-232-290-60	Sequence 60, Appl	960	34.5	42.1	274	1	US-08-860-174A-12	Sequence 12, Appl
888	35	42.7	US-09-240-274-6	Sequence 5, Appli	961	34.5	42.1	282	1	US-08-860-174A-10	Sequence 10, Appl
889	35	42.7	US-09-240-274-6	Sequence 6, Appli	962	34.5	42.1	297	2	US-09-605-703B-296	Sequence 296, App
890	35	42.7	US-09-433-404-3	Sequence 3, Appli	963	34.5	42.1	313	2	US-09-605-703B-294	Sequence 294, App
891	35	42.7	US-09-848-798-5	Sequence 5, Appli	964	34.5	42.1	467	1	US-08-704-744-81	Sequence 81, Appl
892	35	42.7	US-09-489-039A-12841	Sequence 6, Appli	965	34	41.5	17	2	US-09-560-198A-12	Sequence 12, Appl
893	35	42.7	US-09-489-039A-12841	Sequence 12841, A	966	34	41.5	17	2	US-09-383-667-11	Sequence 11, Appl
894	35	42.7	US-10-226-795-32	Sequence 32, Appl	967	34	41.5	17	2	US-09-383-667-16	Sequence 16, Appl
895	35	42.7	US-09-248-796A-15144	Sequence 15144, A	968	34	41.5	17	2	US-09-383-667-18	Sequence 18, Appl
896	35	42.7	US-09-112-498A-3	Sequence 3, Appli	969	34	41.5	17	2	US-09-192-854-60	Sequence 60, Appl
897	35	42.7	US-09-092-160-7	Sequence 7, Appli	970	34	41.5	17	2	US-09-192-854-68	Sequence 68, Appl
898	35	42.7	US-09-112-498A-5	Sequence 5, Appli	971	34	41.5	17	2	US-09-424-840B-36	Sequence 36, Appl
899	35	42.7	US-09-252-991A-19945	Sequence 19945, A	972	34	41.5	17	2	US-09-424-840B-77	Sequence 77, Appl
900	35	42.7	US-08-553-497A-18	Sequence 18, Appl	973	34	41.5	17	2	US-09-424-840B-84	Sequence 84, Appl
901	35	42.7	US-09-071-252-22	Sequence 22, Appl	974	34	41.5	17	2	US-09-424-840B-95	Sequence 95, Appl
902	35	42.7	US-07-690-192-4	Sequence 4, Appli	975	34	41.5	17	2	US-09-424-840B-97	Sequence 97, Appl
903	35	42.7	US-08-564-164A-2	Sequence 2, Appli	976	34	41.5	17	2	US-09-424-840B-108	Sequence 108, App

977 34 41.5 17 2 US-09-424-840B-111 Sequence 111, App
978 34 41.5 17 2 US-09-424-840B-113 Sequence 113, App
979 34 41.5 17 2 US-09-511-939-98 Sequence 98, Appl
980 34 41.5 17 2 US-09-511-939-110 Sequence 110, App
981 34 41.5 17 2 US-09-534-717-3 Sequence 3, Appl
982 34 41.5 17 2 US-09-534-717-19 Sequence 19, Appl
983 34 41.5 17 2 US-09-534-717-27 Sequence 27, Appl
984 34 41.5 17 2 US-09-534-717-335 Sequence 335, App
985 34 41.5 17 2 US-09-534-717-336 Sequence 336, App
986 34 41.5 17 2 US-09-534-717-337 Sequence 337, App
987 34 41.5 17 2 US-09-534-717-338 Sequence 338, App
988 34 41.5 17 2 US-09-534-717-339 Sequence 339, App
989 34 41.5 17 2 US-09-534-717-340 Sequence 340, App
990 34 41.5 17 2 US-09-534-717-341 Sequence 341, App
991 34 41.5 17 2 US-09-534-717-342 Sequence 342, App
992 34 41.5 17 2 US-09-534-717-343 Sequence 343, App
993 34 41.5 17 2 US-09-534-717-344 Sequence 344, App
994 34 41.5 17 2 US-09-534-717-345 Sequence 345, App
995 34 41.5 17 2 US-09-534-717-346 Sequence 346, App
996 34 41.5 17 2 US-09-534-717-347 Sequence 347, App
997 34 41.5 17 2 US-09-534-717-348 Sequence 348, App
998 34 41.5 17 2 US-09-534-717-349 Sequence 349, App
999 34 41.5 17 2 US-09-534-717-350 Sequence 350, App
1000 34 41.5 17 2 US-09-534-717-351 Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-155-106-2
; Sequence 2, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-155-106-2

Query Match 100.0%; Score 82; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
|||||
Db 1 SITSTGGTYHAESVKG 16

RESULT 2
US-09-155-106-18
; Sequence 18, Application US/09155106

; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-18

Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SITSTGGTYHAESVKG 16
|||||
Db 50 SITSTGGTYHAESVKG 66

RESULT 3
US-09-155-106-19
; Sequence 19, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19

Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||||
Db 50 SITSTGGTYHAESVKG 66

RESULT 4
US-09-155-106-20
; Sequence 20, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-20

Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||||
Db 50 SITSTGGTYHAESVKG 66

RESULT 5
US-09-155-106-26
; Sequence 26, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-26

Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||||
Db 50 SITSTGGTYHAESVKG 66

RESULT 6
US-09-155-106-32
; Sequence 32, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-32

Query Match 87.2%; Score 71.5; DB 2; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00016;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||||
Db 50 SITSTGGTYHAESVKG 66

RESULT 7
US-10-194-975-48
; Sequence 48, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-48

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Query Match          64.6%; Score 53; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.16;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
:|:|||||:|||||
Db 50 AIGTGGTYADSVKG 65

RESULT 8
US-09-534-717-617
; Sequence 617, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BB1-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 617
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-617

Query Match          64.6%; Score 53; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.16;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
:|:|||||:|||||
Db 50 AIGTGGTYADSVKG 65

RESULT 9
US-09-534-717-618
; Sequence 618, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BB1-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 618
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-618

Query Match          64.6%; Score 53; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.16;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
:|:|||||:|||||
Db 50 AIGTGGTYADSVKG 65

RESULT 10
US-08-958-201-2
; Sequence 2, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
```

```
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: D12
US-08-958-201-2

Query Match          64.0%; Score 52.5; DB 1; Length 118;
Best Local Similarity 68.8%; Pred. No. 0.24;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 2 ITSTGG-TYHAESVKG 16
:|:|||||:|||||
Db 51 ISGGGGTYHADSVKG 66

RESULT 11
US-08-958-201-4
; Sequence 4, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
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; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 118 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: 1C
 ; US-08-958-201-4

Query Match 64.0%; Score 52.5; DB 1; Length 118;
 Best Local Similarity 68.8%; Pred. No. 0.24;
 Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 ITSTGG-TYHAESVKG 16
 | : ||| ||| : |||
 Db 51 ISGGSGDTYHADVKG 66

RESULT 12
 US-09-840-459-51
 ; Sequence 51, Application US/09840459
 ; Patent No. 6696550
 ; GENERAL INFORMATION:
 ; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; FILE REFERENCE: METHODS OF USE THEREFOR
 ; CURRENT APPLICATION NUMBER: US/09/840,459
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-840-459-51

Query Match 62.2%; Score 51; DB 2; Length 88;
 Best Local Similarity 62.5%; Pred. No. 0.31;
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 ||: ||| : |||
 Db 41 S1SSGGSTYYPDSVKG 56

RESULT 13
 US-09-497-625A-51
 ; Sequence 51, Application US/09497625A
 ; Patent No. 6727349
 ; GENERAL INFORMATION:
 ; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; FILE REFERENCE: METHODS OF USE THEREFOR

; CURRENT APPLICATION NUMBER: US/09/497,625A
 ; CURRENT FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-497-625A-51

Query Match 62.2%; Score 51; DB 2; Length 88;
 Best Local Similarity 62.5%; Pred. No. 0.31;
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 ||: ||| : |||
 Db 41 S1SSGGSTYYPDSVKG 56

RESULT 14
 US-08-259-372A-4
 ; Sequence 4, Application US/08259372A
 ; Patent No. 5565354
 ; GENERAL INFORMATION:
 ; APPLICANT: Ostberg, Lars G.
 ; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/259,372A
 ; FILING DATE: 14-JUN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/871,426
 ; FILING DATE: 21-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/676,036
 ; FILING DATE: 27-MAR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/538,796
 ; FILING DATE: 15-JUN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/192,754
 ; FILING DATE: 11-MAY-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/925,196
 ; FILING DATE: 31-OCT-1986
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/904,517
 ; FILING DATE: 05-SEP-1986
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-50-7
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 576-0300

;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-4

Query Match 62.2%; Score 51; DB 1; Length 131;
Best Local Similarity 62.5%; Pred. No. 0.48;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
:|||:|:|:|:|:|:|
Db 69 AIGPTGDTYYADSVKG 84

RESULT 15
US-08-468-671-4
; Sequence 4, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-671-4
Query Match 62.2%; Score 51; DB 1; Length 131;
Best Local Similarity 62.5%; Pred. No. 0.48;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
:|||:|:|:|:|:|:|
Db 69 AIGPTGDTYYADSVKG 84

RESULT 16
US-08-264-093-22
; Sequence 22, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-22

Query Match 61.6%; Score 50.5; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.06;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
:|||:|:|:|:|:|:|
Db 1 AISSNGSGTYYADSVKG 17

RESULT 17
US-09-424-840B-72
; Sequence 72, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-652-816A-11

Query Match 61.6%; Score 50.5; DB 1; Length 118;
Best Local Similarity 64.7%; Pred. No. 0.52;
Matches 11; Conservative 4; Mismatches 1; Indels

QY 1 SITSTCG-TYHAEVSKG 16
   :|:|:|:|:|:|:|:|
Db 50 AISSNGSTYADSVKG 66

RESULT 24
US-08-264-093-14
; Sequence 14, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
;
US-08-264-093-14

Query Match 61.6%; Score 50.5; DB 1; Length 120;
Best Local Similarity 64.7%; Pred. No. 0.53;

```



```
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-145

Query Match          61.6%; Score 50.5; DB 1; Length 126;
Best Local Similarity 64.7%; Pred. No. 0.56;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGGT-YHAESVKG 16
   ||: |||: ||: |||
Db 48 SISGTGGSNYADSVKG 64

RESULT 28
US-08-899-575-145
; Sequence 145, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-145

Query Match          61.6%; Score 50.5; DB 1; Length 126;
Best Local Similarity 64.7%; Pred. No. 0.56;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGGT-YHAESVKG 16
   ||: |||: ||: |||
```

```
Db 48 SISGTGGSNYADSVKG 64

RESULT 29
PCT-US95-08743-145
; Sequence 145, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08743-145

Query Match          61.6%; Score 50.5; DB 4; Length 126;
Best Local Similarity 64.7%; Pred. No. 0.56;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGGT-YHAESVKG 16
   ||: |||: ||: |||
Db 48 SISGTGGSNYADSVKG 64

RESULT 30
US-09-976-118-1
; Sequence 1, Application US/09976118
; Patent No. 6699473
; GENERAL INFORMATION:
; APPLICANT: Raisch, Kevin Paul
; APPLICANT: Curiel, David T.
; APPLICANT: Bonner, James Allen
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFV
; OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

Query Match          61.6%; Score 50.5; DB 2; Length 268;
Best Local Similarity 64.7%; Pred. No. 1.3;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-YHAESVKG 16
   :||: |||: ||: |||
Db 50 AISNGSGSTYYADSVKG 66
```

```
RESULT 31
US-08-273-146-65
; Sequence 65, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kuten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-65

Query Match 61.0%; Score 50; DB 1; Length 102;
Best Local Similarity 64.3%; Pred. No. 0.54;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
Db 37 SSSGDTYYADSVKG 50

RESULT 32
US-09-043-514-2
; Sequence 2, Application US/09043514A
; Patent No. 6153745
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, David
; APPLICANT: BROWN, Daniel
; APPLICANT: ZACCOLO, Manuela C.
; APPLICANT: GHERARDI, Ermanno
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MUTAGENESIS OF NUCLEIC
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 41301/251704
; CURRENT APPLICATION NUMBER: US/09/043,514A
; CURRENT FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: GB 9519425.4
; EARLIER FILING DATE: 1995-09-22
```

```
; EARLIER APPLICATION NUMBER: GB 9602011.0
; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: PCT/GB96/02333
; EARLIER FILING DATE: 1996-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; FEATURE:
; OTHER INFORMATION: Primer
US-09-043-514-2

Query Match 59.8%; Score 49; DB 2; Length 95;
Best Local Similarity 66.7%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
Db 46 IYSGGSTYYADSVKG 60

RESULT 33
US-10-194-975-29
; Sequence 29, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-29

Query Match 59.8%; Score 49; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.75;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
Db 51 IYSGGSTYYADSVKG 65

RESULT 34
US-10-194-975-31
; Sequence 31, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-31
```

Query Match 59.8%; Score 49; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. NO. 0.75;
Matches 10; Conservative 2; Mismatches 3; Indels

Qy 2 ITSTGGTYHAESVKG 16
db 51 IYSGGSTYYADSVKG 65

```

RESULT 35
US-09-534-717-616
; Sequence 616, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen. Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: EBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 616
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-616

```

Query Match 59.8%; Score 49; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.75;
Matches 10: Conservative 2; Mismatches 3; Indels

Qy	2	ITSTGGTYHAESVKG	16
		:	
d _B	51	IYSGGTTYADSVKG	65

RESULT 36
US-08-545-809A-135
; Sequence 135, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-135

Query Match 59.8%; Score 49; DB 2; Length 116;
Best Local Similarity 66.7%; Pred. No. 0.91;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16
| | | | | : | | |
Db 70 IYSGGSTYYADSVKG 84

```

1  RESULT 37
2  US-09-515-697-135
3  ; Sequence 135, Application US/09515697
4  ; Patent No. 6936705
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Honjo, Tasuku
7  ; Matsuda, Fumihiiko
8  ; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
9  ; SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
10 ;
11 ; NUMBER OF SEQUENCES: 145
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Fish & Richardson, P.C.
14 ; STREET: 225 Franklin Street
15 ; CITY: Boston
16 ; STATE: MA
17 ; COUNTRY: US
18 ; ZIP: 02110-2804
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: Diskette
21 ; COMPUTER: IBM Compatible
22 ; OPERATING SYSTEM: Windows95
23 ; SOFTWARE: FastSeq for Windows Version 2.0
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/09/515,697
26 ; FILING DATE: 23-Feb-2000
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: US/08/545,809
29 ; FILING DATE: 27-MAR-1996
30 ; APPLICATION NUMBER: PCT/JP93/00603
31 ; FILING DATE: 10-MAY-1993
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: Freeman, John W.
34 ; REGISTRATION NUMBER: 29,066
35 ; REFERENCE/DOCKET NUMBER: 06501/004001
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: 617-542-5070
38 ; TELEFAX: 617-542-8906
39 ; TELEX: 200154
40 ; INFORMATION FOR SEQ ID NO: 135:
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 116 amino acids
43 ; TYPE: amino acid
44 ; TOPOLOGY: linear
45 ; MOLECULE TYPE: protein
46 ; SEQUENCE DESCRIPTION: SEQ ID NO: 135:
47 US-09-515-697-135

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Query Match 59.8%; Score 49; DB 2; Length 116;
Best Local Similarity 66.7%; Pred. No. 0.91;
Matches 10: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16
||| ||| : |||
pb 70 IYSGGSTYADSVKG 84

; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-51

Query Match 58.5%; Score 48; DB 2; Length 19;
Best Local Similarity 64.3%; Pred. No. 0.18; 3; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 6 TDGGSTYYADSVKG 19

RESULT 42
US-09-840-459-87
; Sequence 87, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-87

Query Match 58.5%; Score 48; DB 2; Length 127;
Best Local Similarity 69.2%; Pred. No. 1.5;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 54 SDGGSTYYADSVKG 66

RESULT 43
US-09-497-625A-87
; Sequence 87, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-87

Query Match 58.5%; Score 48; DB 2; Length 127;
Best Local Similarity 69.2%; Pred. No. 1.5;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 54 SDGGSTYYADSVKG 66

RESULT 44
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-16

Query Match 58.5%; Score 48; DB 2; Length 135;
Best Local Similarity 56.3%; Pred. No. 1.6;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
||:| ||:| |||
Db 69 SISTGGSTYYPDSVKG 84

RESULT 45
US-08-579-378A-20
Sequence 20, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:

APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIORITY APPLICATION NUMBER: US/08/579,378A
PRIORITY APPLICATION DATA:
FILING DATE: 30-NOV-1993
PRIORITY APPLICATION NUMBER: US 08/160,074
FILING DATE: 01-DEC-1992
PRIORITY APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995

REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-20

Query Match 58.5%; Score 48; DB 2; Length 135;

Best Local Similarity 56.2%; Pred. No. 1.6;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 SITSTGGTYHAESVKG 16
||:| ||:| |||
Db 69 SISTGGSTYYPDSVKG 84

RESULT 46
US-09-069-821-3
Sequence 3, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILFULA, DAVID
APPLICANT: WANG, MAOLIANG
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
FILING DATE: 02-DEC-1997
PRIORITY APPLICATION NUMBER: US 60/067,341
FILING DATE: 27-OCT-1997
PRIORITY APPLICATION DATA:
FILING DATE: 23-JUN-1997
PRIORITY APPLICATION NUMBER: US 60/050,472
FILING DATE: 30-APR-1997
PRIORITY APPLICATION DATA:
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-3

Query Match 58.5%; Score 48; DB 2; Length 263;
Best Local Similarity 64.3%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
| | | | | | | | | |
Db 184 TDGGSTYADSVKG 197


```
RESULT 47
US-09-956-086-3
; Sequence 3, Application US/09956086
; Patent No. 6743896
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
;           WANG, MAOLIANG
;           SHORR, ROBERT
;           WHITLOW, MARC
;           LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
;
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,086
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3
Query Match 58.5%; Score 48; DB 2; Length 263;
Best Local Similarity 64.3%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TSTGGTYHAESVKG 16
Db 184 TDGGSTYYADSVKG 197

RESULT 48
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. 6743908
; GENERAL INFORMATION:
; APPLICANT: FILPULA, DAVID
;           WANG, MAOLIANG
;           SHORR, ROBERT
;           WHITLOW, MARC
;           LEE, LIHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
;
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,087
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: No. 6743896 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3
Query Match 58.5%; Score 48; DB 2; Length 263;
Best Local Similarity 64.3%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TSTGGTYHAESVKG 16
Db 184 TDGGSTYYADSVKG 197

RESULT 49
US-09-420-592A-6
; Sequence 6, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
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; LENGTH: 283
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-420-592A-6

Query Match 58.5%; Score 48; DB 2; Length 283;
Best Local Similarity 64.3%; Pred. No. 3.6;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
| | | | |
Db 184 TDGSGTYADSVKG 197

RESULT 50
US-09-985-442-6
; Sequence 6, Application US/09985442
; Patent No. 6692942
; GENERAL INFORMATION:
; APPLICANT: Filipula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6692942el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977,2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-985-442-6

Query Match 58.5%; Score 48; DB 2; Length 283;
Best Local Similarity 64.3%; Pred. No. 3.6;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
| | | | |
Db 184 TDGSGTYADSVKG 197

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:41 ; Search time 120.656 Seconds
(without alignments)
55.408 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82

Sequence: 1 SITSTGGTTHAESVKG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:*

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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	16	3	US-09-155-106-2
2	82	100.0	16	5	US-10-808-538-2
3	71.5	87.2	122	3	US-09-155-106-18
4	71.5	87.2	122	3	US-09-155-106-19
5	71.5	87.2	122	3	US-09-155-106-20
6	71.5	87.2	122	3	US-09-155-106-26
7	71.5	87.2	122	3	US-09-155-106-32
8	71.5	87.2	122	5	US-10-808-538-18
9	71.5	87.2	122	5	US-10-808-538-19
10	71.5	87.2	122	5	US-10-808-538-20
11	71.5	87.2	122	5	US-10-808-538-26
12	71.5	87.2	122	5	US-10-808-538-32
13	58	70.7	16	4	US-10-327-598-477
14	56	68.3	119	5	US-10-815-443-1
15	56	68.3	119	5	US-10-815-443-3
16	56	68.3	119	5	US-10-815-449-5
17	55.5	67.7	247	3	US-09-880-748-1953
18	55.5	67.7	247	4	US-10-293-418-1953
19	55	67.1	16	4	US-10-031-874A-175
20	55	67.1	17	5	US-10-996-316-166
21	55	67.1	115	5	US-10-727-155-120
22	55	67.1	217	4	US-10-698-041-5
23	54.5	66.5	117	5	US-10-982-359-68
24	54	65.9	116	4	US-10-408-901-6
25	54	65.9	116	4	US-10-408-901-26
26	54	65.9	446	4	US-10-408-901-30
27	54	65.9	446	4	US-10-408-901-50

28	54	65.9	567	4	US-10-214-524-33	Sequence 33, Appl
29	53	64.6	16	4	US-10-031-874A-32	Sequence 32, Appl
30	53	64.6	16	4	US-10-450-036A-32	Sequence 32, Appl
31	53	64.6	95	3	US-09-864-761-47118	Sequence 47118, A
32	53	64.6	97	4	US-10-194-975-48	Sequence 48, Appl
33	53	64.6	97	4	US-10-032-037B-70	Sequence 70, Appl
34	53	64.6	97	4	US-10-032-037B-71	Sequence 71, Appl
35	53	64.6	97	4	US-10-029-988B-71	Sequence 71, Appl
36	53	64.6	97	4	US-10-029-988B-71	Sequence 71, Appl
37	53	64.6	97	4	US-10-032-423A-70	Sequence 70, Appl
38	53	64.6	97	4	US-10-032-423A-71	Sequence 71, Appl
39	53	64.6	97	4	US-10-029-926B-70	Sequence 70, Appl
40	53	64.6	97	4	US-10-029-926B-71	Sequence 71, Appl
41	53	64.6	97	5	US-10-884-830-617	Sequence 617, App
42	53	64.6	97	5	US-10-884-830-618	Sequence 618, App
43	53	64.6	97	5	US-10-911-831-18	Sequence 18, Appl
44	53	64.6	101	3	US-09-864-761-38468	Sequence 38468, A
45	53	64.6	116	4	US-10-687-795-54	Sequence 54, Appl
46	53	64.6	121	4	US-10-309-762-130	Sequence 130, Appl
47	53	64.6	123	5	US-10-982-359-66	Sequence 66, Appl
48	53	64.6	182	4	US-10-309-762-246	Sequence 246, App
49	53	64.6	850	5	US-10-450-763-34993	Sequence 34993, A
50	53	64.6	869	5	US-10-450-763-50017	Sequence 50017, A
51	52.5	64.0	105	5	US-10-911-838-17	Sequence 17, Appl
52	52.5	64.0	116	5	US-10-911-838-13	Sequence 13, Appl
53	52.5	64.0	144	4	US-10-687-799-10	Sequence 10, Appl
54	52	63.4	116	4	US-10-408-901-14	Sequence 14, Appl
55	52	63.4	116	4	US-10-408-901-22	Sequence 22, Appl
56	52	63.4	446	4	US-10-408-901-38	Sequence 38, Appl
57	52	63.4	446	4	US-10-408-901-46	Sequence 46, Appl
58	51.5	62.8	249	3	US-09-880-748-963	Sequence 963, App
59	51.5	62.8	249	4	US-10-293-418-963	Sequence 963, App
60	51	62.2	88	3	US-09-840-459-51	Sequence 51, Appl
61	51	62.2	88	4	US-10-766-773-51	Sequence 51, Appl
62	51	62.2	88	4	US-10-766-610-51	Sequence 51, Appl
63	51	62.2	88	4	US-10-733-563-51	Sequence 51, Appl
64	51	62.2	122	4	US-10-806-419-20	Sequence 20, Appl
65	51	62.2	208	3	US-09-252-150-4	Sequence 4, Appl
66	51	62.2	208	5	US-10-646-381-4	Sequence 4, Appl
67	51	62.2	254	3	US-09-880-748-971	Sequence 971, App
68	51	62.2	254	4	US-10-293-418-971	Sequence 971, App
69	50.5	61.6	17	4	US-10-031-874A-116	Sequence 116, App
70	50.5	61.6	17	4	US-10-844-424-72	Sequence 72, Appl
71	50.5	61.6	17	4	US-10-844-424-88	Sequence 88, Appl
72	50.5	61.6	98	4	US-10-032-037B-72	Sequence 72, Appl
73	50.5	61.6	98	4	US-10-029-988B-72	Sequence 72, Appl
74	50.5	61.6	98	4	US-10-032-423A-72	Sequence 72, Appl
75	50.5	61.6	98	4	US-10-029-926B-72	Sequence 72, Appl
76	50.5	61.6	98	5	US-10-884-830-620	Sequence 620, App
77	50.5	61.6	98	5	US-10-884-830-621	Sequence 621, App
78	50.5	61.6	98	5	US-10-884-830-631	Sequence 631, App
79	50.5	61.6	98	5	US-10-884-830-633	Sequence 633, App
80	50.5	61.6	116	6	US-10-884-830-634	Sequence 634, App
81	50.5	61.6	120	4	US-11-021-438-7	Sequence 7, Appl
82	50.5	61.6	120	4	US-10-779-461-140	Sequence 140, App
83	50.5	61.6	121	4	US-10-844-424-26	Sequence 26, Appl
84	50.5	61.6	122	4	US-10-180-648-13	Sequence 13, Appl
85	50.5	61.6	122	4	US-10-038-591-24	Sequence 24, Appl
86	50.5	61.6	122	4	US-10-775-444A-24	Sequence 24, Appl
87	50.5	61.6	126	4	US-10-016-986-145	Sequence 145, App
88	50.5	61.6	126	5	US-10-451-585A-92	Sequence 92, Appl
89	50.5	61.6	132	5	US-10-451-585A-86	Sequence 86, Appl
90	50.5	61.6	132	5	US-10-451-585A-87	Sequence 87, Appl
91	50.5	61.6	132	5	US-10-451-585A-88	Sequence 88, Appl
92	50.5	61.6	132	5	US-10-451-585A-89	Sequence 89, Appl
93	50.5	61.6	132	5	US-10-451-585A-90	Sequence 90, Appl
94	50.5	61.6	239	6	US-10-021-438-29	Sequence 29, Appl
95	50.5	61.6	240	3	US-09-880-748-1930	Sequence 1930, Ap
96	50.5	61.6	240	4	US-10-293-418-1930	Sequence 1930, Ap
97	50.5	61.6	241	6	US-11-090-847-50	Sequence 50, Appl
98	50.5	61.6	243	3	US-09-880-748-1945	Sequence 1945, Ap
99	50.5	61.6	243	4	US-10-293-418-1945	Sequence 1945, Ap
100	50.5	61.6	268	3	US-09-976-118-1	Sequence 1, Appl

101	50.5	61.6	268	4	US-10-703-277-1	Sequence 1, Appl	174	48.5	59.1	98	4	US-10-379-392-34	Sequence 34, Appl
102	50.5	61.6	467	4	US-10-180-648-2	Sequence 2, Appl	175	48.5	59.1	98	5	US-10-884-830-622	Sequence 622, Appl
103	50	61.0	17	4	US-10-031-874A-112	Sequence 112, Appl	176	48.5	59.1	295	4	US-10-406-830-21	Sequence 21, Appl
104	50	61.0	134	4	US-10-450-295-9	Sequence 9, Appl	177	48	58.5	16	4	US-10-443-466A-15	Sequence 15, Appl
105	50	61.0	219	3	US-09-252-150-12	Sequence 12, Appl	178	48	58.5	16	5	US-10-993-395-3	Sequence 9, Appl
106	50	61.0	219	5	US-10-646-381-12	Sequence 12, Appl	179	48	58.5	17	4	US-10-031-874A-31	Sequence 31, Appl
107	50	61.0	231	4	US-10-327-598-800	Sequence 800, Appl	180	48	58.5	17	4	US-10-031-874A-53	Sequence 53, Appl
108	50	61.0	312	4	US-10-291-265-334	Sequence 334, Appl	181	48	58.5	17	4	US-10-450-036A-31	Sequence 31, Appl
109	49.5	60.4	17	4	US-10-663-244-121	Sequence 121, Appl	182	48	58.5	17	4	US-10-450-036A-53	Sequence 53, Appl
110	49.5	60.4	116	4	US-10-663-244-61	Sequence 61, Appl	183	48	58.5	17	5	US-10-937-882A-2	Sequence 2, Appl
111	49.5	60.4	124	5	US-10-492-668-157	Sequence 157, Appl	184	48	58.5	17	5	US-10-966-097A-9	Sequence 9, Appl
112	49.5	60.4	462	4	US-10-663-244-155	Sequence 155, Appl	185	48	58.5	19	3	US-09-563-222-51	Sequence 51, Appl
113	49	59.8	16	3	US-09-972-656-52	Sequence 52, Appl	186	48	58.5	19	4	US-10-783-950-51	Sequence 51, Appl
114	49	59.8	16	5	US-10-996-316-163	Sequence 163, Appl	187	48	58.5	115	4	US-10-408-901-10	Sequence 10, Appl
115	49	59.8	96	4	US-10-041-860-278	Sequence 278, Appl	188	48	58.5	116	3	US-09-300-425B-19	Sequence 19, Appl
116	49	59.8	97	4	US-10-194-975-29	Sequence 29, Appl	189	48	58.5	116	4	US-10-321-558-30	Sequence 30, Appl
117	49	59.8	97	4	US-10-194-975-31	Sequence 31, Appl	190	48	58.5	126	5	US-10-492-668-150	Sequence 150, Appl
118	49	59.8	97	4	US-10-041-860-5	Sequence 5, Appl	191	48	58.5	127	3	US-09-840-459-87	Sequence 87, Appl
119	49	59.8	97	4	US-10-041-860-277	Sequence 277, Appl	192	48	58.5	127	4	US-10-766-773-87	Sequence 87, Appl
120	49	59.8	97	4	US-10-308-817-70	Sequence 70, Appl	193	48	58.5	127	4	US-10-766-773-87	Sequence 87, Appl
121	49	59.8	97	4	US-10-308-817-72	Sequence 72, Appl	194	48	58.5	127	4	US-10-733-563-87	Sequence 87, Appl
122	49	59.8	97	4	US-10-032-037B-68	Sequence 68, Appl	195	48	58.5	130	4	US-10-118-100-51	Sequence 51, Appl
123	49	59.8	97	4	US-10-032-037B-69	Sequence 69, Appl	196	48	58.5	131	3	US-09-805-290A-22	Sequence 22, Appl
124	49	59.8	97	4	US-10-029-988B-68	Sequence 68, Appl	197	48	58.5	137	4	US-10-443-466A-45	Sequence 45, Appl
125	49	59.8	97	4	US-10-029-988B-69	Sequence 69, Appl	198	48	58.5	137	4	US-10-443-466A-45	Sequence 45, Appl
126	49	59.8	97	4	US-10-032-423A-68	Sequence 68, Appl	199	48	58.5	137	4	US-10-443-466A-112	Sequence 112, Appl
127	49	59.8	97	4	US-10-032-423A-69	Sequence 69, Appl	200	48	58.5	137	5	US-10-993-395-4	Sequence 4, Appl
128	49	59.8	97	4	US-10-453-698-70	Sequence 70, Appl	201	48	58.5	137	5	US-10-993-395-14	Sequence 14, Appl
129	49	59.8	97	4	US-10-453-698-72	Sequence 72, Appl	202	48	58.5	137	5	US-10-986-498-18	Sequence 18, Appl
130	49	59.8	97	4	US-10-029-926B-68	Sequence 68, Appl	203	48	58.5	137	5	US-10-986-498-22	Sequence 22, Appl
131	49	59.8	97	4	US-10-029-926B-69	Sequence 69, Appl	204	48	58.5	238	4	US-10-336-041A-1	Sequence 1, Appl
132	49	59.8	97	4	US-10-379-392-33	Sequence 33, Appl	205	48	58.5	238	5	US-10-966-097A-1	Sequence 1, Appl
133	49	59.8	97	4	US-10-379-392-35	Sequence 35, Appl	206	48	58.5	240	4	US-10-336-041A-10	Sequence 10, Appl
134	49	59.8	97	5	US-10-884-830-616	Sequence 616, Appl	207	48	58.5	240	4	US-10-336-041A-12	Sequence 12, Appl
135	49	59.8	97	5	US-10-869-355-13	Sequence 13, Appl	208	48	58.5	241	4	US-10-336-041A-11	Sequence 11, Appl
136	49	59.8	97	5	US-10-869-355-14	Sequence 14, Appl	209	48	58.5	241	4	US-10-336-041A-13	Sequence 13, Appl
137	49	59.8	98	3	US-09-864-761-44343	Sequence 44343, A	210	48	58.5	241	5	US-10-631-011A-1	Sequence 1, Appl
138	49	59.8	108	5	US-10-727-155-268	Sequence 268, Appl	211	48	58.5	242	5	US-10-966-097A-20	Sequence 20, Appl
139	49	59.8	108	5	US-10-727-155-282	Sequence 282, Appl	212	48	58.5	242	5	US-10-966-097A-22	Sequence 22, Appl
140	49	59.8	108	5	US-10-727-155-286	Sequence 286, Appl	213	48	58.5	242	5	US-10-966-097A-21	Sequence 21, Appl
141	49	59.8	108	5	US-10-727-155-297	Sequence 297, Appl	214	48	58.5	243	5	US-10-966-097A-23	Sequence 23, Appl
142	49	59.8	108	5	US-10-727-155-300	Sequence 300, Appl	215	48	58.5	243	5	US-10-966-097A-27	Sequence 27, Appl
143	49	59.8	115	5	US-10-727-155-136	Sequence 136, Appl	216	48	58.5	244	5	US-10-966-097A-26	Sequence 26, Appl
144	49	59.8	115	5	US-10-727-155-152	Sequence 152, Appl	217	48	58.5	247	4	US-10-336-041A-9	Sequence 9, Appl
145	49	59.8	115	5	US-10-727-155-182	Sequence 182, Appl	218	48	58.5	263	3	US-09-956-086-3	Sequence 3, Appl
146	49	59.8	115	5	US-10-727-155-186	Sequence 186, Appl	219	48	58.5	263	3	US-09-956-087-3	Sequence 3, Appl
147	49	59.8	118	4	US-10-474-832-67	Sequence 67, Appl	220	48	58.5	283	3	US-09-983-580-6	Sequence 6, Appl
148	49	59.8	120	4	US-10-041-860-15	Sequence 15, Appl	221	48	58.5	283	3	US-09-985-442-6	Sequence 6, Appl
149	49	59.8	120	4	US-10-041-860-212	Sequence 212, Appl	222	48	58.5	283	5	US-10-966-097A-24	Sequence 24, Appl
150	49	59.8	120	4	US-10-041-860-276	Sequence 276, Appl	223	48	58.5	307	4	US-10-291-265-332	Sequence 332, Appl
151	49	59.8	120	4	US-10-665-383-10	Sequence 10, Appl	224	48	58.5	363	4	US-10-291-265-335	Sequence 335, Appl
152	49	59.8	120	5	US-10-996-316-200	Sequence 200, Appl	225	48	58.5	365	5	US-10-966-097A-25	Sequence 25, Appl
153	49	59.8	128	4	US-10-264-049-4268	Sequence 4268, Ap	226	48	58.5	443	3	US-09-917-410-4	Sequence 4, Appl
154	49	59.8	160	5	US-10-473-287-64	Sequence 64, Appl	227	48	58.5	445	4	US-10-408-901-34	Sequence 34, Appl
155	49	59.8	220	3	US-09-972-656-78	Sequence 78, Appl	228	48	58.5	533	4	US-10-104-047-3224	Sequence 3224, Ap
156	49	59.8	243	3	US-09-880-748-995	Sequence 995, Appl	229	47.5	57.9	17	3	US-09-192-854-10	Sequence 10, Appl
157	49	59.8	243	4	US-10-293-418-995	Sequence 995, Appl	230	47.5	57.9	17	3	US-09-968-561A-14	Sequence 14, Appl
158	49	59.8	243	5	US-10-935-290-53	Sequence 53, Appl	231	47.5	57.9	17	3	US-09-968-561A-38	Sequence 38, Appl
159	49	59.8	247	3	US-09-880-748-1177	Sequence 1177, Ap	232	47.5	57.9	17	3	US-09-968-561A-68	Sequence 68, Appl
160	49	59.8	247	4	US-10-293-418-1173	Sequence 1173, Ap	233	47.5	57.9	17	3	US-09-968-561A-74	Sequence 74, Appl
161	49	59.8	249	3	US-09-880-748-1335	Sequence 1335, Ap	234	47.5	57.9	17	3	US-09-968-561A-80	Sequence 80, Appl
162	49	59.8	249	4	US-10-293-418-1335	Sequence 1335, Ap	235	47.5	57.9	17	3	US-09-968-561A-86	Sequence 86, Appl
163	49	59.8	252	3	US-09-880-748-1311	Sequence 1311, Ap	236	47.5	57.9	17	3	US-09-968-561A-92	Sequence 92, Appl
164	49	59.8	252	4	US-10-293-418-1311	Sequence 1311, Ap	237	47.5	57.9	17	3	US-09-968-561A-122	Sequence 122, Appl
165	49	59.8	253	3	US-09-880-748-1449	Sequence 1449, Ap	238	47.5	57.9	17	3	US-09-968-561A-128	Sequence 128, Appl
166	49	59.8	253	3	US-09-880-748-1814	Sequence 1814, Ap	239	47.5	57.9	17	3	US-09-968-561A-134	Sequence 134, Appl
167	49	59.8	253	4	US-10-293-418-1449	Sequence 1449, Ap	240	47.5	57.9	17	3	US-09-968-561A-140	Sequence 140, Appl
168	49	59.8	253	4	US-10-293-418-1814	Sequence 1814, Ap	241	47.5	57.9	17	3	US-09-968-561A-146	Sequence 146, Appl
169	49	59.8	255	3	US-09-880-748-1137	Sequence 1137, Ap	242	47.5	57.9	17	3	US-09-968-561A-188	Sequence 188, Appl
170	49	59.8	255	4	US-10-293-418-1137	Sequence 1137, Ap	243	47.5	57.9	17	3	US-09-968-561A-194	Sequence 194, Appl
171	48.5	59.1	16	4	US-10-687-799-26	Sequence 26, Appl	244	47.5	57.9	17	3	US-09-968-561A-212	Sequence 212, Appl
172	48.5	59.1	98	4	US-10-308-817-71	Sequence 71, Appl	245	47.5	57.9	17	3	US-09-968-561A-218	Sequence 218, Appl
173	48.5	59.1	98	4	US-10-453-698-71	Sequence 71, Appl	246	47.5	57.9	17	3	US-09-968-561A-236	Sequence 236, Appl

247	47.5	57.9	17	3	US-09-968-561A-260	Sequence 260, App	320	47.5	57.9	17	6	US-11-115-682-14	Sequence 14, Appl
248	47.5	57.9	17	3	US-09-968-561A-266	Sequence 266, App	321	47.5	57.9	17	6	US-11-115-682-38	Sequence 38, Appl
249	47.5	57.9	17	3	US-09-968-561A-272	Sequence 272, App	322	47.5	57.9	17	6	US-11-115-682-68	Sequence 68, Appl
250	47.5	57.9	17	3	US-09-968-561A-284	Sequence 284, App	323	47.5	57.9	17	6	US-11-115-682-74	Sequence 74, Appl
251	47.5	57.9	17	3	US-09-968-561A-296	Sequence 296, App	324	47.5	57.9	17	6	US-11-115-682-80	Sequence 80, Appl
252	47.5	57.9	17	3	US-09-968-561A-308	Sequence 308, App	325	47.5	57.9	17	6	US-11-115-682-86	Sequence 86, Appl
253	47.5	57.9	17	3	US-09-968-561A-314	Sequence 314, App	326	47.5	57.9	17	6	US-11-115-682-92	Sequence 92, Appl
254	47.5	57.9	17	3	US-09-972-656-45	Sequence 45, Appl	327	47.5	57.9	17	6	US-11-115-682-122	Sequence 122, App
255	47.5	57.9	17	3	US-09-968-744A-14	Sequence 14, Appl	328	47.5	57.9	17	6	US-11-115-682-134	Sequence 134, App
256	47.5	57.9	17	3	US-09-968-744A-38	Sequence 38, Appl	329	47.5	57.9	17	6	US-11-115-682-138	Sequence 138, App
257	47.5	57.9	17	3	US-09-968-744A-68	Sequence 68, Appl	330	47.5	57.9	17	6	US-11-115-682-140	Sequence 140, App
258	47.5	57.9	17	3	US-09-968-744A-74	Sequence 74, Appl	331	47.5	57.9	17	6	US-11-115-682-146	Sequence 146, App
259	47.5	57.9	17	3	US-09-968-744A-80	Sequence 80, Appl	332	47.5	57.9	17	6	US-11-115-682-188	Sequence 188, App
260	47.5	57.9	17	3	US-09-968-744A-86	Sequence 86, Appl	333	47.5	57.9	17	6	US-11-115-682-194	Sequence 194, App
261	47.5	57.9	17	3	US-09-968-744A-92	Sequence 92, Appl	334	47.5	57.9	17	6	US-11-115-682-212	Sequence 212, App
262	47.5	57.9	17	3	US-09-968-744A-112	Sequence 112, App	335	47.5	57.9	17	6	US-11-115-682-218	Sequence 218, App
263	47.5	57.9	17	3	US-09-968-744A-128	Sequence 128, App	336	47.5	57.9	17	6	US-11-115-682-236	Sequence 236, App
264	47.5	57.9	17	3	US-09-968-744A-134	Sequence 134, App	337	47.5	57.9	17	6	US-11-115-682-260	Sequence 260, App
265	47.5	57.9	17	3	US-09-968-744A-140	Sequence 140, App	338	47.5	57.9	17	6	US-11-115-682-266	Sequence 266, App
266	47.5	57.9	17	3	US-09-968-744A-146	Sequence 146, App	339	47.5	57.9	17	6	US-11-115-682-272	Sequence 272, App
267	47.5	57.9	17	3	US-09-968-744A-188	Sequence 188, App	340	47.5	57.9	17	6	US-11-115-682-284	Sequence 284, App
268	47.5	57.9	17	3	US-09-968-744A-194	Sequence 194, App	341	47.5	57.9	17	6	US-11-115-682-296	Sequence 296, App
269	47.5	57.9	17	3	US-09-968-744A-212	Sequence 212, App	342	47.5	57.9	17	6	US-11-115-682-308	Sequence 308, App
270	47.5	57.9	17	3	US-09-968-744A-218	Sequence 218, App	343	47.5	57.9	17	6	US-11-115-682-314	Sequence 314, App
271	47.5	57.9	17	3	US-09-968-744A-236	Sequence 236, App	344	47.5	57.9	19	4	US-10-387-955-62	Sequence 62, Appl
272	47.5	57.9	17	3	US-09-968-744A-260	Sequence 260, App	345	47.5	57.9	19	4	US-10-387-955-68	Sequence 68, Appl
273	47.5	57.9	17	3	US-09-968-744A-266	Sequence 266, App	346	47.5	57.9	19	3	US-09-822-698A-18	Sequence 18, Appl
274	47.5	57.9	17	3	US-09-968-744A-272	Sequence 272, App	347	47.5	57.9	98	4	US-10-194-975-22	Sequence 22, Appl
275	47.5	57.9	17	3	US-09-968-744A-284	Sequence 284, App	348	47.5	57.9	98	4	US-10-125-687-19	Sequence 19, Appl
276	47.5	57.9	17	3	US-09-968-744A-296	Sequence 296, App	349	47.5	57.9	98	4	US-10-010-942B-10	Sequence 10, Appl
277	47.5	57.9	17	3	US-09-968-744A-308	Sequence 308, App	350	47.5	57.9	98	4	US-10-308-817-62	Sequence 62, Appl
278	47.5	57.9	17	3	US-09-968-744A-314	Sequence 314, App	351	47.5	57.9	98	4	US-10-032-037B-77	Sequence 77, Appl
279	47.5	57.9	17	3	US-09-968-561A-14	Sequence 14, Appl	352	47.5	57.9	98	4	US-10-029-988B-77	Sequence 77, Appl
280	47.5	57.9	17	3	US-09-968-561A-38	Sequence 38, Appl	353	47.5	57.9	98	4	US-10-032-423A-77	Sequence 77, Appl
281	47.5	57.9	17	3	US-09-968-561A-68	Sequence 68, Appl	354	47.5	57.9	98	4	US-10-453-698-62	Sequence 62, Appl
282	47.5	57.9	17	3	US-09-968-561A-74	Sequence 74, Appl	355	47.5	57.9	98	4	US-10-029-926B-77	Sequence 77, Appl
283	47.5	57.9	17	3	US-09-968-561A-80	Sequence 80, Appl	356	47.5	57.9	98	4	US-10-038-591-32	Sequence 32, Appl
284	47.5	57.9	17	3	US-09-968-561A-86	Sequence 86, Appl	357	47.5	57.9	98	4	US-10-388-389-10	Sequence 10, Appl
285	47.5	57.9	17	3	US-09-968-561A-92	Sequence 92, Appl	358	47.5	57.9	98	4	US-10-379-392-23	Sequence 23, Appl
286	47.5	57.9	17	3	US-09-968-561A-122	Sequence 122, App	359	47.5	57.9	98	4	US-10-703-713-10	Sequence 10, Appl
287	47.5	57.9	17	3	US-09-968-561A-128	Sequence 128, App	360	47.5	57.9	98	4	US-10-704-070-10	Sequence 10, Appl
288	47.5	57.9	17	3	US-09-968-561A-134	Sequence 134, App	361	47.5	57.9	98	4	US-10-775-444A-32	Sequence 32, Appl
289	47.5	57.9	17	3	US-09-968-561A-140	Sequence 140, App	362	47.5	57.9	98	5	US-10-884-830-619	Sequence 619, App
290	47.5	57.9	17	3	US-09-968-561A-146	Sequence 146, App	363	47.5	57.9	98	5	US-10-232-030-10	Sequence 10, Appl
291	47.5	57.9	17	3	US-09-968-561A-188	Sequence 188, App	364	47.5	57.9	98	5	US-10-869-355-12	Sequence 12, Appl
292	47.5	57.9	17	3	US-09-968-561A-194	Sequence 194, App	365	47.5	57.9	98	5	US-10-492-668-158	Sequence 158, App
293	47.5	57.9	17	3	US-09-968-561A-212	Sequence 212, App	366	47.5	57.9	98	5	US-10-911-838-20	Sequence 20, Appl
294	47.5	57.9	17	3	US-09-968-561A-218	Sequence 218, App	367	47.5	57.9	98	5	US-10-996-191-19	Sequence 19, Appl
295	47.5	57.9	17	3	US-09-968-561A-236	Sequence 236, App	368	47.5	57.9	98	5	US-10-831-459-48	Sequence 48, Appl
296	47.5	57.9	17	3	US-09-968-561A-260	Sequence 260, App	369	47.5	57.9	109	4	US-10-309-764-17	Sequence 17, Appl
297	47.5	57.9	17	3	US-09-968-561A-266	Sequence 266, App	370	47.5	57.9	109	4	US-10-779-461-154	Sequence 154, App
298	47.5	57.9	17	3	US-09-968-561A-272	Sequence 272, App	371	47.5	57.9	109	4	US-10-800-197-149	Sequence 149, App
299	47.5	57.9	17	3	US-09-968-561A-284	Sequence 284, App	372	47.5	57.9	109	5	US-10-727-155-279	Sequence 279, App
300	47.5	57.9	17	3	US-09-968-561A-296	Sequence 296, App	373	47.5	57.9	109	5	US-10-877-773-8	Sequence 8, Appl
301	47.5	57.9	17	3	US-09-968-561A-308	Sequence 308, App	374	47.5	57.9	109	5	US-10-877-774-8	Sequence 8, Appl
302	47.5	57.9	17	3	US-09-968-561A-314	Sequence 314, App	375	47.5	57.9	115	4	US-10-447-331-5	Sequence 5, Appl
303	47.5	57.9	17	4	US-10-401-344-10	Sequence 10, Appl	376	47.5	57.9	116	3	US-09-840-459-80	Sequence 80, Appl
304	47.5	57.9	17	4	US-10-128-520-357	Sequence 357, App	377	47.5	57.9	116	4	US-10-766-773-80	Sequence 80, Appl
305	47.5	57.9	17	4	US-10-688-925-44	Sequence 44, Appl	378	47.5	57.9	116	4	US-10-766-610-80	Sequence 80, Appl
306	47.5	57.9	17	4	US-10-396-578-57	Sequence 57, Appl	379	47.5	57.9	116	4	US-10-733-563-80	Sequence 80, Appl
307	47.5	57.9	17	4	US-10-844-424-107	Sequence 107, App	380	47.5	57.9	116	4	US-10-409-814A-2	Sequence 2, Appl
308	47.5	57.9	17	4	US-10-741-481-51	Sequence 51, Appl	381	47.5	57.9	116	5	US-10-744-774-5	Sequence 5, Appl
309	47.5	57.9	17	5	US-10-798-380-123	Sequence 123, App	382	47.5	57.9	116	5	US-11-031-485-114	Sequence 114, App
310	47.5	57.9	17	5	US-10-726-332-64	Sequence 64, Appl	383	47.5	57.9	117	3	US-09-840-459-83	Sequence 83, Appl
311	47.5	57.9	17	5	US-10-726-332-85	Sequence 85, Appl	384	47.5	57.9	117	4	US-10-766-773-83	Sequence 83, Appl
312	47.5	57.9	17	5	US-10-891-972-56	Sequence 56, Appl	385	47.5	57.9	117	4	US-10-766-610-83	Sequence 83, Appl
313	47.5	57.9	17	5	US-10-891-972-142	Sequence 142, App	386	47.5	57.9	117	4	US-10-733-563-83	Sequence 83, Appl
314	47.5	57.9	17	5	US-10-891-972-148	Sequence 148, App	387	47.5	57.9	118	4	US-10-001-934-39	Sequence 39, Appl
315	47.5	57.9	17	5	US-10-891-973-154	Sequence 154, App	388	47.5	57.9	118	4	US-10-309-762-129	Sequence 129, App
316	47.5	57.9	17	5	US-10-505-313-100	Sequence 100, App	389	47.5	57.9	118	4	US-10-275-046-68	Sequence 68, Appl
317	47.5	57.9	17	5	US-10-505-313-147	Sequence 147, App	390	47.5	57.9	118	5	US-10-798-380-119	Sequence 119, App
318	47.5	57.9	17	5	US-10-505-313-215	Sequence 215, App	391	47.5	57.9	119	4	US-10-401-344-6	Sequence 6, Appl
319	47.5	57.9	17	6	US-11-074-803-57	Sequence 57, Appl	392	47.5	57.9	119	6	US-11-021-438-6	Sequence 6, Appl

393	47.5	57.9	120	3	US-09-840-459-85	Sequence 85, Appl	466	47.5	57.9	218	4	US-10-128-520-144	Sequence 144, App
394	47.5	57.9	120	4	US-10-125-687-4	Sequence 4, Appl	467	47.5	57.9	220	4	US-10-128-520-154	Sequence 154, App
395	47.5	57.9	120	4	US-10-275-046-80	Sequence 80, Appl	468	47.5	57.9	220	4	US-10-128-520-156	Sequence 156, App
396	47.5	57.9	120	4	US-10-766-773-85	Sequence 85, Appl	469	47.5	57.9	221	4	US-10-128-520-143	Sequence 143, App
397	47.5	57.9	120	4	US-10-766-610-85	Sequence 85, Appl	470	47.5	57.9	221	4	US-10-128-520-171	Sequence 171, App
398	47.5	57.9	120	4	US-10-733-563-85	Sequence 85, Appl	471	47.5	57.9	222	4	US-10-128-520-145	Sequence 145, App
399	47.5	57.9	120	5	US-10-492-668-117	Sequence 117, App	472	47.5	57.9	222	4	US-10-128-520-152	Sequence 152, App
400	47.5	57.9	120	5	US-10-938-353-104	Sequence 104, App	473	47.5	57.9	223	3	US-09-972-656-86	Sequence 86, Appl
401	47.5	57.9	120	5	US-10-891-972-23	Sequence 23, Appl	474	47.5	57.9	224	3	US-09-972-656-68	Sequence 68, Appl
402	47.5	57.9	120	5	US-10-996-191-4	Sequence 4, Appl	475	47.5	57.9	224	4	US-10-128-520-148	Sequence 148, App
403	47.5	57.9	121	3	US-09-840-459-92	Sequence 92, Appl	476	47.5	57.9	224	4	US-10-128-520-150	Sequence 150, App
404	47.5	57.9	121	4	US-10-010-942B-9	Sequence 9, Appl	477	47.5	57.9	236	3	US-09-453-234-64	Sequence 64, Appl
405	47.5	57.9	121	4	US-10-275-046-78	Sequence 78, Appl	478	47.5	57.9	236	3	US-09-453-234-104	Sequence 104, App
406	47.5	57.9	121	4	US-10-388-389-9	Sequence 9, Appl	479	47.5	57.9	238	4	US-10-779-461-1	Sequence 1, Appl
407	47.5	57.9	121	4	US-10-766-773-92	Sequence 92, Appl	480	47.5	57.9	239	3	US-09-880-748-1922	Sequence 1922, Ap
408	47.5	57.9	121	4	US-10-766-610-92	Sequence 92, Appl	481	47.5	57.9	239	3	US-09-880-748-2018	Sequence 2018, Ap
409	47.5	57.9	121	4	US-10-733-563-92	Sequence 92, Appl	482	47.5	57.9	239	3	US-09-880-748-2022	Sequence 2022, Ap
410	47.5	57.9	121	4	US-10-703-713-9	Sequence 9, Appl	483	47.5	57.9	239	3	US-09-880-748-2023	Sequence 2023, Ap
411	47.5	57.9	121	4	US-10-704-070-9	Sequence 9, Appl	484	47.5	57.9	239	3	US-09-880-748-2035	Sequence 2035, Ap
412	47.5	57.9	121	4	US-10-800-197-128	Sequence 128, App	485	47.5	57.9	239	4	US-10-293-418-1922	Sequence 1922, Ap
413	47.5	57.9	121	5	US-10-232-030-9	Sequence 9, Appl	486	47.5	57.9	239	4	US-10-293-418-2018	Sequence 2018, Ap
414	47.5	57.9	121	6	US-11-031-485-118	Sequence 118, App	487	47.5	57.9	239	4	US-10-293-418-2022	Sequence 2022, Ap
415	47.5	57.9	122	4	US-10-800-197-134	Sequence 134, App	488	47.5	57.9	239	4	US-10-293-418-2023	Sequence 2023, Ap
416	47.5	57.9	122	5	US-10-727-155-262	Sequence 262, App	489	47.5	57.9	239	4	US-10-293-418-2035	Sequence 2035, Ap
417	47.5	57.9	122	5	US-10-891-972-33	Sequence 33, Appl	490	47.5	57.9	240	3	US-09-192-854-2	Sequence 2, Appl
418	47.5	57.9	122	5	US-10-505-313-4	Sequence 4, Appl	491	47.5	57.9	240	3	US-09-968-561A-2	Sequence 2, Appl
419	47.5	57.9	123	4	US-10-268-805-1	Sequence 1, Appl	492	47.5	57.9	240	3	US-09-880-748-2047	Sequence 2, Appl
420	47.5	57.9	123	4	US-10-268-805-23	Sequence 23, Appl	493	47.5	57.9	240	3	US-09-968-744A-2	Sequence 2, Appl
421	47.5	57.9	123	4	US-10-269-805-59	Sequence 59, Appl	494	47.5	57.9	240	3	US-09-968-561A-2	Sequence 2, Appl
422	47.5	57.9	124	3	US-09-840-459-89	Sequence 89, Appl	495	47.5	57.9	240	4	US-10-293-418-2047	Sequence 2047, Ap
423	47.5	57.9	124	4	US-10-040-244-16	Sequence 16, Appl	496	47.5	57.9	240	4	US-10-450-012-2	Sequence 2, Appl
424	47.5	57.9	124	4	US-10-766-773-89	Sequence 89, Appl	497	47.5	57.9	240	5	US-10-744-774-1	Sequence 1, Appl
425	47.5	57.9	124	4	US-10-766-610-89	Sequence 89, Appl	498	47.5	57.9	240	6	US-11-115-682-2	Sequence 2, Appl
426	47.5	57.9	124	4	US-10-688-925-4	Sequence 4, Appl	499	47.5	57.9	241	3	US-09-880-748-2060	Sequence 2060, Ap
427	47.5	57.9	124	4	US-10-733-563-89	Sequence 89, Appl	500	47.5	57.9	241	4	US-10-293-418-2060	Sequence 2060, Ap
428	47.5	57.9	125	4	US-10-505-313-8	Sequence 8, Appl	501	47.5	57.9	242	4	US-11-017-030-58	Sequence 9, Appl
429	47.5	57.9	125	3	US-09-840-459-76	Sequence 76, Appl	502	47.5	57.9	242	6	US-11-017-030-58	Sequence 58, Appl
430	47.5	57.9	125	3	US-09-840-459-84	Sequence 84, Appl	503	47.5	57.9	242	6	US-11-017-030-56	Sequence 66, Appl
431	47.5	57.9	125	3	US-09-850-165-107	Sequence 107, App	504	47.5	57.9	243	3	US-09-880-748-1969	Sequence 1969, Ap
432	47.5	57.9	125	4	US-10-038-591-16	Sequence 16, Appl	505	47.5	57.9	243	3	US-09-880-748-2056	Sequence 2056, Ap
433	47.5	57.9	125	4	US-10-766-773-76	Sequence 76, Appl	506	47.5	57.9	243	4	US-10-322-673-51	Sequence 51, Appl
434	47.5	57.9	125	4	US-10-766-773-84	Sequence 84, Appl	507	47.5	57.9	243	4	US-10-322-673-55	Sequence 55, Appl
435	47.5	57.9	125	4	US-10-766-610-76	Sequence 76, Appl	508	47.5	57.9	243	4	US-10-293-418-1969	Sequence 1969, Ap
436	47.5	57.9	125	4	US-10-766-610-84	Sequence 84, Appl	509	47.5	57.9	243	4	US-10-293-418-2056	Sequence 2056, Ap
437	47.5	57.9	125	4	US-10-733-563-76	Sequence 76, Appl	510	47.5	57.9	243	4	US-10-779-461-46	Sequence 46, Appl
438	47.5	57.9	125	4	US-10-733-563-84	Sequence 84, Appl	511	47.5	57.9	243	5	US-10-935-260-69	Sequence 69, Appl
439	47.5	57.9	125	4	US-10-775-444A-16	Sequence 16, Appl	512	47.5	57.9	243	5	US-10-981-465-51	Sequence 51, Appl
440	47.5	57.9	125	4	US-10-741-481-47	Sequence 47, Appl	513	47.5	57.9	243	5	US-10-981-465-55	Sequence 55, Appl
441	47.5	57.9	126	5	US-10-725-962-20	Sequence 20, Appl	514	47.5	57.9	243	5	US-10-981-621-51	Sequence 51, Appl
442	47.5	57.9	126	5	US-10-505-313-6	Sequence 6, Appl	515	47.5	57.9	243	5	US-10-981-621-55	Sequence 55, Appl
443	47.5	57.9	127	4	US-10-320-231A-36	Sequence 36, Appl	516	47.5	57.9	243	5	US-10-981-673-51	Sequence 51, Appl
444	47.5	57.9	127	4	US-10-800-197-124	Sequence 124, App	517	47.5	57.9	243	5	US-10-981-673-55	Sequence 55, Appl
445	47.5	57.9	127	5	US-10-725-962-6	Sequence 6, Appl	518	47.5	57.9	243	5	US-10-981-691-51	Sequence 51, Appl
446	47.5	57.9	127	5	US-10-867-506-36	Sequence 36, Appl	519	47.5	57.9	243	5	US-10-981-691-55	Sequence 55, Appl
447	47.5	57.9	128	3	US-10-505-313-235	Sequence 335, App	520	47.5	57.9	243	6	US-11-021-438-26	Sequence 26, Appl
448	47.5	57.9	128	3	US-09-840-459-77	Sequence 77, Appl	521	47.5	57.9	243	6	US-11-021-438-28	Sequence 28, Appl
449	47.5	57.9	128	3	US-09-840-459-79	Sequence 79, Appl	522	47.5	57.9	244	4	US-10-120-414-77	Sequence 77, Appl
450	47.5	57.9	128	4	US-10-766-773-77	Sequence 77, Appl	523	47.5	57.9	244	4	US-10-322-673-45	Sequence 45, Appl
451	47.5	57.9	128	4	US-10-766-773-79	Sequence 79, Appl	524	47.5	57.9	244	5	US-10-935-290-121	Sequence 121, App
452	47.5	57.9	128	4	US-10-766-610-77	Sequence 77, Appl	525	47.5	57.9	244	5	US-10-981-465-45	Sequence 45, Appl
453	47.5	57.9	128	4	US-10-766-610-79	Sequence 79, Appl	526	47.5	57.9	244	5	US-10-981-621-45	Sequence 45, Appl
454	47.5	57.9	128	4	US-10-733-563-77	Sequence 77, Appl	527	47.5	57.9	244	5	US-10-981-673-45	Sequence 45, Appl
455	47.5	57.9	128	4	US-10-733-563-79	Sequence 79, Appl	528	47.5	57.9	244	5	US-10-981-691-45	Sequence 45, Appl
456	47.5	57.9	130	4	US-10-118-100-54	Sequence 54, Appl	529	47.5	57.9	244	5	US-10-992-135-77	Sequence 77, Appl
457	47.5	57.9	136	3	US-09-837-306-184	Sequence 184, App	530	47.5	57.9	244	6	US-11-017-030-49	Sequence 49, Appl
458	47.5	57.9	136	4	US-10-045-674-487	Sequence 487, App	531	47.5	57.9	244	6	US-11-090-847-142	Sequence 142, App
459	47.5	57.9	147	5	US-10-473-287-60	Sequence 60, Appl	532	47.5	57.9	245	4	US-10-322-673-43	Sequence 43, App
460	47.5	57.9	156	5	US-10-473-287-59	Sequence 59, Appl	533	47.5	57.9	245	4	US-10-322-673-47	Sequence 47, App
461	47.5	57.9	177	4	US-10-693-629-64	Sequence 64, Appl	534	47.5	57.9	245	4	US-10-779-461-10	Sequence 10, Appl
462	47.5	57.9	217	4	US-10-128-520-140	Sequence 140, App	535	47.5	57.9	245	4	US-10-779-461-24	Sequence 24, Appl
463	47.5	57.9	217	4	US-10-128-520-141	Sequence 141, App	536	47.5	57.9	245	4	US-10-779-461-59	Sequence 59, Appl
464	47.5	57.9	217	4	US-10-128-520-142	Sequence 142, App	537	47.5	57.9	245	4	US-10-800-197-11	Sequence 11, Appl
465	47.5	57.9	217	4	US-10-128-520-146	Sequence 146, App	538	47.5	57.9	245	5	US-10-798-380-121	Sequence 121, App

539	47.5	57.9	Sequence 43, Appl	612	47.5	57.9	US-11-017-030-59	Sequence 59, Appl
540	47.5	57.9	Sequence 43, Appl	613	47.5	57.9	US-11-017-030-61	Sequence 61, Appl
541	47.5	57.9	Sequence 43, Appl	614	47.5	57.9	US-09-880-748-1431	Sequence 1431, Ap
542	47.5	57.9	Sequence 43, Appl	615	47.5	57.9	US-10-293-418-1431	Sequence 1431, Ap
543	47.5	57.9	Sequence 48, Appl	616	47.5	57.9	US-11-017-030-12	Sequence 12, Appl
544	47.5	57.9	Sequence 53, Appl	617	47.5	57.9	US-09-880-748-858	Sequence 858, App
545	47.5	57.9	Sequence 53, Appl	618	47.5	57.9	US-09-880-748-989	Sequence 989, App
546	47.5	57.9	Sequence 65, Appl	619	47.5	57.9	US-10-120-414-76	Sequence 76, Appl
547	47.5	57.9	Sequence 137, App	620	47.5	57.9	US-10-293-418-858	Sequence 858, App
548	47.5	57.9	Sequence 1324, Ap	621	47.5	57.9	US-10-293-418-989	Sequence 989, App
549	47.5	57.9	Sequence 1975, Ap	622	47.5	57.9	US-10-800-197-9	Sequence 9, Appl
550	47.5	57.9	Sequence 1324, Ap	623	47.5	57.9	US-10-992-195-76	Sequence 76, Appl
551	47.5	57.9	Sequence 1975, Ap	624	47.5	57.9	US-11-017-030-17	Sequence 17, Appl
552	47.5	57.9	Sequence 45, Appl	625	47.5	57.9	US-11-017-030-20	Sequence 20, Appl
553	47.5	57.9	Sequence 47, Appl	626	47.5	57.9	US-11-017-030-57	Sequence 57, Appl
554	47.5	57.9	Sequence 80, Appl	627	47.5	57.9	US-11-017-030-1	Sequence 1, Appl
555	47.5	57.9	Sequence 145, App	628	47.5	57.9	US-11-090-847-148	Sequence 148, App
556	47.5	57.9	Sequence 996, App	629	47.5	57.9	US-09-880-748-1701	Sequence 1701, Ap
557	47.5	57.9	Sequence 996, App	630	47.5	57.9	US-09-880-748-1739	Sequence 1739, Ap
558	47.5	57.9	Sequence 1923, Ap	631	47.5	57.9	US-10-293-418-1701	Sequence 1701, Ap
559	47.5	57.9	Sequence 81, Appl	632	47.5	57.9	US-10-293-418-1739	Sequence 1739, Ap
560	47.5	57.9	Sequence 996, App	633	47.5	57.9	US-11-017-030-1	Sequence 1, Appl
561	47.5	57.9	Sequence 1923, Ap	634	47.5	57.9	US-11-017-030-45	Sequence 45, Appl
562	47.5	57.9	Sequence 81, Appl	635	47.5	57.9	US-11-017-030-52	Sequence 52, Appl
563	47.5	57.9	Sequence 16, Appl	636	47.5	57.9	US-11-017-030-3	Sequence 3, Appl
564	47.5	57.9	Sequence 50, Appl	637	47.5	57.9	US-11-090-847-139	Sequence 139, App
565	47.5	57.9	Sequence 60, Appl	638	47.5	57.9	US-11-090-847-143	Sequence 143, App
566	47.5	57.9	Sequence 67, Appl	639	47.5	57.9	US-09-880-748-1183	Sequence 1183, Ap
567	47.5	57.9	Sequence 138, App	640	47.5	57.9	US-10-293-418-1183	Sequence 1183, Ap
568	47.5	57.9	Sequence 141, App	641	47.5	57.9	US-11-090-847-66	Sequence 66, Appl
569	47.5	57.9	Sequence 921, App	642	47.5	57.9	US-11-090-847-140	Sequence 140, App
570	47.5	57.9	Sequence 1456, Ap	643	47.5	57.9	US-11-068-925-2	Sequence 2, Appl
571	47.5	57.9	Sequence 78, Appl	644	47.5	57.9	US-09-818-247-22	Sequence 22, Appl
572	47.5	57.9	Sequence 921, App	645	47.5	57.9	US-11-038-956-22	Sequence 22, Appl
573	47.5	57.9	Sequence 1456, Ap	646	47.5	57.9	US-09-969-748C-2	Sequence 2, Appl
574	47.5	57.9	Sequence 32, Appl	647	47.5	57.9	US-09-949-039-2	Sequence 2, Appl
575	47.5	57.9	Sequence 78, Appl	648	47.5	57.9	US-10-470-987-42	Sequence 42, Appl
576	47.5	57.9	Sequence 4, Appl	649	47.5	57.9	US-10-406-830-9	Sequence 9, Appl
577	47.5	57.9	Sequence 11, Appl	650	47.5	57.9	US-10-406-830-10	Sequence 10, Appl
578	47.5	57.9	Sequence 18, Appl	651	47.5	57.9	US-09-969-748C-12	Sequence 12, Appl
579	47.5	57.9	Sequence 46, Appl	652	47.5	57.9	US-09-949-039-75	Sequence 75, Appl
580	47.5	57.9	Sequence 47, Appl	653	47.5	57.9	US-10-291-265-427	Sequence 427, App
581	47.5	57.9	Sequence 51, Appl	654	47.5	57.9	US-10-045-674-453	Sequence 453, App
582	47.5	57.9	Sequence 56, Appl	655	47.5	57.9	US-09-837-306-196	Sequence 196, App
583	47.5	57.9	Sequence 63, Appl	656	47.5	57.9	US-10-320-231A-79	Sequence 79, Appl
584	47.5	57.9	Sequence 64, Appl	657	47.5	57.9	US-10-867-506-79	Sequence 79, Appl
585	47.5	57.9	Sequence 53, Appl	658	47.5	57.9	US-10-401-344-2	Sequence 2, Appl
586	47.5	57.9	Sequence 53, Appl	659	47.5	57.9	US-10-038-591-46	Sequence 46, Appl
587	47.5	57.9	Sequence 53, Appl	660	47.5	57.9	US-10-775-444A-46	Sequence 46, Appl
588	47.5	57.9	Sequence 53, Appl	661	47.5	57.9	US-10-505-313-254	Sequence 254, App
589	47.5	57.9	Sequence 53, Appl	662	47.5	57.9	US-10-031-874A-176	Sequence 176, App
590	47.5	57.9	Sequence 15, Appl	663	47.5	57.9	US-10-031-874A-30	Sequence 30, Appl
591	47.5	57.9	Sequence 54, Appl	664	47.5	57.9	US-10-031-874A-40	Sequence 40, Appl
592	47.5	57.9	Sequence 62, Appl	665	47.5	57.9	US-10-031-874A-43	Sequence 43, Appl
593	47.5	57.9	Sequence 132, App	666	47.5	57.9	US-10-450-036A-30	Sequence 30, Appl
594	47.5	57.9	Sequence 1420, Ap	667	47.5	57.9	US-10-450-036A-40	Sequence 40, Appl
595	47.5	57.9	Sequence 72, Appl	668	47.5	57.9	US-10-450-036A-43	Sequence 43, Appl
596	47.5	57.9	Sequence 1420, Ap	669	47.5	57.9	US-10-396-578-63	Sequence 63, Appl
597	47.5	57.9	Sequence 8, Appl	670	47.5	57.9	US-10-783-311-228	Sequence 228, App
598	47.5	57.9	Sequence 72, Appl	671	47.5	57.9	US-10-783-311-232	Sequence 232, App
599	47.5	57.9	Sequence 74, Appl	672	47.5	57.9	US-10-726-332-52	Sequence 52, Appl
600	47.5	57.9	Sequence 82, Appl	673	47.5	57.9	US-11-074-803-63	Sequence 63, Appl
601	47.5	57.9	Sequence 136, App	674	47.5	57.9	US-09-972-656-123	Sequence 123, App
602	47.5	57.9	Sequence 908, App	675	47.5	57.9	US-09-972-656-127	Sequence 127, App
603	47.5	57.9	Sequence 1605, Ap	676	47.5	57.9	US-10-489-477-31	Sequence 31, Appl
604	47.5	57.9	Sequence 1740, Ap	677	47.5	57.9	US-09-822-698A-3	Sequence 3, Appl
605	47.5	57.9	Sequence 1740, Ap	678	47.5	57.9	US-10-733-532-130	Sequence 130, App
606	47.5	57.9	Sequence 908, App	679	47.5	57.9	US-09-840-459-78	Sequence 78, Appl
607	47.5	57.9	Sequence 1605, Ap	680	47.5	57.9	US-10-766-773-78	Sequence 78, Appl
608	47.5	57.9	Sequence 1708, Ap	681	47.5	57.9	US-10-766-610-78	Sequence 78, Appl
609	47.5	57.9	Sequence 1740, Ap	682	47.5	57.9	US-10-733-563-78	Sequence 78, Appl
610	47.5	57.9	Sequence 15, Appl	683	47.5	57.9	US-10-916-840-76	Sequence 76, Appl
611	47.5	57.9	Sequence 55, Appl	684	47.5	57.9	US-10-492-668-128	Sequence 128, App

685	47	57.3	131	5	US-10-915-490-14	Sequence 14, Appl	758	45.5	55.5	127	5	US-10-452-593-2	Sequence 2, Appl
686	47	57.3	138	5	US-10-783-311-223	Sequence 283, App	759	45.5	55.5	127	5	US-10-452-593-103	Sequence 103, App
687	47	57.3	138	5	US-10-783-311-287	Sequence 287, App	760	45.5	55.5	129	5	US-10-916-758-24	Sequence 24, Appl
688	47	57.3	152	3	US-09-737-476B-7	Sequence 7, Appl	761	45.5	55.5	131	5	US-10-916-840-24	Sequence 24, Appl
689	47	57.3	240	3	US-09-880-748-2013	Sequence 2013, Ap	762	45.5	55.5	190	5	US-10-894-194A-9	Sequence 9, Appl
690	47	57.3	240	3	US-10-293-418-2013	Sequence 2013, Ap	763	45.5	55.5	190	5	US-10-894-194A-10	Sequence 10, Appl
691	47	57.3	242	3	US-09-880-748-1949	Sequence 1949, Ap	764	45.5	55.5	190	5	US-10-894-194A-12	Sequence 12, Appl
692	47	57.3	242	3	US-10-293-418-1949	Sequence 1949, Ap	765	45.5	55.5	190	5	US-10-894-194A-13	Sequence 13, Appl
693	47	57.3	243	3	US-09-880-748-1940	Sequence 1940, Ap	766	45.5	55.5	237	3	US-09-880-748-1941	Sequence 1941, Ap
694	47	57.3	243	3	US-10-293-418-1940	Sequence 1940, Ap	767	45.5	55.5	237	3	US-10-293-418-1941	Sequence 1941, Ap
695	47	57.3	246	3	US-09-880-748-1980	Sequence 1980, Ap	768	45.5	55.5	246	3	US-09-880-748-1314	Sequence 1314, Ap
696	47	57.3	246	3	US-10-293-418-1980	Sequence 1980, Ap	769	45.5	55.5	246	3	US-10-293-418-1314	Sequence 1314, Ap
697	47	57.3	250	3	US-09-880-748-883	Sequence 883, App	770	45.5	55.5	252	6	US-11-017-030-29	Sequence 29, Appl
698	47	57.3	250	3	US-10-293-418-883	Sequence 883, App	771	45.5	55.5	254	3	US-09-880-748-1673	Sequence 1673, Ap
699	47	57.3	251	3	US-09-880-748-1171	Sequence 1171, Ap	772	45.5	55.5	254	3	US-10-293-418-1673	Sequence 1673, Ap
700	47	57.3	251	3	US-10-293-418-1171	Sequence 1171, Ap	773	45.5	55.5	471	4	US-10-292-088-6	Sequence 6, Appl
701	47	57.3	367	4	US-10-291-265-899	Sequence 899, App	774	45	54.9	16	4	US-10-327-598-479	Sequence 479, App
702	47	57.3	381	3	US-09-822-698A-5	Sequence 5, Appl	775	45	54.9	16	5	US-10-505-313-114	Sequence 114, App
703	47	57.3	451	3	US-09-822-698A-26	Sequence 26, Appl	776	45	54.9	16	6	US-11-102-403-33	Sequence 33, Appl
704	47	57.3	2066	4	US-10-437-963-176144	Sequence 176144,	777	45	54.9	17	3	US-09-736-371B-4	Sequence 4, Appl
705	47	57.3	3161	4	US-10-437-963-176140	Sequence 176140,	778	45	54.9	17	4	US-10-060-714-2	Sequence 2, Appl
706	46.5	56.7	17	5	US-10-783-311-132	Sequence 132, App	779	45	54.9	17	4	US-10-031-874A-103	Sequence 103, App
707	46.5	56.7	98	4	US-10-194-975-30	Sequence 30, Appl	780	45	54.9	17	4	US-10-031-874A-106	Sequence 106, App
708	46.5	56.7	123	5	US-10-783-311-127	Sequence 127, App	781	45	54.9	17	4	US-10-384-060-55	Sequence 55, Appl
709	46.5	56.7	128	5	US-10-916-840-102	Sequence 102, App	782	45	54.9	17	4	US-10-463-442-4	Sequence 4, Appl
710	46.5	56.7	131	5	US-10-916-840-92	Sequence 92, Appl	783	45	54.9	17	4	US-10-743-423B-2	Sequence 2, Appl
711	46.5	56.7	132	5	US-10-916-840-32	Sequence 32, Appl	784	45	54.9	17	5	US-10-491-112-2	Sequence 2, Appl
712	46.5	56.7	143	5	US-10-916-840-48	Sequence 48, Appl	785	45	54.9	98	4	US-10-032-037B-62	Sequence 62, Appl
713	46.5	56.7	147	4	US-10-624-884-27	Sequence 27, Appl	786	45	54.9	98	4	US-10-029-828B-62	Sequence 62, Appl
714	46.5	56.7	147	4	US-10-624-884-28	Sequence 28, Appl	787	45	54.9	98	4	US-10-032-423A-62	Sequence 62, Appl
715	46.5	56.7	147	5	US-10-895-183-27	Sequence 27, Appl	788	45	54.9	98	4	US-10-029-926B-62	Sequence 62, Appl
716	46.5	56.7	147	5	US-10-895-183-28	Sequence 28, Appl	789	45	54.9	98	5	US-10-884-830-600	Sequence 600, App
717	46.5	56.7	147	5	US-10-916-840-52	Sequence 52, Appl	790	45	54.9	99	4	US-10-194-975-27	Sequence 27, Appl
718	46.5	56.7	282	4	US-10-427-805-1	Sequence 1, Appl	791	45	54.9	99	4	US-10-308-817-67	Sequence 67, Appl
719	46.5	56.7	397	4	US-10-427-805-3	Sequence 3, Appl	792	45	54.9	99	4	US-10-453-698-67	Sequence 67, Appl
720	46.5	56.7	418	4	US-10-427-805-2	Sequence 2, Appl	793	45	54.9	99	4	US-10-379-392-29	Sequence 29, Appl
721	46	56.1	16	4	US-10-443-466A-38	Sequence 38, Appl	794	45	54.9	111	3	US-09-899-896-7	Sequence 7, Appl
722	46	56.1	16	5	US-10-864-818-10	Sequence 10, Appl	795	45	54.9	112	5	US-10-492-668-137	Sequence 137, App
723	46	56.1	16	5	US-10-996-316-164	Sequence 164, App	796	45	54.9	112	5	US-10-492-668-140	Sequence 140, App
724	46	56.1	115	4	US-10-408-901-18	Sequence 18, Appl	797	45	54.9	113	3	US-09-056-160B-11	Sequence 11, Appl
725	46	56.1	119	6	US-11-056-776-4	Sequence 4, Appl	798	45	54.9	113	3	US-09-795-798-6	Sequence 6, Appl
726	46	56.1	120	5	US-10-864-818-4	Sequence 4, Appl	799	45	54.9	113	4	US-10-727-737-6	Sequence 6, Appl
727	46	56.1	121	3	US-09-920-171-3	Sequence 3, Appl	800	45	54.9	113	5	US-10-974-591-11	Sequence 3, Appl
728	46	56.1	121	4	US-10-113-996-3	Sequence 3, Appl	801	45	54.9	113	5	US-09-811-123-3	Sequence 3, Appl
729	46	56.1	121	5	US-10-791-619-3	Sequence 3, Appl	802	45	54.9	119	3	US-09-736-371B-17	Sequence 17, Appl
730	46	56.1	125	5	US-10-489-477-25	Sequence 25, Appl	803	45	54.9	119	3	US-10-060-714-17	Sequence 17, Appl
731	46	56.1	133	4	US-10-364-743-104	Sequence 104, App	804	45	54.9	119	4	US-10-268-501-6	Sequence 6, Appl
732	46	56.1	133	5	US-10-452-593-104	Sequence 104, App	805	45	54.9	119	4	US-10-044-896-6	Sequence 6, Appl
733	46	56.1	140	4	US-10-443-466A-27	Sequence 27, Appl	806	45	54.9	119	4	US-10-463-442-17	Sequence 17, Appl
734	46	56.1	245	5	US-10-864-818-1	Sequence 1, Appl	807	45	54.9	119	4	US-10-608-626-6	Sequence 6, Appl
735	46	56.1	373	3	US-09-828-995B-35	Sequence 35, Appl	808	45	54.9	119	4	US-10-600-152-15	Sequence 15, Appl
736	46	56.1	373	4	US-10-753-139-35	Sequence 35, Appl	809	45	54.9	119	4	US-10-639-754-6	Sequence 6, Appl
737	46	56.1	449	6	US-10-408-901-42	Sequence 42, Appl	810	45	54.9	119	4	US-10-743-423B-11	Sequence 11, Appl
738	46	56.1	449	6	US-11-056-776-5	Sequence 5, Appl	811	45	54.9	119	5	US-10-719-310-6	Sequence 6, Appl
739	46	56.1	453	3	US-09-802-077-8	Sequence 8, Appl	812	45	54.9	119	5	US-10-491-112-11	Sequence 11, Appl
740	46	56.1	453	3	US-09-802-096-8	Sequence 8, Appl	813	45	54.9	119	5	US-10-861-049-42	Sequence 42, Appl
741	46	56.1	453	3	US-09-925-179-8	Sequence 8, Appl	814	45	54.9	119	5	US-11-021-874-42	Sequence 42, Appl
742	46	56.1	453	5	US-10-968-237-8	Sequence 8, Appl	815	45	54.9	119	6	US-11-044-749-6	Sequence 6, Appl
743	46	56.1	468	6	US-11-056-776-6	Sequence 6, Appl	816	45	54.9	119	6	US-11-154-465-6	Sequence 6, Appl
744	46	56.1	470	3	US-09-828-995B-11	Sequence 11, Appl	817	45	54.9	119	6	US-10-492-668-111	Sequence 111, App
745	46	56.1	470	4	US-10-753-159-11	Sequence 11, Appl	818	45	54.9	121	5	US-10-492-668-111	Sequence 111, App
746	45.5	55.5	17	4	US-10-844-424-76	Sequence 76, Appl	819	45	54.9	122	5	US-10-835-641-21	Sequence 21, Appl
747	45.5	55.5	110	5	US-10-916-758-81	Sequence 81, Appl	820	45	54.9	124	3	US-09-530-139-58	Sequence 2, Appl
748	45.5	55.5	114	5	US-10-916-758-37	Sequence 37, Appl	821	45	54.9	124	6	US-11-102-403-2	Sequence 2, Appl
749	45.5	55.5	123	5	US-10-915-490-24	Sequence 24, Appl	822	45	54.9	125	4	US-10-353-721-9	Sequence 9, Appl
750	45.5	55.5	125	5	US-10-492-668-153	Sequence 153, App	823	45	54.9	125	4	US-10-251-085B-149	Sequence 149, App
751	45.5	55.5	126	4	US-10-292-088-2	Sequence 2, Appl	824	45	54.9	126	4	US-10-737-252-149	Sequence 149, App
752	45.5	55.5	126	4	US-10-292-088-90	Sequence 90, Appl	825	45	54.9	126	4	US-10-353-721-7	Sequence 7, Appl
753	45.5	55.5	126	4	US-10-292-088-92	Sequence 92, Appl	826	45	54.9	127	4	US-10-104-473A-19	Sequence 19, Appl
754	45.5	55.5	126	6	US-11-001-980-9	Sequence 1, Appl	827	45	54.9	128	3	US-09-805-290A-32	Sequence 32, Appl
755	45.5	55.5	126	6	US-11-001-980-9	Sequence 1, Appl	828	45	54.9	130	5	US-10-683-451-21	Sequence 21, Appl
756	45.5	55.5	127	4	US-10-364-743-2	Sequence 2, Appl	829	45	54.9	137	5	US-10-916-840-80	Sequence 80, Appl
757	45.5	55.5	127	4	US-10-364-743-103	Sequence 103, App	830	45	54.9	146	4	US-10-353-721-11	Sequence 11, Appl

831	45	54.9	147	4	US-10-353-721-10	Sequence 10, Appl	904	44.5	54.3	126	5	US-10-725-962-21	Sequence 21, Appl
832	45	54.9	159	4	US-10-291-265-333	Sequence 33, App	905	44.5	54.3	130	3	US-09-764-304-8	Sequence 8, Appl
833	45	54.9	183	4	US-10-124-903-2	Sequence 2, Appl	906	44.5	54.3	130	3	US-09-764-304-18	Sequence 18, Appl
834	45	54.9	194	5	US-10-894-194A-8	Sequence 8, Appl	907	44.5	54.3	130	4	US-10-265-713-8	Sequence 8, Appl
835	45	54.9	216	3	US-09-252-150A-13	Sequence 13, Appl	908	44.5	54.3	130	4	US-10-265-713-18	Sequence 18, Appl
836	45	54.9	216	5	US-10-646-381-13	Sequence 13, Appl	909	44.5	54.3	130	4	US-10-166-626-8	Sequence 8, Appl
837	45	54.9	217	3	US-09-252-150-11	Sequence 11, Appl	910	44.5	54.3	130	4	US-10-166-626-18	Sequence 18, Appl
838	45	54.9	217	5	US-10-646-381-11	Sequence 11, Appl	911	44.5	54.3	130	5	US-10-885-492-5	Sequence 5, Appl
839	45	54.9	246	6	US-11-090-847-67	Sequence 67, Appl	912	44.5	54.3	131	3	US-09-988-115A-53	Sequence 53, Appl
840	45	54.9	247	3	US-09-880-748-1652	Sequence 1652, Ap	913	44.5	54.3	131	5	US-10-705-519-53	Sequence 53, Appl
841	45	54.9	247	4	US-10-293-418-1652	Sequence 1652, Ap	914	44.5	54.3	136	4	US-10-364-743-18	Sequence 18, Appl
842	45	54.9	249	3	US-09-880-748-941	Sequence 941, App	915	44.5	54.3	136	4	US-10-364-743-80	Sequence 80, Appl
843	45	54.9	249	4	US-10-293-418-941	Sequence 941, App	916	44.5	54.3	136	5	US-10-452-593-18	Sequence 18, Appl
844	45	54.9	249	6	US-11-090-847-68	Sequence 68, Appl	917	44.5	54.3	136	5	US-10-452-593-80	Sequence 80, Appl
845	45	54.9	249	6	US-11-090-847-71	Sequence 71, Appl	918	44.5	54.3	141	5	US-10-893-576-25	Sequence 25, Appl
846	45	54.9	249	6	US-11-090-847-77	Sequence 77, Appl	919	44.5	54.3	150	3	US-09-737-476B-9	Sequence 9, Appl
847	45	54.9	249	6	US-11-090-847-80	Sequence 80, Appl	920	44.5	54.3	152	5	US-10-473-287-33	Sequence 33, Appl
848	45	54.9	249	6	US-11-090-847-85	Sequence 85, Appl	921	44.5	54.3	152	5	US-10-473-287-61	Sequence 61, Appl
849	45	54.9	249	6	US-11-090-847-91	Sequence 91, Appl	922	44.5	54.3	153	3	US-09-737-476B-11	Sequence 11, Appl
850	45	54.9	251	6	US-11-090-847-92	Sequence 92, Appl	923	44.5	54.3	190	5	US-10-894-194A-11	Sequence 11, Appl
851	45	54.9	324	6	US-11-097-143-5682	Sequence 5682, Ap	924	44.5	54.3	236	3	US-09-880-748-2010	Sequence 2010, Ap
852	45	54.9	408	4	US-10-353-721-15	Sequence 15, Appl	925	44.5	54.3	236	4	US-10-293-418-2010	Sequence 2010, Ap
853	45	54.9	409	4	US-10-353-721-14	Sequence 14, Appl	926	44.5	54.3	237	3	US-09-880-748-1906	Sequence 1906, Ap
854	45	54.9	449	3	US-09-736-371B-21	Sequence 21, Appl	927	44.5	54.3	237	3	US-09-880-748-2003	Sequence 2003, Ap
855	45	54.9	449	4	US-10-463-442-21	Sequence 21, Appl	928	44.5	54.3	237	3	US-09-880-748-2005	Sequence 2005, Ap
856	45	54.9	467	6	US-11-031-485-10	Sequence 10, Appl	929	44.5	54.3	237	3	US-09-880-748-2006	Sequence 2006, Ap
857	45	54.9	469	5	US-10-858-186-14	Sequence 14, Appl	930	44.5	54.3	237	3	US-09-880-748-2017	Sequence 2017, Ap
858	44.5	54.3	17	5	US-10-725-962-73	Sequence 73, Appl	931	44.5	54.3	237	3	US-09-880-748-2019	Sequence 2019, Ap
859	44.5	54.3	17	5	US-10-893-576-100	Sequence 100, App	932	44.5	54.3	237	3	US-09-880-748-2020	Sequence 2020, Ap
860	44.5	54.3	17	5	US-10-505-313-222	Sequence 222, App	933	44.5	54.3	237	3	US-09-880-748-2027	Sequence 2027, Ap
861	44.5	54.3	22	5	US-10-778-394-16	Sequence 16, App	934	44.5	54.3	237	3	US-09-880-748-2028	Sequence 2028, Ap
862	44.5	54.3	89	3	US-09-840-459-48	Sequence 48, Appl	935	44.5	54.3	237	3	US-09-880-748-2036	Sequence 2036, Ap
863	44.5	54.3	89	4	US-10-766-773-48	Sequence 48, Appl	936	44.5	54.3	237	3	US-09-880-748-2039	Sequence 2039, Ap
864	44.5	54.3	89	4	US-10-766-610-48	Sequence 48, Appl	937	44.5	54.3	237	3	US-09-880-748-2040	Sequence 2040, Ap
865	44.5	54.3	89	4	US-10-733-563-48	Sequence 48, Appl	938	44.5	54.3	237	3	US-09-880-748-2043	Sequence 2043, Ap
866	44.5	54.3	88	4	US-10-066-895-4	Sequence 4, Appl	939	44.5	54.3	237	3	US-09-880-748-2104	Sequence 2104, Ap
867	44.5	54.3	98	4	US-10-194-975-17	Sequence 17, Appl	940	44.5	54.3	237	3	US-09-880-748-2110	Sequence 2110, Ap
868	44.5	54.3	98	4	US-10-308-817-57	Sequence 57, Appl	941	44.5	54.3	237	3	US-09-880-748-2111	Sequence 2111, Ap
869	44.5	54.3	98	4	US-10-032-037B-63	Sequence 63, Appl	942	44.5	54.3	237	3	US-09-880-748-2112	Sequence 2112, Ap
870	44.5	54.3	98	4	US-10-032-037B-79	Sequence 79, Appl	943	44.5	54.3	237	3	US-09-880-748-2114	Sequence 2114, Ap
871	44.5	54.3	98	4	US-10-029-988B-63	Sequence 63, Appl	944	44.5	54.3	237	3	US-09-880-748-2115	Sequence 2115, Ap
872	44.5	54.3	98	4	US-10-029-988B-79	Sequence 79, Appl	945	44.5	54.3	237	3	US-09-880-748-2118	Sequence 2118, Ap
873	44.5	54.3	98	4	US-10-032-423A-63	Sequence 63, Appl	946	44.5	54.3	237	4	US-10-293-418-1906	Sequence 1906, Ap
874	44.5	54.3	98	4	US-10-032-423A-79	Sequence 79, Appl	947	44.5	54.3	237	4	US-10-293-418-2003	Sequence 2003, Ap
875	44.5	54.3	98	4	US-10-453-698-57	Sequence 57, Appl	948	44.5	54.3	237	4	US-10-293-418-2005	Sequence 2005, Ap
876	44.5	54.3	98	4	US-10-029-926B-63	Sequence 63, Appl	949	44.5	54.3	237	4	US-10-293-418-2006	Sequence 2006, Ap
877	44.5	54.3	98	4	US-10-029-926B-79	Sequence 79, Appl	950	44.5	54.3	237	4	US-10-293-418-2017	Sequence 2017, Ap
878	44.5	54.3	98	4	US-10-038-591-30	Sequence 30, Appl	951	44.5	54.3	237	4	US-10-293-418-2019	Sequence 2019, Ap
879	44.5	54.3	98	4	US-10-379-392-16	Sequence 16, Appl	952	44.5	54.3	237	4	US-10-293-418-2020	Sequence 2020, Ap
880	44.5	54.3	98	4	US-10-775-444A-30	Sequence 30, Appl	953	44.5	54.3	237	4	US-10-293-418-2027	Sequence 2027, Ap
881	44.5	54.3	98	5	US-10-884-830-601	Sequence 601, App	954	44.5	54.3	237	4	US-10-293-418-2028	Sequence 2028, Ap
882	44.5	54.3	98	5	US-10-884-830-639	Sequence 639, App	955	44.5	54.3	237	4	US-10-293-418-2036	Sequence 2036, Ap
883	44.5	54.3	98	5	US-10-887-954-4	Sequence 4, Appl	956	44.5	54.3	237	4	US-10-293-418-2039	Sequence 2039, Ap
884	44.5	54.3	98	5	US-10-461-576-6	Sequence 6, Appl	957	44.5	54.3	237	4	US-10-293-418-2040	Sequence 2040, Ap
885	44.5	54.3	109	4	US-10-309-764-23	Sequence 23, Appl	958	44.5	54.3	237	4	US-10-293-418-2043	Sequence 2043, Ap
886	44.5	54.3	109	5	US-10-727-155-288	Sequence 288, App	959	44.5	54.3	237	4	US-10-293-418-2104	Sequence 2104, Ap
887	44.5	54.3	114	5	US-10-938-353-115	Sequence 115, App	960	44.5	54.3	237	4	US-10-293-418-2110	Sequence 2110, Ap
888	44.5	54.3	115	5	US-10-938-353-108	Sequence 108, App	961	44.5	54.3	237	4	US-10-293-418-2111	Sequence 2111, Ap
889	44.5	54.3	115	5	US-10-938-353-116	Sequence 116, App	962	44.5	54.3	237	4	US-10-293-418-2112	Sequence 2112, Ap
890	44.5	54.3	117	4	US-10-663-244-77	Sequence 77, Appl	963	44.5	54.3	237	4	US-10-293-418-2114	Sequence 2114, Ap
891	44.5	54.3	117	5	US-10-938-353-106	Sequence 106, App	964	44.5	54.3	237	4	US-10-293-418-2115	Sequence 2115, Ap
892	44.5	54.3	120	5	US-10-433-349-2	Sequence 2, Appl	965	44.5	54.3	237	4	US-10-293-418-2118	Sequence 2118, Ap
893	44.5	54.3	120	5	US-10-433-349-34	Sequence 34, Appl	966	44.5	54.3	238	3	US-09-880-748-2024	Sequence 2024, Ap
894	44.5	54.3	120	5	US-10-893-576-186	Sequence 186, App	967	44.5	54.3	238	4	US-10-293-418-2024	Sequence 2024, Ap
895	44.5	54.3	122	4	US-10-269-805-7	Sequence 7, Appl	968	44.5	54.3	239	3	US-09-880-748-2034	Sequence 2034, Ap
896	44.5	54.3	122	4	US-10-269-805-11	Sequence 11, Appl	969	44.5	54.3	239	4	US-10-293-418-2034	Sequence 2034, Ap
897	44.5	54.3	122	4	US-10-269-805-53	Sequence 53, Appl	970	44.5	54.3	240	3	US-09-880-748-1905	Sequence 1905, Ap
898	44.5	54.3	122	4	US-10-016-986-80	Sequence 80, Appl	971	44.5	54.3	240	3	US-09-880-748-2007	Sequence 2007, Ap
899	44.5	54.3	122	5	US-10-888-959-5	Sequence 5, Appl	972	44.5	54.3	240	3	US-09-880-748-2016	Sequence 2016, Ap
900	44.5	54.3	123	4	US-10-364-743-116	Sequence 116, App	973	44.5	54.3	240	3	US-09-880-748-2025	Sequence 2025, Ap
901	44.5	54.3	123	4	US-10-364-743-118	Sequence 118, App	974	44.5	54.3	240	3	US-09-880-748-2029	Sequence 2029, Ap
902	44.5	54.3	123	5	US-10-452-593-116	Sequence 116, App	975	44.5	54.3	240	3	US-09-880-748-2031	Sequence 2031, Ap
903	44.5	54.3	123	5	US-10-452-593-118	Sequence 118, App	976	44.5	54.3	240	3	US-09-880-748-2041	Sequence 2041, Ap

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977 44.5 54.3 240 3 US-09-880-748-2044 Sequence 2044, Ap
978 44.5 54.3 240 3 US-09-880-748-2045 Sequence 2045, Ap
979 44.5 54.3 240 3 US-09-880-748-2048 Sequence 2048, Ap
980 44.5 54.3 240 3 US-09-880-748-2105 Sequence 2105, Ap
981 44.5 54.3 240 3 US-09-880-748-2108 Sequence 2108, Ap
982 44.5 54.3 240 3 US-09-880-748-2113 Sequence 2113, Ap
983 44.5 54.3 240 3 US-09-880-748-2117 Sequence 2117, Ap
984 44.5 54.3 240 4 US-10-293-418-1905 Sequence 1905, Ap
985 44.5 54.3 240 4 US-10-293-418-2007 Sequence 2007, Ap
986 44.5 54.3 240 4 US-10-293-418-2016 Sequence 2016, Ap
987 44.5 54.3 240 4 US-10-293-418-2025 Sequence 2025, Ap
988 44.5 54.3 240 4 US-10-293-418-2029 Sequence 2029, Ap
989 44.5 54.3 240 4 US-10-293-418-2030 Sequence 2030, Ap
990 44.5 54.3 240 4 US-10-293-418-2041 Sequence 2041, Ap
991 44.5 54.3 240 4 US-10-293-418-2044 Sequence 2044, Ap
992 44.5 54.3 240 4 US-10-293-418-2045 Sequence 2045, Ap
993 44.5 54.3 240 4 US-10-293-418-2048 Sequence 2048, Ap
994 44.5 54.3 240 4 US-10-293-418-2105 Sequence 2105, Ap
995 44.5 54.3 240 4 US-10-293-418-2108 Sequence 2108, Ap
996 44.5 54.3 240 4 US-10-293-418-2113 Sequence 2113, Ap
997 44.5 54.3 240 4 US-10-293-418-2117 Sequence 2117, Ap
998 44.5 54.3 240 4 US-10-779-461-23 Sequence 23, Appl
999 44.5 54.3 242 6 US-11-090-847-88 Sequence 88, Appl
1000 44.5 54.3 243 4 US-10-689-921-2 Sequence 2, Appli

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ALIGNMENTS

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RESULT 1
US-09-155-106-2
; Sequence 2, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-2
Query Match 100.0%; Score 82; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | |
Db 1 SITSTGGTYHAESVKG 16

RESULT 2
US-10-808-538-2
; Sequence 2, Application US/10808538

```

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; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-808-538-2
Query Match 100.0%; Score 82; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
| | | | | | | | | | | | | | | |
Db 1 SITSTGGTYHAESVKG 16

RESULT 3
US-09-155-106-18
; Sequence 18, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-18

Query Match      87.2%; Score 71.5; DB 3; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
   ||||| ||||| ||||| |||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 4
US-09-155-106-19
; Sequence 19, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19

Query Match      87.2%; Score 71.5; DB 3; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
   ||||| ||||| ||||| |||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 5
US-09-155-106-20
; Sequence 20, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-20

Query Match      87.2%; Score 71.5; DB 3; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
   ||||| ||||| ||||| |||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 6
US-09-155-106-26
; Sequence 26, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-26

Query Match      87.2%; Score 71.5; DB 3; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
   ||||| ||||| ||||| |||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 7
US-09-155-106-32
; Sequence 32, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-155-106-32

Query Match 87.2%; Score 71.5; DB 3; Length 122;
Best Local Similarity 94.1%; Pred. NO. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SITST-GGTYHAESVKG 16
||||| |||||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 8

US-10-808-538-18
Sequence 18, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-808-538-18

Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. NO. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SITST-GGTYHAESVKG 16
||||| |||||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 9

US-10-808-538-19
Sequence 19, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-808-538-19

Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. NO. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SITST-GGTYHAESVKG 16
||||| |||||||
Db 50 SITSTGGGTYHAESVKG 66

RESULT 10

US-10-808-538-20
Sequence 20, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Immunomedics, Inc.
FILING DATE: 25-Mar-2004
PUBLICATION NO. US20050048053A1
PRIORITY APPLICATION DATA:
APPLICANT: Krah, Eugene
FILING DATE: 17-NOV-1998
PUBLICATION NO. US20040181039A1
PRIORITY APPLICATION DATA:
APPLICANT: Guo, Honliang
FILING DATE: 19-MAR-1997
PUBLICATION NO. US60/013,708
PRIORITY APPLICATION DATA:
APPLICANT: Lawton, Robert
FILING DATE: 20-MAR-1996
PUBLICATION NO. US60/344,874
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||
DB 50 SITSTGGTYHAESVKG 66

RESULT 11

US-10-808-538-26
Sequence 26, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:

APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Immunomedics, Inc.
FILING DATE: 25-Mar-2004

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-10-808-538-26
Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||
DB 50 SITSTGGTYHAESVKG 66

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||
DB 50 SITSTGGTYHAESVKG 66

RESULT 12

US-10-808-538-32
Sequence 32, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:

APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Immunomedics, Inc.
FILING DATE: 25-Mar-2004

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-808-538-32

Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||
DB 50 SITSTGGTYHAESVKG 66

RESULT 13

US-10-327-598-477
Sequence 477, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:

APPLICANT: Krah, Eugene
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-10-327-598-477
Query Match 87.2%; Score 71.5; DB 5; Length 122;
Best Local Similarity 94.1%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITST-GGTYHAESVKG 16
||||| |||||||
DB 50 SITSTGGTYHAESVKG 66

```
; LENGTH: 16
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-477

Query Match      70.7%; Score 58; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.017;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
   ||:||||:|:||||
Db 1 SSSSGGTYADAVKG 16

RESULT 14
US-10-815-449-1
; Sequence 1, Application US/10815449
; Publication No. US20040228859A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, Yvo
; APPLICANT: KOPETZKI, Erhard
; APPLICANT: KUENKELE, Klaus-Peter
; APPLICANT: MUNDIGL, Olaf
; APPLICANT: PARREN, Paul
; APPLICANT: REERS, Frank
; APPLICANT: SCHUMACHER, Ralf
; APPLICANT: Van de WINKEL, Jan
; APPLICANT: Van VUGT, Martine
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE REFERENCE: 21655 US2
; CURRENT APPLICATION NUMBER: US/10/815,449
; PRIOR APPLICATION NUMBER: US 60/459,837
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/463,003
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-449-1

Query Match      68.3%; Score 56; DB 5; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.31;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
   :|||:||||:|:||||
Db 50 AIGSGGTYADSVKG 65

RESULT 15
US-10-815-449-3
; Sequence 3, Application US/10815449
; Publication No. US20040228859A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, Yvo
; APPLICANT: KOPETZKI, Erhard
; APPLICANT: KUENKELE, Klaus-Peter
; APPLICANT: MUNDIGL, Olaf
; APPLICANT: PARREN, Paul
; APPLICANT: REERS, Frank
; APPLICANT: SCHUMACHER, Ralf
; APPLICANT: Van de WINKEL, Jan
; APPLICANT: Van VUGT, Martine
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE REFERENCE: 21655 US2
; CURRENT APPLICATION NUMBER: US/10/815,449
; CURRENT FILING DATE: 2004-04-01
```

```
; PRIOR APPLICATION NUMBER: US 60/459,837
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/463,003
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-449-3

Query Match      68.3%; Score 56; DB 5; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.31;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
   :|||:||||:|:||||
Db 50 AIGSGGTYADSVKG 65

RESULT 16
US-10-815-449-5
; Sequence 5, Application US/10815449
; Publication No. US20040228859A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, Yvo
; APPLICANT: KOPETZKI, Erhard
; APPLICANT: KUENKELE, Klaus-Peter
; APPLICANT: MUNDIGL, Olaf
; APPLICANT: PARREN, Paul
; APPLICANT: REERS, Frank
; APPLICANT: SCHUMACHER, Ralf
; APPLICANT: Van de WINKEL, Jan
; APPLICANT: Van VUGT, Martine
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE REFERENCE: 21655 US2
; CURRENT APPLICATION NUMBER: US/10/815,449
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 60/459,837
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/463,003
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-815-449-5

Query Match      68.3%; Score 56; DB 5; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.31;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
   :|||:||||:|:||||
Db 50 AIGSGGTYADSVKG 65

RESULT 17
US-09-880-748-1953
; Sequence 1953, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
```

; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1953
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-880-748-1953

Query Match 67.7%; Score 55.5; DB 3; Length 247;
 Best Local Similarity 70.6%; Pred. No. 0.82;
 Matches 12; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|||:|||||:|:|:|
 Db 50 AITSSGGATYYADSVKG 66

RESULT 18
 US-10-293-418-1953
 ; Sequence 1953, Application US/10293418
 ; Publication No. US20030223996A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1953
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-418-1953

Query Match 67.7%; Score 55.5; DB 4; Length 247;
 Best Local Similarity 70.6%; Pred. No. 0.82;
 Matches 12; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
 :|||:|||||:|:|:|
 Db 50 AITSSGGATYYADSVKG 66

RESULT 19
 US-10-031-874A-175
 ; Sequence 175, Application US/10031874A
 ; Publication No. US20030190598A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANHA, JAMSHID

; APPLICANT: DUBUC, GINETTE
 ; APPLICANT: NARANG, SARAN
 ; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
 ; FILE REFERENCE: 11054-1
 ; CURRENT APPLICATION NUMBER: US/10/031,874A
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/207,234
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 175
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Lama glama
 US-10-031-874A-175

Query Match 67.1%; Score 55; DB 4; Length 16;
 Best Local Similarity 73.3%; Pred. No. 0.052;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
 :|||:|||||:|:|:|
 Db 2 ITSSGGTDYADSVKG 16

RESULT 20
 US-10-996-316-166
 ; Sequence 166, Application US/10996316
 ; Publication No. US20050129690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexion Pharmaceuticals, Inc.
 ; APPLICANT: Bowdish, Katherine S.
 ; APPLICANT: McWhirter, John
 ; APPLICANT: Kretz-Rommel, Anke
 ; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
 ; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
 ; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
 ; CURRENT APPLICATION NUMBER: US/10/996,316
 ; CURRENT FILING DATE: 2004-11-23
 ; PRIOR APPLICATION NUMBER: US 10/894,672
 ; PRIOR FILING DATE: 2004-07-20
 ; PRIOR APPLICATION NUMBER: US 10/736,188
 ; PRIOR FILING DATE: 2003-12-15
 ; PRIOR APPLICATION NUMBER: US 10/379,151
 ; PRIOR FILING DATE: 2003-03-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/47931
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/254,113
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 211
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 166
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: murine
 US-10-996-316-166

Query Match 67.1%; Score 55; DB 5; Length 17;
 Best Local Similarity 68.8%; Pred. No. 0.055;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
 :|||:|||||:|:|:|
 Db 1 SITSSGGTYYPNSVKG 16

RESULT 21
 US-10-727-155-120
 ; Sequence 120, Application US/10727155
 ; Publication No. US20050049402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. Babcook

; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-26

Query Match 65.9%; Score 54; DB 4; Length 116;
Best Local Similarity 66.7%; Pred. No. 0.64;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| : ||||:||||
DB 51 IGTAGGTYADSVKG 65

RESULT 26
US-10-408-901-30
; Sequence 30, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:

; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-30

Query Match 65.9%; Score 54; DB 4; Length 446;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| : ||||:||||
DB 51 IGTAGGTYADSVKG 65

RESULT 27
US-10-408-901-50
; Sequence 50, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:

; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 446
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-408-901-50

Query Match 65.9%; Score 54; DB 4; Length 446;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
| : ||||:||||
DB 51 IGTAGGTYADSVKG 65

RESULT 28
US-10-214-524-33
; Sequence 33, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Pig (Sus scrofa)
US-10-214-524-33

Query Match 65.9%; Score 54; DB 4; Length 567;
Best Local Similarity 71.4%; Pred. No. 3.5;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 TSTGGTYHAESVKG 16
|| : ||||:||||
DB 72 TSAGSTTYADSVKG 85

RESULT 29
US-10-031-874A-32
; Sequence 32, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID
; APPLICANT: DUBUC, GINETTE
; APPLICANT: NARANG, SARAN
; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
; FILE REFERENCE: 11054-1
; CURRENT APPLICATION NUMBER: US/10/031,874A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/207,234
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Lama glama
US-10-031-874A-32

Query Match 64.6%; Score 53; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.11;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITSTGGTYHAESVKG 16
||| : ||||:||||

Db 2 ITSGGATYADSMKG 16

RESULT 30

US-10-450-036A-32

; Sequence 32, Application US/10450036A

; Publication No. US20040161738A1

; GENERAL INFORMATION:

; APPLICANT: MURUGANANDAM, ARUMUGAM

; APPLICANT: TANHA, JASMID

; APPLICANT: NARANG, SARAM

; APPLICANT: STANIMIROVIC, DANICA

; TITLE OF INVENTION: SINGLE-DOMAIN BRAIN TARGETING ANTIBODY FRAGMENTS

; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES

; FILE REFERENCE: 1339-25

; CURRENT APPLICATION NUMBER: US/10/450,036A

; CURRENT FILING DATE: 2004-01-09

; PRIOR APPLICATION NUMBER: PCT/CA01/00783

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/263,108

; PRIOR FILING DATE: 2001-01-22

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: Patent In Ver. 3.2

; SEQ ID NO 32

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Lama glama

US-10-450-036A-32

Query Match 64.6%; Score 53; DB 4; Length 16;

Best Local Similarity 66.7%; Pred. No. 0.11;

Matches 10; Conservative 3; Mismatches 2; Indels 2; Gaps 0;

Qy 2 ITSTGGTYHAESVKG 16

||| ||| ||| ||| |||

Db 2 ITSGGATYADSMKG 16

RESULT 31

US-09-864-761-47118

; Sequence 47118, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aecmica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 47118

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC004529.1

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 48

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

; OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUATE 1.00e-42

US-09-864-761-47118

Query Match 64.6%; Score 53; DB 3; Length 95;

Best Local Similarity 62.5%; Pred. No. 0.75;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16

:|: |||: |||

Db 46 AIGTGGGTYADSVKG 61

RESULT 32

US-10-194-975-48

; Sequence 48, Application US/10194975

; Publication No. US20030039649A1

; GENERAL INFORMATION:

; APPLICANT: Foote, Jefferson

; TITLE OF INVENTION: Super Humanized Antibodies

; FILE REFERENCE: 501231.01

; CURRENT APPLICATION NUMBER: US/10/194,975

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/305,111

; PRIOR FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 48

; LENGTH: 97

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-194-975-48

Query Match 64.6%; Score 53; DB 4; Length 97;

Best Local Similarity 62.5%; Pred. No. 0.77;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16

:|: |||: |||

Db 50 AIGTGGGTYADSVKG 65

RESULT 33

US-10-032-037B-70

; Sequence 70, Application US/10032037B

; Publication No. US20040001822A1

; GENERAL INFORMATION:

```
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-70

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65

RESULT 34
US-10-032-037B-71
; Sequence 71, Application US/10032037B
; Publication No. US2004000182A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-71

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65

RESULT 35
US-10-029-988B-70
; Sequence 70, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-70

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65

RESULT 36
US-10-029-988B-71
; Sequence 71, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-71

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65

RESULT 37
US-10-032-423A-70
; Sequence 70, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-70

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65

RESULT 38
US-10-032-423A-70

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SITSTGGTYHAESVKG 16
      :|: ||||:|:||||
Db      50 AIGTGGTYADSVKG 65
```

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US-10-032-423A-71
; Sequence 71, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-71

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
Db      50 AIGTGGGTYADSVKG 65

RESULT 39
US-10-029-926B-70
; Sequence 70, Application US/10029926B
; Publication No. US2004007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-70

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
Db      50 AIGTGGGTYADSVKG 65

RESULT 39
US-10-029-926B-70
; Sequence 70, Application US/10029926B
; Publication No. US2004007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-71

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
Db      50 AIGTGGGTYADSVKG 65

RESULT 40
US-10-029-926B-71
; Sequence 71, Application US/10029926B
; Publication No. US2004007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 71
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; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-71

Query Match      64.6%; Score 53; DB 4; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
Db      50 AIGTGGGTYADSVKG 65

RESULT 41
US-10-884-830-617
; Sequence 617, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 617
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-617

Query Match      64.6%; Score 53; DB 5; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
Db      50 AIGTGGGTYADSVKG 65

RESULT 42
US-10-884-830-618
; Sequence 618, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 618
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-618

Query Match      64.6%; Score 53; DB 5; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
       :|:||||:||||
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Db 50 AIGTGGTYADSVKVG 65

RESULT 43

US-10-911-838-18
; Sequence 18, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJ1-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 97
; TYPE: PRT
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-18

Query Match 64.6%; Score 53; DB 5; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.77;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKVG 16
:|:||||:||||
Db 50 AIGTGGTYADSVKVG 65

RESULT 44

US-09-864-761-38468
; Sequence 38468, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38468
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006352.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUE 5.00e-47
; OTHER INFORMATION: EST_HUMAN HIT: AW408304.1, EVALUE 1.00e-45
US-09-864-761-38468

Query Match 64.6%; Score 53; DB 3; Length 101;
Best Local Similarity 62.5%; Pred. No. 0.8;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKVG 16
:|:||||:||||
Db 52 AIGTGGTYADSVKVG 67

RESULT 45

US-10-687-799-54
; Sequence 54, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parzen, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687,799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02

; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-54

Query Match 64.6%; Score 53; DB 4; Length 116;
Best Local Similarity 62.5%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
: | : ||||:|:|
Db 69 AIGTGGTYADSVKG 84

RESULT 46

US-10-309-762-130
; Sequence 130, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-130

Query Match 64.6%; Score 53; DB 4; Length 121;
Best Local Similarity 76.9%; Pred. No. 0.97;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
| ||||:|:|
Db 54 SGGGTYADSVKG 66

RESULT 47

US-10-982-359-66
; Sequence 66, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAI heavy chain variable region
US-10-982-359-66

Query Match 64.6%; Score 53; DB 5; Length 123;
Best Local Similarity 62.5%; Pred. No. 0.99;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGGTYHAESVKG 16
: | : ||||:|:|
Db 50 AIGTGGTYADSVKG 65

RESULT 48

US-10-309-762-246
; Sequence 246, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-246

Query Match 64.6%; Score 53; DB 4; Length 182;
Best Local Similarity 76.9%; Pred. No. 1.5;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
| ||||:|:|
Db 54 SGGGTYADSVKG 66

RESULT 49

US-10-450-763-34993
; Sequence 34993, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34993
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (466)..(514)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031A, p-value=1.000e-40, raw score of 16.80
US-10-450-763-34993

Query Match 64.6%; Score 53; DB 5; Length 850;
Best Local Similarity 62.5%; Pred. No. 7.9;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
:|:||||:|
Db 515 AIGTGGGTYADSVKG 530

RESULT 50
US-10-450-763-50017
; Sequence 50017, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50017
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (472)..(520)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031A, p-value=1.000e-40, raw score of 16.80
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (92)..(568)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
; OTHER INFORMATION: E-value=1.6e-12, Pfam score of 45.4
US-10-450-763-50017

Query Match 64.6%; Score 53; DB 5; Length 869;
Best Local Similarity 62.5%; Pred. No. 8.1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
:|:||||:|
Db 121 AIGAGGGTYADSVKG 136

Search completed: May 11, 2006, 16:48:57
Job time : 127.656 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:42:11 ; Search time 19.9344 Seconds
(without alignments)
37.683 Million cell updates/sec

Title: US-10-808-538-2

Perfect score: 82

Sequence: 1 SITSTGCTVHAESVKG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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6	55.5	67.7	247 11	US-11-266-444-1953 Sequence 1953, Ap
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165	47.5	57.9	123	11	US-11-098-758-216	Sequence 216, Appl	238	47.5	57.9	470	11	US-11-144-222-46	Sequence 46, Appl
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255	47	57.3	122	11	US-11-199-739-574	Sequence 574, App	328	46.5	56.7	130	11	US-11-199-739-270	Sequence 270, App
256	47	57.3	123	11	US-11-102-512-56	Sequence 56, Appl	329	46.5	56.7	131	11	US-11-049-536-92	Sequence 92, Appl
257	47	57.3	123	11	US-11-049-536-478	Sequence 478, App	330	46.5	56.7	131	11	US-11-199-739-92	Sequence 92, Appl
258	47	57.3	125	11	US-11-199-739-478	Sequence 478, App	331	46.5	56.7	132	11	US-11-049-536-32	Sequence 32, Appl
259	47	57.3	126	11	US-11-049-536-422	Sequence 422, App	332	46.5	56.7	132	11	US-11-199-739-32	Sequence 32, Appl
260	47	57.3	126	11	US-11-199-739-422	Sequence 422, App	333	46.5	56.7	143	11	US-11-049-536-48	Sequence 48, Appl
261	47	57.3	128	11	US-11-049-536-76	Sequence 76, Appl	334	46.5	56.7	143	11	US-11-199-739-48	Sequence 48, Appl
262	47	57.3	128	11	US-11-049-536-76	Sequence 76, Appl	335	46.5	56.7	147	11	US-11-049-536-52	Sequence 52, Appl
263	47	57.3	129	11	US-11-049-536-554	Sequence 554, App	336	46.5	56.7	147	11	US-11-199-739-52	Sequence 52, Appl
264	47	57.3	129	11	US-11-199-739-554	Sequence 554, App	337	46	56.1	16	9	US-10-238-051-11	Sequence 11, Appl
265	47	57.3	152	11	US-11-267-310-7	Sequence 7, Appl	338	46	56.1	16	11	US-11-171-567-164	Sequence 164, App
266	47	57.3	152	11	US-11-267-191-7	Sequence 7, Appl	339	46	56.1	116	11	US-11-102-512-24	Sequence 24, Appl
267	47	57.3	240	11	US-11-054-515-2013	Sequence 2013, Ap	340	46	56.1	118	9	US-10-771-257-15	Sequence 15, Appl
268	47	57.3	240	11	US-11-266-444-2013	Sequence 2013, Ap	341	46	56.1	118	11	US-11-137-677-15	Sequence 15, Appl
269	47	57.3	242	11	US-11-054-515-1949	Sequence 1949, Ap	342	46	56.1	120	9	US-10-925-366A-5	Sequence 5, Appl
270	47	57.3	242	11	US-11-266-444-1949	Sequence 1949, Ap	343	46	56.1	120	9	US-10-925-366A-280	Sequence 280, App
271	47	57.3	243	11	US-11-054-515-1940	Sequence 1940, Ap	344	46	56.1	120	11	US-11-102-512-5	Sequence 5, Appl
272	47	57.3	243	11	US-11-266-444-1940	Sequence 1940, Ap	345	46	56.1	120	11	US-11-217-919-85	Sequence 85, Appl
273	47	57.3	246	11	US-11-054-515-1980	Sequence 1980, Ap	346	46	56.1	120	11	US-11-098-758-5	Sequence 5, Appl
274	47	57.3	246	11	US-11-266-444-1980	Sequence 1980, Ap	347	46	56.1	120	11	US-11-098-758-280	Sequence 280, App
275	47	57.3	250	11	US-11-054-515-883	Sequence 883, App	348	46	56.1	131	11	US-11-166-496-12	Sequence 12, Appl
276	47	57.3	250	11	US-11-266-444-883	Sequence 883, App	349	46	56.1	676	10	US-11-181-115-28	Sequence 28, Appl
277	47	57.3	251	11	US-11-266-444-1171	Sequence 1171, Ap	350	46	56.1	676	10	US-11-181-115-29	Sequence 29, Appl
278	47	57.3	251	11	US-11-054-515-1171	Sequence 1171, Ap	351	46	56.1	676	10	US-11-181-115-48	Sequence 48, Appl
279	47	57.3	367	11	US-11-266-444-83-899	Sequence 899, App	352	45.5	55.5	89	9	US-10-925-366A-342	Sequence 342, App
280	46.5	56.7	98	11	US-11-054-669-30	Sequence 30, Appl	353	45.5	55.5	89	11	US-11-098-758-342	Sequence 342, App
281	46.5	56.7	116	11	US-11-049-536-614	Sequence 614, App	354	45.5	55.5	116	11	US-11-102-512-21	Sequence 21, Appl
282	46.5	56.7	116	11	US-11-199-739-614	Sequence 614, App	355	45.5	55.5	118	11	US-11-217-919-156	Sequence 156, App
283	46.5	56.7	116	11	US-11-102-512-25	Sequence 25, Appl	356	45.5	55.5	119	9	US-10-925-366A-352	Sequence 352, App
284	46.5	56.7	116	11	US-11-102-512-30	Sequence 30, Appl	357	45.5	55.5	119	11	US-11-217-919-168	Sequence 168, App
285	46.5	56.7	116	11	US-11-102-512-80	Sequence 80, Appl	358	45.5	55.5	119	11	US-11-098-758-352	Sequence 352, App
286	46.5	56.7	117	11	US-11-049-536-190	Sequence 190, App	359	45.5	55.5	126	10	US-11-211-917-2	Sequence 2, Appl
287	46.5	56.7	117	11	US-11-049-536-274	Sequence 274, App	360	45.5	55.5	126	10	US-11-211-917-90	Sequence 90, Appl
288	46.5	56.7	117	11	US-11-049-536-414	Sequence 414, App	361	45.5	55.5	126	10	US-11-211-917-92	Sequence 92, Appl
289	46.5	56.7	117	11	US-11-049-536-462	Sequence 462, App	362	45.5	55.5	131	11	US-11-049-536-24	Sequence 24, Appl
290	46.5	56.7	117	11	US-11-049-536-530	Sequence 530, App	363	45.5	55.5	131	11	US-11-199-739-24	Sequence 24, Appl
291	46.5	56.7	117	11	US-11-199-739-190	Sequence 190, App	364	45.5	55.5	137	9	US-10-993-543-100	Sequence 100, App
292	46.5	56.7	117	11	US-11-199-739-274	Sequence 274, App	365	45.5	55.5	237	11	US-11-054-515-1941	Sequence 1941, Ap
293	46.5	56.7	117	11	US-11-199-739-414	Sequence 414, App	366	45.5	55.5	237	11	US-11-266-444-1941	Sequence 1941, Ap
294	46.5	56.7	117	11	US-11-199-739-462	Sequence 462, App	367	45.5	55.5	246	11	US-11-054-515-1314	Sequence 1314, Ap
295	46.5	56.7	117	11	US-11-199-739-530	Sequence 530, App	368	45.5	55.5	246	11	US-11-266-444-1314	Sequence 1314, Ap
296	46.5	56.7	118	9	US-10-771-257-8	Sequence 8, Appl	369	45.5	55.5	254	11	US-11-054-515-1673	Sequence 1673, Ap
297	46.5	56.7	118	11	US-11-127-677-8	Sequence 8, Appl	370	45.5	55.5	254	11	US-11-266-444-1673	Sequence 1673, Ap
298	46.5	56.7	118	11	US-11-049-536-546	Sequence 546, App	371	45.5	55.5	471	10	US-11-211-917-6	Sequence 6, Appl
299	46.5	56.7	118	11	US-11-199-739-546	Sequence 546, App	372	45	54.9	17	10	US-11-300-563-2	Sequence 2, Appl
300	46.5	56.7	119	11	US-11-049-536-330	Sequence 330, App	373	45	54.9	22	11	US-11-149-943-29	Sequence 29, Appl
301	46.5	56.7	119	11	US-11-049-536-362	Sequence 362, App	374	45	54.9	37	11	US-11-143-077-12	Sequence 12, Appl
302	46.5	56.7	119	11	US-11-049-536-402	Sequence 402, App	375	45	54.9	37	11	US-11-187-364-12	Sequence 12, Appl
303	46.5	56.7	119	11	US-11-049-536-638	Sequence 638, App	376	45	54.9	99	11	US-11-054-669-27	Sequence 27, Appl
304	46.5	56.7	119	11	US-11-199-739-330	Sequence 330, App	377	45	54.9	99	11	US-11-084-554-38	Sequence 38, Appl
305	46.5	56.7	119	11	US-11-199-739-362	Sequence 362, App	378	45	54.9	99	11	US-11-004-590-29	Sequence 29, Appl
306	46.5	56.7	119	11	US-11-199-739-402	Sequence 402, App	379	45	54.9	99	11	US-11-136-250-38	Sequence 38, Appl
307	46.5	56.7	119	11	US-11-199-739-638	Sequence 638, App	380	45	54.9	113	9	US-10-665-658-6	Sequence 6, Appl
308	46.5	56.7	120	11	US-11-049-536-586	Sequence 586, App	381	45	54.9	113	10	US-11-219-121-24	Sequence 24, Appl
309	46.5	56.7	120	11	US-11-049-536-666	Sequence 666, App	382	45	54.9	116	9	US-10-925-366A-213	Sequence 213, App
310	46.5	56.7	120	11	US-11-199-739-586	Sequence 586, App	383	45	54.9	116	9	US-10-925-366A-214	Sequence 214, App
311	46.5	56.7	120	11	US-11-199-739-666	Sequence 666, App	384	45	54.9	116	11	US-11-098-758-213	Sequence 213, App
312	46.5	56.7	122	11	US-11-049-536-278	Sequence 278, App	385	45	54.9	117	11	US-11-098-758-214	Sequence 214, App
313	46.5	56.7	122	11	US-11-049-536-302	Sequence 302, App	386	45	54.9	117	9	US-10-834-397-24	Sequence 24, Appl

387	45	54.9	117	9	US-10-981-356A-6	Sequence 6, Appli	460	44.5	54.3	119	9	US-10-473-037-49	Sequence 49, Appl
388	45	54.9	117	11	US-11-096-046-6	Sequence 6, Appli	461	44.5	54.3	121	9	US-10-925-366A-212	Sequence 212, App
389	45	54.9	117	11	US-11-049-536-458	Sequence 458, App	462	44.5	54.3	121	11	US-11-098-758-212	Sequence 212, App
390	45	54.9	117	11	US-11-049-536-610	Sequence 610, App	463	44.5	54.3	122	9	US-10-982-440-7	Sequence 7, Appli
391	45	54.9	117	11	US-11-199-739-458	Sequence 458, App	464	44.5	54.3	122	9	US-10-982-440-11	Sequence 11, Appl
392	45	54.9	117	11	US-11-199-739-610	Sequence 610, App	465	44.5	54.3	122	9	US-10-982-440-53	Sequence 53, Appl
393	45	54.9	118	11	US-11-049-536-198	Sequence 198, App	466	44.5	54.3	123	9	US-10-925-366A-218	Sequence 218, App
394	45	54.9	118	11	US-11-049-536-334	Sequence 334, App	467	44.5	54.3	123	11	US-11-098-758-218	Sequence 218, App
395	45	54.9	118	11	US-11-199-739-198	Sequence 198, App	468	44.5	54.3	130	11	US-11-228-293-8	Sequence 8, Appli
396	45	54.9	118	11	US-11-199-739-334	Sequence 334, App	469	44.5	54.3	130	11	US-11-228-293-18	Sequence 18, Appli
397	45	54.9	119	10	US-11-254-182-6	Sequence 6, Appli	470	44.5	54.3	130	11	US-11-228-319-8	Sequence 8, Appli
398	45	54.9	119	10	US-11-254-182-30	Sequence 30, Appl	471	44.5	54.3	130	11	US-11-228-319-18	Sequence 18, Appli
399	45	54.9	119	10	US-11-300-563-11	Sequence 11, Appl	472	44.5	54.3	138	9	US-10-473-037-1	Sequence 1, Appli
400	45	54.9	119	11	US-11-120-338-9	Sequence 9, Appli	473	44.5	54.3	150	11	US-11-267-310-9	Sequence 9, Appli
401	45	54.9	119	11	US-11-106-820-9	Sequence 9, Appli	474	44.5	54.3	150	11	US-11-267-310-9	Sequence 9, Appli
402	45	54.9	119	11	US-11-154-337-6	Sequence 6, Appli	475	44.5	54.3	153	11	US-11-267-310-11	Sequence 11, Appli
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404	45	54.9	119	11	US-11-049-536-418	Sequence 418, App	477	44.5	54.3	236	11	US-11-054-515-2010	Sequence 2010, App
405	45	54.9	119	11	US-11-049-536-538	Sequence 538, App	478	44.5	54.3	236	11	US-11-266-444-2010	Sequence 2010, App
406	45	54.9	119	11	US-11-049-536-562	Sequence 562, App	479	44.5	54.3	237	11	US-11-054-515-1906	Sequence 1906, App
407	45	54.9	119	11	US-11-143-077-9	Sequence 9, Appli	480	44.5	54.3	237	11	US-11-054-515-2003	Sequence 2003, App
408	45	54.9	119	11	US-11-190-364-9	Sequence 9, Appli	481	44.5	54.3	237	11	US-11-054-515-2005	Sequence 2005, App
409	45	54.9	119	11	US-11-102-120-6	Sequence 6, Appli	482	44.5	54.3	237	11	US-11-054-515-2006	Sequence 2006, App
410	45	54.9	119	11	US-11-147-780-9	Sequence 9, Appli	483	44.5	54.3	237	11	US-11-054-515-2017	Sequence 2017, App
411	45	54.9	119	11	US-11-223-361-6	Sequence 6, Appli	484	44.5	54.3	237	11	US-11-054-515-2019	Sequence 2019, App
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413	45	54.9	119	11	US-11-199-739-418	Sequence 418, App	486	44.5	54.3	237	11	US-11-054-515-2027	Sequence 2027, App
414	45	54.9	119	11	US-11-199-739-538	Sequence 538, App	487	44.5	54.3	237	11	US-11-054-515-2028	Sequence 2028, App
415	45	54.9	119	11	US-11-199-739-562	Sequence 562, App	488	44.5	54.3	237	11	US-11-054-515-2036	Sequence 2036, App
416	45	54.9	119	11	US-11-187-364-9	Sequence 9, Appli	489	44.5	54.3	237	11	US-11-054-515-2039	Sequence 2039, App
417	45	54.9	119	11	US-11-222-587-6	Sequence 6, Appli	490	44.5	54.3	237	11	US-11-054-515-2040	Sequence 2040, App
418	45	54.9	119	11	US-11-234-586-6	Sequence 6, Appli	491	44.5	54.3	237	11	US-11-054-515-2043	Sequence 2043, App
419	45	54.9	121	11	US-11-049-536-622	Sequence 622, App	492	44.5	54.3	237	11	US-11-054-515-2104	Sequence 2104, App
420	45	54.9	121	11	US-11-199-739-622	Sequence 622, App	493	44.5	54.3	237	11	US-11-054-515-2110	Sequence 2110, App
421	45	54.9	122	11	US-11-049-536-186	Sequence 186, App	494	44.5	54.3	237	11	US-11-054-515-2111	Sequence 2111, App
422	45	54.9	122	11	US-11-199-739-186	Sequence 186, App	495	44.5	54.3	237	11	US-11-054-515-2112	Sequence 2112, App
423	45	54.9	123	11	US-11-049-536-238	Sequence 238, App	496	44.5	54.3	237	11	US-11-054-515-2114	Sequence 2114, App
424	45	54.9	123	11	US-11-049-536-378	Sequence 378, App	497	44.5	54.3	237	11	US-11-054-515-2115	Sequence 2115, App
425	45	54.9	123	11	US-11-049-536-398	Sequence 398, App	498	44.5	54.3	237	11	US-11-054-515-2118	Sequence 2118, App
426	45	54.9	123	11	US-11-199-739-238	Sequence 238, App	499	44.5	54.3	237	11	US-11-266-444-1906	Sequence 1906, App
427	45	54.9	123	11	US-11-199-739-378	Sequence 378, App	500	44.5	54.3	237	11	US-11-266-444-2003	Sequence 2003, App
428	45	54.9	123	11	US-11-199-739-398	Sequence 398, App	501	44.5	54.3	237	11	US-11-266-444-2005	Sequence 2005, App
429	45	54.9	123	11	US-11-102-512-79	Sequence 79, Appl	502	44.5	54.3	237	11	US-11-266-444-2006	Sequence 2006, App
430	45	54.9	124	11	US-11-049-536-298	Sequence 298, App	503	44.5	54.3	237	11	US-11-266-444-2017	Sequence 2017, App
431	45	54.9	124	11	US-11-199-739-298	Sequence 298, App	504	44.5	54.3	237	11	US-11-266-444-2019	Sequence 2019, App
432	45	54.9	124	11	US-11-102-512-61	Sequence 61, Appl	505	44.5	54.3	237	11	US-11-266-444-2020	Sequence 2020, App
433	45	54.9	127	11	US-11-049-536-446	Sequence 446, App	506	44.5	54.3	237	11	US-11-266-444-2027	Sequence 2027, App
434	45	54.9	127	11	US-11-199-739-446	Sequence 446, App	507	44.5	54.3	237	11	US-11-266-444-2028	Sequence 2028, App
435	45	54.9	135	9	US-10-993-543-36	Sequence 36, Appl	508	44.5	54.3	237	11	US-11-266-444-2036	Sequence 2036, App
436	45	54.9	137	11	US-11-049-536-80	Sequence 80, Appl	509	44.5	54.3	237	11	US-11-266-444-2039	Sequence 2039, App
437	45	54.9	137	11	US-11-199-739-80	Sequence 80, Appl	510	44.5	54.3	237	11	US-11-266-444-2040	Sequence 2040, App
438	45	54.9	159	11	US-11-000-463-333	Sequence 333, App	511	44.5	54.3	237	11	US-11-266-444-2043	Sequence 2043, App
439	45	54.9	216	11	US-11-128-440-13	Sequence 13, Appl	512	44.5	54.3	237	11	US-11-266-444-2104	Sequence 2104, App
440	45	54.9	217	11	US-11-128-440-11	Sequence 11, Appl	513	44.5	54.3	237	11	US-11-266-444-2110	Sequence 2110, App
441	45	54.9	247	11	US-11-054-515-1652	Sequence 1652, App	514	44.5	54.3	237	11	US-11-266-444-2111	Sequence 2111, App
442	45	54.9	247	11	US-11-266-444-1652	Sequence 1652, App	515	44.5	54.3	237	11	US-11-266-444-2112	Sequence 2112, App
443	45	54.9	249	11	US-11-084-515-941	Sequence 941, App	516	44.5	54.3	237	11	US-11-266-444-2114	Sequence 2114, App
444	45	54.9	249	11	US-11-266-444-941	Sequence 941, App	517	44.5	54.3	237	11	US-11-266-444-2115	Sequence 2115, App
445	45	54.9	448	10	US-11-219-121-28	Sequence 28, Appl	518	44.5	54.3	237	11	US-11-266-444-2118	Sequence 2118, App
446	45	54.9	470	11	US-11-041-095-22	Sequence 22, Appl	519	44.5	54.3	238	11	US-11-054-515-2034	Sequence 2034, App
447	45	54.9	475	11	US-11-041-095-16	Sequence 16, Appl	520	44.5	54.3	238	11	US-11-266-444-2034	Sequence 2034, App
448	45	54.9	526	11	US-11-041-095-10	Sequence 10, Appl	521	44.5	54.3	239	11	US-11-054-515-2034	Sequence 2034, App
449	44.5	54.3	17	9	US-10-473-037-4	Sequence 4, Appli	522	44.5	54.3	239	11	US-11-266-444-2034	Sequence 1905, App
450	44.5	54.3	17	9	US-10-982-440-11	Sequence 11, App	523	44.5	54.3	240	11	US-11-054-515-1905	Sequence 2007, App
451	44.5	54.3	22	11	US-11-149-943-16	Sequence 16, Appl	524	44.5	54.3	240	11	US-11-054-515-2007	Sequence 2016, App
452	44.5	54.3	98	11	US-11-144-248-30	Sequence 30, Appl	525	44.5	54.3	240	11	US-11-054-515-2016	Sequence 2025, App
453	44.5	54.3	98	11	US-11-054-669-17	Sequence 17, Appl	526	44.5	54.3	240	11	US-11-054-515-2025	Sequence 2029, App
454	44.5	54.3	98	11	US-11-084-554-27	Sequence 27, Appl	527	44.5	54.3	240	11	US-11-054-515-2029	Sequence 2030, App
455	44.5	54.3	98	11	US-11-144-222-30	Sequence 30, Appl	528	44.5	54.3	240	11	US-11-054-515-2030	Sequence 2041, App
456	44.5	54.3	98	11	US-11-004-590-16	Sequence 16, Appl	529	44.5	54.3	240	11	US-11-054-515-2041	Sequence 2044, App
457	44.5	54.3	98	11	US-11-136-250-27	Sequence 27, Appl	530	44.5	54.3	240	11	US-11-054-515-2044	Sequence 2045, App
458	44.5	54.3	98	11	US-11-182-343-30	Sequence 30, Appl	531	44.5	54.3	240	11	US-11-054-515-2045	Sequence 2048, App
459	44.5	54.3	119	9	US-10-473-037-9	Sequence 9, Appli	532	44.5	54.3	240	11	US-11-054-515-2048	

533	44.5	54.3	240	11	US-11-054-515-2105	Sequence 2105, Ap	606	43.5	53.0	125	11	US-11-127-903-46	Sequence 46, Appl
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536	44.5	54.3	240	11	US-11-054-515-2117	Sequence 2117, Ap	609	43.5	53.0	138	9	US-10-789-273-12	Sequence 12, Appl
537	44.5	54.3	240	11	US-11-266-444-1905	Sequence 1905, Ap	610	43.5	53.0	139	9	US-10-721-763-33	Sequence 33, Appl
538	44.5	54.3	240	11	US-11-266-444-2007	Sequence 2007, Ap	611	43.5	53.0	240	11	US-11-054-515-1886	Sequence 1886, Ap
539	44.5	54.3	240	11	US-11-266-444-2016	Sequence 2016, Ap	612	43.5	53.0	240	11	US-11-054-515-2059	Sequence 2059, Ap
540	44.5	54.3	240	11	US-11-266-444-2025	Sequence 2025, Ap	613	43.5	53.0	240	11	US-11-054-515-2061	Sequence 2061, Ap
541	44.5	54.3	240	11	US-11-266-444-2029	Sequence 2029, Ap	614	43.5	53.0	240	11	US-11-266-444-1886	Sequence 1886, Ap
542	44.5	54.3	240	11	US-11-266-444-2030	Sequence 2030, Ap	615	43.5	53.0	240	11	US-11-266-444-2059	Sequence 2059, Ap
543	44.5	54.3	240	11	US-11-266-444-2041	Sequence 2041, Ap	616	43.5	53.0	240	11	US-11-266-444-2061	Sequence 2061, Ap
544	44.5	54.3	240	11	US-11-266-444-2044	Sequence 2044, Ap	617	43.5	53.0	244	11	US-11-054-515-1924	Sequence 1924, Ap
545	44.5	54.3	240	11	US-11-266-444-2045	Sequence 2045, Ap	618	43.5	53.0	244	11	US-11-266-444-1924	Sequence 1924, Ap
546	44.5	54.3	240	11	US-11-266-444-2048	Sequence 2048, Ap	619	43.5	53.0	250	11	US-11-054-515-1461	Sequence 1461, Ap
547	44.5	54.3	240	11	US-11-266-444-2105	Sequence 2105, Ap	620	43.5	53.0	250	11	US-11-266-444-1461	Sequence 1461, Ap
548	44.5	54.3	240	11	US-11-266-444-2108	Sequence 2108, Ap	621	43.5	53.0	469	10	US-11-211-917-54	Sequence 54, Appl
549	44.5	54.3	240	11	US-11-266-444-2113	Sequence 2113, Ap	622	43.5	53.0	470	11	US-11-144-248-45	Sequence 45, Appl
550	44.5	54.3	240	11	US-11-266-444-2117	Sequence 2117, Ap	623	43.5	53.0	470	11	US-11-144-222-45	Sequence 45, Appl
551	44.5	54.3	248	11	US-11-054-515-1965	Sequence 1965, Ap	624	43.5	53.0	470	11	US-11-182-343-45	Sequence 45, Appl
552	44.5	54.3	248	11	US-11-054-515-1974	Sequence 1974, Ap	625	43.5	53.0	16	11	US-11-093-274-6	Sequence 6, Appl
553	44.5	54.3	248	11	US-11-266-444-1965	Sequence 1965, Ap	626	43	52.4	110	9	US-10-771-257-1	Sequence 1, Appl
554	44.5	54.3	248	11	US-11-266-444-1974	Sequence 1974, Ap	627	43	52.4	110	11	US-11-127-677-1	Sequence 1, Appl
555	44.5	54.3	250	11	US-11-054-515-1179	Sequence 1179, Ap	628	43	52.4	114	11	US-11-217-919-153	Sequence 153, Ap
556	44.5	54.3	250	11	US-11-266-444-1179	Sequence 1179, Ap	629	43	52.4	116	11	US-11-093-274-21	Sequence 21, Appl
557	44.5	54.3	256	11	US-11-054-515-2119	Sequence 2119, Ap	630	43	52.4	116	11	US-11-093-274-36	Sequence 36, Appl
558	44.5	54.3	256	11	US-11-266-444-2119	Sequence 2119, Ap	631	43	52.4	117	11	US-11-127-903-44	Sequence 44, Appl
559	44.5	54.3	473	11	US-11-144-248-50	Sequence 50, Appl	632	43	52.4	117	11	US-11-049-536-686	Sequence 686, Ap
560	44.5	54.3	473	11	US-11-144-248-50	Sequence 50, Appl	633	43	52.4	117	11	US-11-199-739-686	Sequence 686, Ap
561	44.5	54.3	473	11	US-11-182-343-50	Sequence 50, Appl	634	43	52.4	119	9	US-10-771-257-10	Sequence 10, Appl
562	44	53.7	117	11	US-11-049-536-354	Sequence 354, Ap	635	43	52.4	119	11	US-11-127-677-10	Sequence 10, Appl
563	44	53.7	117	11	US-11-049-536-390	Sequence 390, Ap	636	43	52.4	123	9	US-10-993-543-92	Sequence 92, Appl
564	44	53.7	117	11	US-11-049-536-558	Sequence 558, Ap	637	43	52.4	126	11	US-11-127-932-5	Sequence 5, Appl
565	44	53.7	117	11	US-11-049-536-634	Sequence 634, Ap	638	43	52.4	126	11	US-11-127-903-5	Sequence 5, Appl
566	44	53.7	117	11	US-11-049-536-662	Sequence 642, Ap	639	43	52.4	132	9	US-10-993-543-12	Sequence 12, Appl
567	44	53.7	117	11	US-11-049-536-698	Sequence 698, Ap	640	43	52.4	137	11	US-11-049-536-72	Sequence 72, Appl
568	44	53.7	117	11	US-11-199-739-354	Sequence 354, Ap	641	43	52.4	137	11	US-11-199-739-72	Sequence 72, Appl
569	44	53.7	117	11	US-11-199-739-390	Sequence 390, Ap	642	42.5	51.8	96	9	US-10-993-543-236	Sequence 236, Ap
570	44	53.7	117	11	US-11-199-739-558	Sequence 558, Ap	643	42.5	51.8	96	9	US-10-993-543-238	Sequence 238, Ap
571	44	53.7	117	11	US-11-199-739-634	Sequence 634, Ap	644	42.5	51.8	115	11	US-11-127-932-2	Sequence 2, Appl
572	44	53.7	117	11	US-11-199-739-662	Sequence 642, Ap	645	42.5	51.8	115	11	US-11-127-932-3	Sequence 3, Appl
573	44	53.7	117	11	US-11-199-739-698	Sequence 698, Ap	646	42.5	51.8	115	11	US-11-127-932-6	Sequence 6, Appl
574	44	53.7	119	11	US-11-049-536-502	Sequence 502, Ap	647	42.5	51.8	115	11	US-11-127-932-7	Sequence 7, Appl
575	44	53.7	119	11	US-11-049-536-650	Sequence 650, Ap	648	42.5	51.8	115	11	US-11-127-932-8	Sequence 8, Appl
576	44	53.7	119	11	US-11-199-739-502	Sequence 502, Ap	649	42.5	51.8	115	11	US-11-127-932-9	Sequence 9, Appl
577	44	53.7	119	11	US-11-199-739-650	Sequence 650, Ap	650	42.5	51.8	115	11	US-11-127-932-10	Sequence 10, Appl
578	44	53.7	123	11	US-11-049-536-410	Sequence 410, Ap	651	42.5	51.8	115	11	US-11-127-903-2	Sequence 2, Appl
579	44	53.7	123	11	US-11-199-739-410	Sequence 410, Ap	652	42.5	51.8	115	11	US-11-127-903-3	Sequence 3, Appl
580	44	53.7	125	11	US-11-049-536-214	Sequence 214, Ap	653	42.5	51.8	115	11	US-11-127-903-6	Sequence 6, Appl
581	44	53.7	125	11	US-11-199-739-214	Sequence 214, Ap	654	42.5	51.8	115	11	US-11-127-903-7	Sequence 7, Appl
582	44	53.7	127	11	US-11-049-536-454	Sequence 454, Ap	655	42.5	51.8	115	11	US-11-127-903-8	Sequence 8, Appl
583	44	53.7	127	11	US-11-199-739-454	Sequence 454, Ap	656	42.5	51.8	115	11	US-11-127-903-9	Sequence 9, Appl
584	44	53.7	146	11	US-11-049-536-16	Sequence 16, Appl	657	42.5	51.8	115	11	US-11-127-903-10	Sequence 10, Appl
585	44	53.7	146	11	US-11-199-739-16	Sequence 16, Appl	658	42.5	51.8	116	11	US-11-102-512-16	Sequence 16, Appl
586	44	53.7	247	11	US-11-054-515-915	Sequence 915, Ap	659	42.5	51.8	116	11	US-11-102-512-43	Sequence 43, Appl
587	44	53.7	247	11	US-11-054-515-923	Sequence 923, Ap	660	42.5	51.8	116	11	US-11-102-512-81	Sequence 81, Appl
588	44	53.7	247	11	US-11-266-444-915	Sequence 915, Ap	661	42.5	51.8	119	11	US-11-102-512-20	Sequence 20, Appl
589	44	53.7	247	11	US-11-266-444-923	Sequence 923, Ap	662	42.5	51.8	123	9	US-10-993-543-112	Sequence 112, Ap
590	44	53.7	384	11	US-11-000-463-804	Sequence 804, Ap	663	42.5	51.8	126	9	US-10-993-543-96	Sequence 96, Appl
591	44	53.7	384	11	US-11-000-463-805	Sequence 805, Ap	664	42.5	51.8	129	9	US-10-771-257-61	Sequence 61, Appl
592	44	53.7	384	11	US-11-000-463-806	Sequence 806, Ap	665	42.5	51.8	129	9	US-10-993-543-180	Sequence 180, Ap
593	44	53.7	384	11	US-11-000-463-807	Sequence 807, Ap	666	42.5	51.8	129	11	US-11-127-677-59	Sequence 59, Appl
594	43.5	53.0	119	11	US-11-102-512-46	Sequence 46, Appl	667	42.5	51.8	130	11	US-10-993-543-20	Sequence 20, Appl
595	43.5	53.0	120	11	US-11-049-536-258	Sequence 258, Ap	668	42.5	51.8	130	11	US-11-109-264-52	Sequence 52, Appl
596	43.5	53.0	120	11	US-11-199-739-258	Sequence 258, Ap	669	42.5	51.8	130	11	US-11-109-264-53	Sequence 53, Appl
597	43.5	53.0	123	11	US-11-049-536-510	Sequence 510, Ap	670	42.5	51.8	135	9	US-10-993-543-44	Sequence 44, Appl
598	43.5	53.0	123	11	US-11-199-739-510	Sequence 510, Ap	671	42.5	51.8	239	11	US-11-054-515-1882	Sequence 1882, Ap
599	43.5	53.0	124	10	US-11-211-917-50	Sequence 50, Appl	672	42.5	51.8	239	11	US-11-266-444-1882	Sequence 1882, Ap
600	43.5	53.0	124	10	US-11-211-917-96	Sequence 96, Appl	673	42.5	51.8	256	11	US-11-054-515-1392	Sequence 1392, Ap
601	43.5	53.0	124	11	US-11-144-248-8	Sequence 8, Appl	674	42.5	51.8	256	11	US-11-266-444-1392	Sequence 1392, Ap
602	43.5	53.0	124	11	US-11-144-248-8	Sequence 8, Appl	675	42	51.2	15	11	US-11-171-567-67	Sequence 67, Appl
603	43.5	53.0	124	11	US-11-144-248-8	Sequence 8, Appl	676	42	51.2	16	9	US-10-982-440-140	Sequence 140, Ap
604	43.5	53.0	125	9	US-10-771-257-6	Sequence 6, Appl	677	42	51.2	19	9	US-10-880-238-115	Sequence 115, Ap
605	43.5	53.0	125	11	US-11-127-677-6	Sequence 6, Appl	678	42	51.2	19	11	US-11-108-135-30	Sequence 30, Appl

679	42	51.2	19	11	US-11-126-978-30	Sequence 30, Appl	752	41	50.0	243	11	US-11-054-515-1942	Sequence 1942, Ap
680	42	51.2	19	11	US-11-171-567-161	Sequence 161, App	753	41	50.0	243	11	US-11-054-515-1944	Sequence 1944, Ap
681	42	51.2	19	11	US-11-217-995-2	Sequence 2, Appl	754	41	50.0	243	11	US-11-266-444-1929	Sequence 1929, Ap
682	42	51.2	95	8	US-10-489-071-23	Sequence 23, Appl	755	41	50.0	243	11	US-11-266-444-1942	Sequence 1942, Ap
683	42	51.2	112	9	US-10-982-440-57	Sequence 57, Appl	756	41	50.0	243	11	US-11-266-444-1944	Sequence 1944, Ap
684	42	51.2	115	11	US-11-108-135-37	Sequence 37, Appl	757	41	50.0	444	11	US-11-172-320-6	Sequence 6, Appl
685	42	51.2	115	11	US-11-126-978-37	Sequence 37, Appl	758	41	50.0	444	11	US-11-172-320-6	Sequence 6, Appl
686	42	51.2	125	11	US-11-041-471-14	Sequence 14, Appl	759	41	50.0	979	11	US-11-072-512-2446	Sequence 2446, Ap
687	42	51.2	131	9	US-10-993-543-140	Sequence 140, App	760	40.5	49.4	17	11	US-11-097-812-167	Sequence 167, App
688	42	51.2	149	11	US-11-267-310-67	Sequence 67, Appl	761	40.5	49.4	115	11	US-11-097-812-22	Sequence 22, Appl
689	42	51.2	149	11	US-11-267-191-67	Sequence 67, Appl	762	40.5	49.4	115	11	US-11-097-812-26	Sequence 26, Appl
690	42	51.2	222	11	US-11-217-995-7	Sequence 7, Appl	763	40.5	49.4	116	11	US-11-102-512-22	Sequence 22, Appl
691	42	51.2	459	9	US-10-496-284-64	Sequence 64, Appl	764	40.5	49.4	116	11	US-11-102-512-44	Sequence 44, Appl
692	42	51.2	722	11	US-11-079-463-9749	Sequence 9749, Ap	765	40.5	49.4	119	11	US-11-097-812-149	Sequence 149, App
693	41.5	50.6	113	11	US-11-049-536-106	Sequence 106, App	766	40.5	49.4	119	11	US-11-097-812-150	Sequence 150, App
694	41.5	50.6	113	11	US-11-199-739-106	Sequence 106, App	767	40.5	49.4	119	11	US-11-049-536-394	Sequence 394, App
695	41.5	50.6	116	11	US-11-102-512-66	Sequence 66, Appl	768	40.5	49.4	119	11	US-11-199-739-394	Sequence 394, App
696	41.5	50.6	117	11	US-11-049-536-178	Sequence 178, App	769	40.5	49.4	120	11	US-11-049-536-230	Sequence 230, App
697	41.5	50.6	117	11	US-11-049-536-222	Sequence 222, App	770	40.5	49.4	120	11	US-11-199-739-230	Sequence 230, App
698	41.5	50.6	117	11	US-11-049-536-226	Sequence 226, App	771	40.5	49.4	123	9	US-10-925-366A-217	Sequence 217, App
699	41.5	50.6	117	11	US-11-199-739-178	Sequence 178, App	772	40.5	49.4	123	11	US-11-098-758-217	Sequence 217, App
700	41.5	50.6	117	11	US-11-199-739-222	Sequence 222, App	773	40.5	49.4	125	9	US-10-993-543-168	Sequence 168, App
701	41.5	50.6	117	11	US-11-199-739-226	Sequence 226, App	774	40.5	49.4	131	11	US-11-049-536-84	Sequence 84, Appl
702	41.5	50.6	118	11	US-11-049-536-266	Sequence 266, App	775	40.5	49.4	131	11	US-11-199-739-84	Sequence 84, Appl
703	41.5	50.6	118	11	US-11-199-739-266	Sequence 266, App	776	40.5	49.4	135	9	US-10-993-543-60	Sequence 60, Appl
704	41.5	50.6	119	11	US-11-049-536-282	Sequence 282, App	777	40.5	49.4	140	9	US-10-504-389A-51	Sequence 51, Appl
705	41.5	50.6	119	11	US-11-049-536-306	Sequence 306, App	778	40.5	49.4	240	11	US-11-054-515-2052	Sequence 2052, Ap
706	41.5	50.6	119	11	US-11-049-536-550	Sequence 550, App	779	40.5	49.4	240	11	US-11-266-444-2052	Sequence 2052, Ap
707	41.5	50.6	119	11	US-11-199-739-282	Sequence 282, App	780	40.5	49.4	247	11	US-11-054-515-1978	Sequence 1978, Ap
708	41.5	50.6	119	11	US-11-199-739-306	Sequence 306, App	781	40.5	49.4	247	11	US-11-266-444-1978	Sequence 1978, Ap
709	41.5	50.6	119	11	US-11-199-739-550	Sequence 550, App	782	40.5	49.4	256	11	US-11-054-515-1604	Sequence 1604, Ap
710	41.5	50.6	121	9	US-10-771-257-7	Sequence 7, Appl	783	40.5	49.4	256	11	US-11-266-444-1604	Sequence 1604, Ap
711	41.5	50.6	121	11	US-11-127-677-7	Sequence 7, Appl	784	40	48.8	15	9	US-10-507-662-6	Sequence 6, Appl
712	41.5	50.6	122	9	US-10-771-257-57	Sequence 57, Appl	785	40	48.8	20	11	US-11-149-943-28	Sequence 28, Appl
713	41.5	50.6	122	11	US-11-127-677-55	Sequence 55, Appl	786	40	48.8	20	11	US-11-149-943-38	Sequence 38, Appl
714	41.5	50.6	123	9	US-10-771-257-84	Sequence 84, Appl	787	40	48.8	115	9	US-10-925-366A-227	Sequence 227, App
715	41.5	50.6	123	9	US-10-771-257-88	Sequence 88, Appl	788	40	48.8	115	11	US-11-098-758-227	Sequence 227, App
716	41.5	50.6	123	9	US-10-771-257-90	Sequence 90, Appl	789	40	48.8	116	9	US-10-925-366A-209	Sequence 209, App
717	41.5	50.6	123	9	US-10-771-257-95	Sequence 95, Appl	790	40	48.8	116	11	US-11-102-512-34	Sequence 34, Appl
718	41.5	50.6	124	11	US-11-049-536-594	Sequence 594, App	791	40	48.8	116	11	US-11-098-758-209	Sequence 209, App
719	41.5	50.6	124	11	US-11-199-739-594	Sequence 594, App	792	40	48.8	117	11	US-11-037-199-28	Sequence 28, Appl
720	41.5	50.6	127	11	US-11-049-536-64	Sequence 64, Appl	793	40	48.8	117	11	US-11-037-199-36	Sequence 36, Appl
721	41.5	50.6	127	11	US-11-199-739-64	Sequence 64, Appl	794	40	48.8	120	9	US-10-507-662-24	Sequence 24, Appl
722	41.5	50.6	128	9	US-10-993-543-72	Sequence 72, Appl	795	40	48.8	120	11	US-11-005-726-3	Sequence 3, Appl
723	41.5	50.6	131	9	US-10-993-543-80	Sequence 80, Appl	796	40	48.8	123	11	US-11-102-512-18	Sequence 18, Appl
724	41.5	50.6	132	9	US-10-993-543-152	Sequence 152, App	797	40	48.8	125	11	US-11-127-903-21	Sequence 21, Appl
725	41.5	50.6	134	9	US-10-993-543-172	Sequence 172, App	798	40	48.8	125	11	US-11-049-536-326	Sequence 326, App
726	41.5	50.6	142	9	US-10-993-543-132	Sequence 132, App	799	40	48.8	127	11	US-11-199-739-326	Sequence 326, App
727	41.5	50.6	148	11	US-11-049-536-20	Sequence 20, Appl	800	40	48.8	154	9	US-10-496-284-53	Sequence 53, Appl
728	41.5	50.6	148	11	US-11-199-739-20	Sequence 20, Appl	801	40	48.8	237	9	US-10-073-301A-9	Sequence 9, Appl
729	41.5	50.6	157	11	US-11-049-536-110	Sequence 110, App	802	40	48.8	237	11	US-11-203-137-9	Sequence 9, Appl
730	41.5	50.6	157	11	US-11-199-739-110	Sequence 110, App	803	40	48.8	242	11	US-11-170-653-41	Sequence 41, Appl
731	41.5	50.6	254	11	US-11-054-515-1295	Sequence 1295, Ap	804	40	48.8	246	11	US-11-054-515-2075	Sequence 2075, Ap
732	41.5	50.6	254	11	US-11-266-444-1295	Sequence 1295, Ap	805	40	48.8	246	11	US-11-266-444-2075	Sequence 2075, Ap
733	41.5	50.6	256	11	US-11-054-515-1209	Sequence 1209, Ap	806	40	48.8	253	11	US-11-054-515-938	Sequence 938, App
734	41.5	50.6	256	11	US-11-266-444-1209	Sequence 1209, Ap	807	40	48.8	253	11	US-11-266-444-938	Sequence 938, App
735	41.5	50.6	258	11	US-11-054-515-1841	Sequence 1841, Ap	808	40	48.8	323	11	US-11-087-099-2157	Sequence 2157, Ap
736	41.5	50.6	258	11	US-11-266-444-1841	Sequence 1841, Ap	809	40	48.8	434	9	US-10-530-386-174	Sequence 174, App
737	41	50.0	96	11	US-11-084-554-37	Sequence 37, Appl	810	40	48.8	514	9	US-10-467-657-2664	Sequence 2664, Ap
738	41	50.0	96	11	US-11-004-590-38	Sequence 38, Appl	811	40	48.8	678	11	US-11-087-099-9248	Sequence 9248, Ap
739	41	50.0	96	11	US-11-136-250-37	Sequence 37, Appl	812	40	48.8	860	11	US-11-079-463-9959	Sequence 9959, Ap
740	41	50.0	97	11	US-11-004-590-28	Sequence 28, Appl	813	39.5	48.2	17	8	US-10-614-959-28	Sequence 28, Appl
741	41	50.0	102	9	US-10-997-201A-6	Sequence 6, Appl	814	39.5	48.2	115	11	US-11-127-903-24	Sequence 24, Appl
742	41	50.0	112	9	US-10-771-257-3	Sequence 3, Appl	815	39.5	48.2	116	9	US-10-925-366A-215	Sequence 215, App
743	41	50.0	112	11	US-11-127-677-3	Sequence 3, Appl	816	39.5	48.2	116	11	US-11-049-536-674	Sequence 674, App
744	41	50.0	112	11	US-11-137-932-1	Sequence 1, Appl	817	39.5	48.2	116	11	US-11-199-739-674	Sequence 674, App
745	41	50.0	112	11	US-11-127-903-1	Sequence 1, Appl	818	39.5	48.2	116	11	US-11-102-512-32	Sequence 32, Appl
746	41	50.0	125	11	US-11-127-903-43	Sequence 43, Appl	819	39.5	48.2	116	11	US-11-102-512-33	Sequence 33, Appl
747	41	50.0	133	9	US-10-993-543-184	Sequence 184, App	820	39.5	48.2	116	11	US-11-102-512-73	Sequence 73, Appl
748	41	50.0	137	11	US-11-049-536-68	Sequence 68, Appl	821	39.5	48.2	116	11	US-11-098-758-215	Sequence 215, App
749	41	50.0	137	11	US-11-199-739-68	Sequence 68, Appl	822	39.5	48.2	117	11	US-11-165-023-30	Sequence 30, Appl
750	41	50.0	228	11	US-11-170-653-39	Sequence 39, Appl	823	39.5	48.2	119	11	US-11-049-536-246	Sequence 246, App
751	41	50.0	243	11	US-11-054-515-1929	Sequence 1929, Ap	824	39.5	48.2	119	11	US-11-199-739-246	Sequence 246, App

825	39.5	48.2	123	11	US-11-102-512-78	Sequence 78, Appl	898	39	47.6	310	11	US-11-297-327-11	Sequence 11, Appl
826	39.5	48.2	124	11	US-11-102-512-71	Sequence 71, Appl	899	39	47.6	310	11	US-11-297-448-11	Sequence 11, Appl
827	39.5	48.2	131	9	US-10-993-543-88	Sequence 88, Appl	900	39	47.6	354	9	US-10-517-939-216	Sequence 216, Appl
828	39.5	48.2	250	11	US-11-054-515-842	Sequence 842, Appl	901	39	47.6	493	9	US-10-915-002-209	Sequence 209, Appl
829	39.5	48.2	250	11	US-11-266-444-842	Sequence 842, Appl	902	39	47.6	1821	8	US-10-505-928-451	Sequence 451, Appl
830	39.5	48.2	253	11	US-11-054-515-1000	Sequence 1000, Ap	903	38.5	47.0	22	11	US-11-149-943-30	Sequence 30, Appl
831	39.5	48.2	253	11	US-11-054-515-1006	Sequence 1006, Ap	904	38.5	47.0	98	11	US-11-054-669-28	Sequence 28, Appl
832	39.5	48.2	253	11	US-11-054-515-1180	Sequence 1180, Ap	905	38.5	47.0	98	11	US-11-084-554-39	Sequence 39, Appl
833	39.5	48.2	253	11	US-11-054-515-1399	Sequence 1399, Ap	906	38.5	47.0	98	11	US-11-004-590-30	Sequence 30, Appl
834	39.5	48.2	253	11	US-11-266-444-1000	Sequence 1000, Ap	907	38.5	47.0	98	11	US-11-136-250-39	Sequence 39, Appl
835	39.5	48.2	253	11	US-11-266-444-1006	Sequence 1006, Ap	908	38.5	47.0	116	11	US-11-049-536-318	Sequence 318, Appl
836	39.5	48.2	253	11	US-11-266-444-1180	Sequence 1180, Ap	909	38.5	47.0	116	11	US-11-199-739-318	Sequence 318, Appl
837	39.5	48.2	253	11	US-11-266-444-1399	Sequence 1399, Ap	910	38.5	47.0	118	11	US-11-049-536-382	Sequence 382, Appl
838	39	47.6	17	11	US-11-170-453-2	Sequence 2, Appl	911	38.5	47.0	118	11	US-11-199-739-382	Sequence 382, Appl
839	39	47.6	19	10	US-11-121-282-46	Sequence 46, Appl	912	38.5	47.0	119	11	US-11-049-536-490	Sequence 490, Appl
840	39	47.6	21	11	US-11-149-943-17	Sequence 17, Appl	913	38.5	47.0	119	11	US-11-199-739-490	Sequence 490, Appl
841	39	47.6	27	10	US-11-121-282-126	Sequence 126, Appl	914	38.5	47.0	121	11	US-11-049-536-194	Sequence 194, Appl
842	39	47.6	97	11	US-11-054-669-18	Sequence 18, Appl	915	38.5	47.0	121	11	US-11-199-739-194	Sequence 194, Appl
843	39	47.6	97	11	US-11-084-554-28	Sequence 28, Appl	916	38.5	47.0	123	9	US-10-771-257-59	Sequence 59, Appl
844	39	47.6	97	11	US-11-004-590-17	Sequence 17, Appl	917	38.5	47.0	123	11	US-11-127-677-57	Sequence 57, Appl
845	39	47.6	97	11	US-11-136-250-28	Sequence 28, Appl	918	38.5	47.0	123	11	US-11-127-903-45	Sequence 45, Appl
846	39	47.6	115	11	US-11-127-903-33	Sequence 33, Appl	919	38.5	47.0	123	11	US-11-127-903-47	Sequence 47, Appl
847	39	47.6	115	11	US-11-127-903-38	Sequence 38, Appl	920	38.5	47.0	125	11	US-11-049-536-366	Sequence 366, Appl
848	39	47.6	116	11	US-11-049-536-218	Sequence 218, Appl	921	38.5	47.0	125	11	US-11-049-536-486	Sequence 486, Appl
849	39	47.6	116	11	US-11-199-739-218	Sequence 218, Appl	922	38.5	47.0	125	11	US-11-199-739-366	Sequence 366, Appl
850	39	47.6	116	11	US-11-102-512-13	Sequence 13, Appl	923	38.5	47.0	125	11	US-11-199-739-486	Sequence 486, Appl
851	39	47.6	116	11	US-11-102-512-60	Sequence 60, Appl	924	38.5	47.0	132	11	US-11-049-536-8	Sequence 8, Appl
852	39	47.6	116	11	US-11-102-512-72	Sequence 72, Appl	925	38.5	47.0	132	11	US-11-199-739-8	Sequence 8, Appl
853	39	47.6	117	11	US-11-127-903-29	Sequence 29, Appl	926	38.5	47.0	133	9	US-10-993-543-4	Sequence 4, Appl
854	39	47.6	117	11	US-11-127-903-30	Sequence 30, Appl	927	38.5	47.0	134	9	US-10-993-543-24	Sequence 24, Appl
855	39	47.6	117	11	US-11-127-903-32	Sequence 32, Appl	928	38.5	47.0	137	11	US-11-230-462-39	Sequence 39, Appl
856	39	47.6	117	11	US-11-127-903-34	Sequence 34, Appl	929	38.5	47.0	240	11	US-11-054-515-1918	Sequence 1918, Ap
857	39	47.6	117	11	US-11-127-903-36	Sequence 36, Appl	930	38.5	47.0	240	11	US-11-266-444-1918	Sequence 1918, Ap
858	39	47.6	117	11	US-11-127-903-37	Sequence 37, Appl	931	38.5	47.0	243	11	US-11-054-515-2102	Sequence 2102, Ap
859	39	47.6	117	11	US-11-049-536-434	Sequence 434, Appl	932	38.5	47.0	243	11	US-11-266-444-2102	Sequence 2102, Ap
860	39	47.6	117	11	US-11-199-739-434	Sequence 434, Appl	933	38	46.3	17	11	US-11-049-536-120	Sequence 120, Appl
861	39	47.6	117	11	US-11-102-512-12	Sequence 12, Appl	934	38	46.3	17	11	US-11-049-536-122	Sequence 122, Appl
862	39	47.6	118	11	US-11-049-536-670	Sequence 670, Appl	935	38	46.3	17	11	US-11-199-739-120	Sequence 120, Appl
863	39	47.6	118	11	US-11-199-739-670	Sequence 670, Appl	936	38	46.3	17	11	US-11-199-739-122	Sequence 122, Appl
864	39	47.6	118	11	US-11-102-512-14	Sequence 14, Appl	937	38	46.3	115	9	US-10-925-366A-225	Sequence 225, Appl
865	39	47.6	119	9	US-10-925-366A-210	Sequence 210, Appl	938	38	46.3	115	9	US-10-925-366A-229	Sequence 229, Appl
866	39	47.6	119	9	US-10-956-008-74	Sequence 74, Appl	939	38	46.3	115	11	US-11-098-758-225	Sequence 225, Appl
867	39	47.6	119	11	US-11-127-903-31	Sequence 31, Appl	940	38	46.3	115	11	US-11-098-758-229	Sequence 229, Appl
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869	39	47.6	119	11	US-11-102-512-42	Sequence 42, Appl	942	38	46.3	118	11	US-11-049-536-514	Sequence 514, Appl
870	39	47.6	119	11	US-11-098-758-210	Sequence 210, Appl	943	38	46.3	119	11	US-11-199-739-514	Sequence 514, Appl
871	39	47.6	120	11	US-11-102-512-17	Sequence 17, Appl	944	38	46.3	119	11	US-11-010-954-5	Sequence 5, Appl
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873	39	47.6	122	11	US-11-102-512-48	Sequence 48, Appl	946	38	46.3	119	11	US-11-053-749-5	Sequence 5, Appl
874	39	47.6	122	11	US-11-102-512-75	Sequence 75, Appl	947	38	46.3	119	11	US-11-170-753-5	Sequence 5, Appl
875	39	47.6	123	11	US-11-102-512-69	Sequence 69, Appl	948	38	46.3	119	11	US-11-179-359-5	Sequence 5, Appl
876	39	47.6	123	11	US-11-102-512-70	Sequence 70, Appl	949	38	46.3	119	11	US-11-181-030-5	Sequence 5, Appl
877	39	47.6	124	9	US-10-925-366A-211	Sequence 211, Appl	950	38	46.3	119	11	US-11-182-033-5	Sequence 5, Appl
878	39	47.6	124	9	US-10-771-257-19	Sequence 19, Appl	951	38	46.3	120	11	US-11-195-589-5	Sequence 5, Appl
879	39	47.6	124	11	US-11-127-677-19	Sequence 19, Appl	952	38	46.3	120	11	US-11-005-726-1	Sequence 1, Appl
880	39	47.6	124	11	US-11-049-536-358	Sequence 358, Appl	953	38	46.3	120	11	US-11-005-726-9	Sequence 9, Appl
881	39	47.6	124	11	US-11-199-739-358	Sequence 358, Appl	954	38	46.3	121	11	US-11-049-536-522	Sequence 522, Appl
882	39	47.6	124	11	US-11-102-512-74	Sequence 74, Appl	955	38	46.3	121	11	US-11-199-739-522	Sequence 522, Appl
883	39	47.6	124	11	US-11-098-758-211	Sequence 211, Appl	956	38	46.3	128	9	US-10-993-543-108	Sequence 108, Appl
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886	39	47.6	129	9	US-10-993-543-28	Sequence 28, Appl	959	38	46.3	128	11	US-11-199-739-234	Sequence 234, Appl
887	39	47.6	135	9	US-10-993-543-120	Sequence 120, Appl	960	38	46.3	129	9	US-10-993-543-8	Sequence 8, Appl
888	39	47.6	142	11	US-11-170-453-7	Sequence 7, Appl	961	38	46.3	129	9	US-10-993-543-156	Sequence 156, Appl
889	39	47.6	153	11	US-11-267-310-5	Sequence 5, Appl	962	38	46.3	130	9	US-10-993-543-55	Sequence 55, Appl
890	39	47.6	153	11	US-11-267-191-5	Sequence 5, Appl	963	38	46.3	132	9	US-10-993-543-176	Sequence 176, Appl
891	39	47.6	252	11	US-11-054-515-1612	Sequence 1612, Ap	964	38	46.3	132	11	US-11-005-726-11	Sequence 11, Appl
892	39	47.6	252	11	US-11-266-444-1612	Sequence 1612, Ap	965	38	46.3	134	11	US-11-188-298-15603	Sequence 15603, A
893	39	47.6	254	11	US-11-054-515-1195	Sequence 1195, Ap	966	38	46.3	164	9	US-10-517-939-190	Sequence 190, Appl
894	39	47.6	254	11	US-11-054-515-1578	Sequence 1578, Ap	967	38	46.3	189	9	US-10-517-939-376	Sequence 376, Appl
895	39	47.6	254	11	US-11-266-444-1195	Sequence 1195, Ap	968	38	46.3	189	9	US-10-517-939-378	Sequence 378, Appl
896	39	47.6	254	11	US-11-266-444-1578	Sequence 1578, Ap	969	38	46.3	189	9	US-10-517-939-380	Sequence 380, Appl
897	39	47.6	310	11	US-11-245-053-11	Sequence 11, Appl	970	38	46.3	208	11	US-11-031-206-6	Sequence 6, Appl


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971 38 46.3 211 9 US-10-517-939-198 Sequence 198, App
972 38 46.3 214 9 US-10-517-939-158 Sequence 158, App
973 38 46.3 225 9 US-10-517-939-172 Sequence 172, App
974 38 46.3 226 10 US-11-183-218-42 Sequence 42, Appl
975 38 46.3 226 11 US-11-183-205-42 Sequence 42, Appl
976 38 46.3 238 11 US-11-054-515-2067 Sequence 2067, Ap
977 38 46.3 238 11 US-11-266-444-2067 Sequence 2067, Ap
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979 38 46.3 254 11 US-11-266-444-1846 Sequence 1846, Ap
980 38 46.3 255 11 US-11-054-515-1849 Sequence 1849, Ap
981 38 46.3 255 11 US-11-266-444-1849 Sequence 1849, Ap
982 38 46.3 309 11 US-11-188-298-11429 Sequence 11429, A
983 38 46.3 309 11 US-11-005-726-161 Sequence 161, App
984 38 46.3 450 11 US-11-072-512-3233 Sequence 3233, Ap
985 38 46.3 508 11 US-11-072-512-3233 Sequence 3233, Ap
986 38 46.3 695 11 US-11-079-463-9639 Sequence 9639, Ap
987 38 46.3 953 9 US-10-966-846-2 Sequence 2, Appli
988 38 46.3 1419 11 US-11-114-962-3 Sequence 3, Appli
989 38 46.3 2471 11 US-11-050-346-68 Sequence 68, Appl
990 37.5 45.7 17 9 US-10-925-366A-89 Sequence 89, Appl
991 37.5 45.7 17 11 US-11-201-825-38 Sequence 38, Appl
992 37.5 45.7 17 11 US-11-224-823-16 Sequence 16, Appl
993 37.5 45.7 17 11 US-11-217-919-80 Sequence 80, Appl
994 37.5 45.7 17 11 US-11-098-758-89 Sequence 89, Appl
995 37.5 45.7 115 9 US-10-925-366A-334 Sequence 334, App
996 37.5 45.7 115 11 US-11-217-919-147 Sequence 147, App
997 37.5 45.7 115 11 US-11-098-758-334 Sequence 334, App
998 37.5 45.7 116 9 US-10-925-366A-282 Sequence 282, App
999 37.5 45.7 116 9 US-10-496-845A-4 Sequence 4, Appli
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ALIGNMENTS

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RESULT 1
US-11-102-512-26
; Sequence 26, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-26

Query Match 68.9%; Score 56.5; DB 11; Length 116;
Best Local Similarity 76.5%; Pred. No. 0.031;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
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Db 50 SITSEGGSTYYADSVKG 66

RESULT 2
US-11-102-512-28
; Sequence 28, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-88

Query Match 68.9%; Score 56.5; DB 11; Length 123;
Best Local Similarity 76.5%; Pred. No. 0.033;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
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Db 53 SITSEGGSTYYADSVKG 69

RESULT 4
US-11-102-512-88
; Sequence 88, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-88

Query Match 68.9%; Score 56.5; DB 11; Length 123;
Best Local Similarity 76.5%; Pred. No. 0.033;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
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Db 53 SITSEGGSTYYADSVKG 69

RESULT 4
US-11-102-512-88
; Sequence 88, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-88
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; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-28

Query Match 68.9%; Score 56.5; DB 11; Length 116;
Best Local Similarity 76.5%; Pred. No. 0.031;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
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Db 50 SITSEGGSTYYADSVKG 66

RESULT 3
US-11-102-512-85
; Sequence 85, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (120)..(121)
; OTHER INFORMATION: X corresponds to stop codon in coding sequence
US-11-102-512-85

Query Match 68.9%; Score 56.5; DB 11; Length 123;
Best Local Similarity 76.5%; Pred. No. 0.033;
Matches 13; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
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Db 53 SITSEGGSTYYADSVKG 69

RESULT 4
US-11-102-512-88
; Sequence 88, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-88
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Query Match      68.9%; Score 56.5; DB 11; Length 241;
Best Local Similarity 76.5%; Pred. No. 0.066; 1; Indels 1; Gaps 1;
Matches 13; Conservative 2; Mismatches 1;

QY      1 SITSTGG-TYHAESVKG 16
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Db      175 SITSEGGSTYYADSVKG 191

RESULT 5
US-11-054-515-1953
; Sequence 1953, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1953
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1953

Query Match      67.7%; Score 55.5; DB 11; Length 247;
Best Local Similarity 70.6%; Pred. No. 0.098; 0; Indels 1; Gaps 1;
Matches 12; Conservative 4; Mismatches 0;

QY      1 SITSTGG-TYHAESVKG 16
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Db      50 AITSSGGATYYADSVKG 66

RESULT 6
US-11-266-444-1953
; Sequence 1953, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1953
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1953

Query Match      67.7%; Score 55.5; DB 11; Length 247;
Best Local Similarity 70.6%; Pred. No. 0.098; 0; Indels 1; Gaps 1;
Matches 12; Conservative 4; Mismatches 0;

QY      1 SITSTGG-TYHAESVKG 16
      :|||:||| |||:|||
Db      50 AITSSGGATYYADSVKG 66

RESULT 7
US-11-171-567-166
; Sequence 166, Application US/11171567
; Publication No. US20060057651A1
; GENERAL INFORMATION:
; APPLICANT: McWhirter, Katherine S.
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCTIC LEU
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: ALEX-P06-060
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 166
; LENGTH: 17
; TYPE: PRT
; ORGANISM: murine
US-11-171-567-166

Query Match      67.1%; Score 55; DB 11; Length 17;
Best Local Similarity 68.8%; Pred. No. 0.0078; 3; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 0;

QY      1 SITSTGGTYHAESVKG 16
      |||:|||:|||
Db      1 SITSSGGTYYPNSVKG 16

RESULT 8
US-11-102-512-64
; Sequence 64, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
```

; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-64

Query Match 65.2%; Score 53.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.097;
Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTG-GTYHAESVKG 16
:|:|||||:|:
Db 50 TITSEGGTYADSVKG 66

RESULT 9
US-11-054-669-48
; Sequence 48, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-48

Query Match 64.6%; Score 53; DB 11; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.098;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGTYHAESVKG 16
:|:|||||:|:
Db 50 AIGTGGTYADSVKG 65

RESULT 10
US-11-093-274-32
; Sequence 32, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-32

Query Match 64.6%; Score 53; DB 11; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.098;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SITSTGTYHAESVKG 16
:|:|||||:|:
Db 50 AIGTGGTYADSVKG 65

RESULT 11
US-11-049-536-524
; Sequence 524, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 119
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-049-536-524

Query Match 64.6%; Score 53; DB 11; Length 119;
Best Local Similarity 76.9%; Pred. No. 0.12;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 STGGTYHAESVKG 16
|:|:|:|:|:|:
Db 54 SGGGTYADSVKG 66

RESULT 12
US-11-199-739-524
; Sequence 524, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 119
; TYPE: PRT
; ORGANISM: ARTIFICIAL

```
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-199-739-524

Query Match      64.6%; Score 53; DB 11; Length 119;
Best Local Similarity 76.9%; Pred. No. 0.12;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  4 STGGTYHAESVKG 16
Db   54 SGGGTYADSVKG 66

RESULT 13
US-11-049-536-310
; Sequence 310, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 124
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-049-536-310

Query Match      64.6%; Score 53; DB 11; Length 124;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  4 STGGTYHAESVKG 16
Db   54 SGGGTYADSVKG 66

RESULT 14
US-11-199-739-310
; Sequence 310, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310

; LENGTH: 124
; TYPE: PRT
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-199-739-310

Query Match      64.6%; Score 53; DB 11; Length 124;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  4 STGGTYHAESVKG 16
Db   54 SGGGTYADSVKG 66

RESULT 15
US-11-102-512-31
; Sequence 31, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-31

Query Match      64.0%; Score 52.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.14;
Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY  1 SITST-GGTYHAESVKG 16
Db   50 SISDGGGTYADSVKG 66

RESULT 16
US-11-102-512-67
; Sequence 67, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-67

Query Match      64.0%; Score 52.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.14;
Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY  1 SITSTG-GTYHAESVKG 16
Db   50 SISSTGQSTYYADSVKG 66
```

```
RESULT 17
US-11-102-512-77
; Sequence 77, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/21328
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-77

Query Match      64.0%; Score 52.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.14;
Matches 12; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy      1 SITST-GTTHAESVKG 16
      |||:|||||:|||||
Db      50 SISDGGGTYADSVKG 66

RESULT 18
US-11-054-515-963
; Sequence 963, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 963
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-963

Query Match      62.8%; Score 51.5; DB 11; Length 249;
Best Local Similarity 64.7%; Pred. No. 0.45;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy      1 SITSTGG-TYHAESVKG 16
      |||:|||||:|||||
Db      50 SISDGGGTYADSVKG 66

RESULT 19
US-11-266-444-963
; Sequence 963, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 963
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-963

Query Match      62.8%; Score 51.5; DB 11; Length 249;
Best Local Similarity 64.7%; Pred. No. 0.45;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy      1 SITSTGG-TYHAESVKG 16
      |||:|||||:|||||
Db      50 TITDSGGNTYYADSVKG 66

RESULT 20
US-10-507-662-5
; Sequence 5, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-5

Query Match      62.2%; Score 51; DB 9; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.033;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 SITSTGGTYHAESVKG 16
      |||:|||||:|||||
Db      1 SITSGGSGTYTPDSVKG 16
```

RESULT 21
US-11-149-309-23
; Sequence 23, Application US/11149309
; Publication No. US20060063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasaiian, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertruida M.
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lin, Laura Long
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepui
; APPLICANT: Feyfant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
; APPLICANT: Widom, Angela M.
; APPLICANT: Parris, Kevin D.
; APPLICANT: Goldman, Samuel J.
; TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
; FILE REFERENCE: 16158-048001 / AM101493
; CURRENT APPLICATION NUMBER: US/11/149,309
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/578,473
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/581,375
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/578,736
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: This fragment corresponds to residues 50-65 (linear) of, e.g.,
; OTHER INFORMATION: Figure 29.
US-11-149-309-23

Query Match 62.2%; Score 51; DB 11; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.033;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
DB 1 SISSGGNTYYPDSVKG 16
|||:|:|:|:|:|:|

RESULT 22
US-11-102-512-76
; Sequence 76, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-76

Query Match 62.2%; Score 51; DB 11; Length 116;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTTHAESVKG 16
DB 56 GGTYYADSVKG 66
|||:|:|:|:|:|:|

RESULT 23
US-11-149-309-13
; Sequence 13, Application US/11149309
; Publication No. US20060063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasaiian, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertruida M.
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lin, Laura Long
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepui
; APPLICANT: Feyfant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
; APPLICANT: Widom, Angela M.
; APPLICANT: Parris, Kevin D.
; APPLICANT: Goldman, Samuel J.
; TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
; FILE REFERENCE: 16158-048001 / AM101493
; CURRENT APPLICATION NUMBER: US/11/149,309
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/578,473
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/581,375
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: US 60/578,736
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-149-309-13

Query Match 62.2%; Score 51; DB 11; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.25;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SITSTGGTYHAESVKG 16
DB 50 SISSGGNTYYPDSVKG 65
|||:|:|:|:|:|:|

RESULT 24
US-11-149-309-14
; Sequence 14, Application US/11149309
; Publication No. US20060063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasaiian, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertruida M.
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lin, Laura Long
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepui
; APPLICANT: Feyfant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
US-11-149-309-14

RESULT 27
US-11-149-308-36
Sequence 36, Application US/11149309
; Publication No. US2006063228A1
; GENERAL INFORMATION:
; APPLICANT: Kasalan, Marion T.
; APPLICANT: Tchistiakova, Lioudmila
; APPLICANT: Veldman, Geertruida M.
; APPLICANT: Marquette, Kimberly Ann
; APPLICANT: Tan, Xiang-Yang
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lin, Laura Long
; APPLICANT: Shane, Tania
; APPLICANT: Tam, Amy Szepei
; APPLICANT: Peffiant, Eric
; APPLICANT: Wood, Nancy L.
; APPLICANT: Fitz, Lori J.
; APPLICANT: Widom, Angela M.

Qy 3 TSTGGTYHAESVKG 16
:||:|:|:|:|:|:|
Db 53 SSSGSTYYADSVKG 66

RESULT 31
US-11-266-444-971
; Sequence 971, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; CURRENT APPLICATION NUMBER: US/11/266,444
; FILE REFERENCE: PF523P1D1
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 971
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-971

Query Match 62.2%; Score 51; DB 11; Length 254;
Best Local Similarity 64.3%; Pred. No. 0.55;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TSTGGTYHAESVKG 16
:||:|:|:|:|:|:|
Db 53 SSSGSTYYADSVKG 66

RESULT 32
US-11-084-554-42
; Sequence 42, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENTX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-42

Query Match 61.6%; Score 50.5; DB 11; Length 98;
Best Local Similarity 64.7%; Pred. No. 0.25;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
:||:|:|:|:|:|:|
Db 50 AISNGGSTYYADSVKG 66

RESULT 33
US-11-136-250-42
; Sequence 42, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENTX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-42

Query Match 61.6%; Score 50.5; DB 11; Length 98;
Best Local Similarity 64.7%; Pred. No. 0.25;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
:||:|:|:|:|:|:|
Db 50 AISNGGSTYYADSVKG 66

RESULT 34
US-11-102-512-8
; Sequence 8, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/21328
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-8

Query Match 61.6%; Score 50.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.3;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SITSTG-GTYHAESVKG 16
:||:|:|:|:|:|:|
Db 50 SITSDGTSTYYADSVKG 66

RESULT 35

```
US-11-102-512-9
; Sequence 9, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-9

Query Match      61.6%; Score 50.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.3;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 SITSTG-GTYHAESVKG 16
      ||||| | ||:||||
Db      50 SITSDGVTYYADSVKG 66

RESULT 36
US-11-102-512-10
; Sequence 10, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-10

Query Match      61.6%; Score 50.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.3;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 SITSTG-GTYHAESVKG 16
      ||||| | ||:||||
Db      50 SITSDGVTYYADSVKG 66

RESULT 37
US-11-102-512-29
; Sequence 29, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-29

Query Match      61.6%; Score 50.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.3;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 SITSTG-GTYHAESVKG 16
      ||||| | ||:||||
Db      50 SITSDGVTYYADSVKG 66

RESULT 38
US-11-102-512-63
; Sequence 63, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-63

Query Match      61.6%; Score 50.5; DB 11; Length 116;
Best Local Similarity 70.6%; Pred. No. 0.3;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY      1 SITSTG-GTYHAESVKG 16
      ||||| | ||:||||
Db      50 SITSDGVTYYADSVKG 66

RESULT 39
US-11-144-248-24
; Sequence 24, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-24

Query Match      61.6%; Score 50.5; DB 11; Length 122;
Best Local Similarity 68.8%; Pred. No. 0.32;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
```

Qy 2 ITSTGG-TYHAESVKG 16
||:|||||
Db 51 ITSGGGTYADSVKG 66

RESULT 40

US-11-144-222-24
; Sequence 24, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D. R.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-24

Query Match 61.6%; Score 50.5; DB 11; Length 122;
Best Local Similarity 68.8%; Pred. No. 0.32;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 2 ITSTGG-TYHAESVKG 16
||:|||||
Db 51 ITSGGGTYADSVKG 66

RESULT 41

US-11-182-343-24
; Sequence 24, Application US/11182343
; Publication No. US20060018910A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce
; APPLICANT: Gualberto, Antonio
; APPLICANT: Melvin, Carrie
; APPLICANT: Roberts, Luisa M.
; TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
; FILE REFERENCE: PC32226A
; CURRENT APPLICATION NUMBER: US/11/182,343
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 60/588,721
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-343-24

Query Match 61.6%; Score 50.5; DB 11; Length 122;
Best Local Similarity 68.8%; Pred. No. 0.32;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 2 ITSTGG-TYHAESVKG 16
||:|||||
Db 51 ITSGGGTYADSVKG 66

RESULT 42

US-11-054-515-1930
; Sequence 1930, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1930
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1930

Query Match 61.6%; Score 50.5; DB 11; Length 240;
Best Local Similarity 64.7%; Pred. No. 0.63;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SITSTGG-TYHAESVKG 16
||:|||||
Db 50 SITSGGGTYADSVKG 66

RESULT 43

US-11-266-444-1930
; Sequence 1930, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulators
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1930
; LENGTH: 240

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1930

Query Match          61.6%; Score 50.5; DB 11; Length 240;
Best Local Similarity 64.7%; Pred. No. 0.63;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   ||: || ||: ||: |||
Db 50 SISGGSGTYADSVKG 66

RESULT 44
US-11-054-515-1945
; Sequence 1945, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1945
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1945

Query Match          61.6%; Score 50.5; DB 11; Length 243;
Best Local Similarity 64.7%; Pred. No. 0.64;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   ||: || ||: ||: |||
Db 50 AISNGSGTYADSVKG 66

RESULT 45
US-11-266-444-1945
; Sequence 1945, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
```

```
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1945
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1945

Query Match          61.6%; Score 50.5; DB 11; Length 243;
Best Local Similarity 64.7%; Pred. No. 0.64;
Matches 11; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 SITSTGG-TYHAESVKG 16
   ||: || ||: ||: |||
Db 50 AISNGSGTYADSVKG 66

RESULT 46
US-11-041-095-58
; Sequence 58, Application US/11041095
; Publication No. US20060024782A1
; GENERAL INFORMATION:
; APPLICANT: Lehmbrecht, Jan
; TITLE OF INVENTION: Production of a Monoclonal Antibody in a Heterokaryon Fungus or
; FILE REFERENCE: 10453-200-US
; CURRENT APPLICATION NUMBER: US/11/041,095
; CURRENT FILING DATE: 2005-01-20
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-041-095-58

Query Match          61.6%; Score 50.5; DB 11; Length 524;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 ITSTGG-TYHAESVKG 16
   ||: || ||: ||: |||
Db 127 ITSGSGTYADSVKG 142

RESULT 47
US-11-084-554-43
; Sequence 43, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
```

```
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-43

Query Match          61.0%; Score 50; DB 11; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 ITSTGGTYHAESVKG 16
       |||||:|||||
Db      51 IYSCGTYADSVKG 65

RESULT 48
US-11-136-250-43
; Sequence 43, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-43

Query Match          61.0%; Score 50; DB 11; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 ITSTGGTYHAESVKG 16
       |||||:|||||
Db      51 IYSCGTYADSVKG 65

RESULT 49
US-11-128-440-12
; Sequence 12, Application US/11128440
; Publication No. US20050261478A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaire, Laura S.
; APPLICANT: Law, Che-Leung
; APPLICANT: Dua, Raj
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: LYMPHOCTE ACTIVATION
; FILE REFERENCE: 980034.40BD1
; CURRENT APPLICATION NUMBER: US/11/128,440
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/646,381
; PRIOR FILING DATE: 2003-08-21
```

```
; PRIOR APPLICATION NUMBER: US 09/252,150
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/108,683
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/075,274
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Llama llama
US-11-128-440-12

Query Match          61.0%; Score 50; DB 11; Length 219;
Best Local Similarity 60.0%; Pred. No. 0.69;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 ITSTGGTYHAESVKG 16
       ||:|||||
Db      52 ISTRGTYADSVKG 66

RESULT 50
US-11-000-463-334
; Sequence 334, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
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; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
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; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-334

Query Match          61.0%; Score 50; DB 11; Length 312;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db      71 ISSGGTYADSVKG 85
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Job time : 24.9344 secs

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OM protein - protein search, using sw model									
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Scoring table:	BLOSUM62								
	Gapop 10.0 , Gapext 0.5								
Searched:	2443163 seqs, 439378781 residues								
Total number of hits satisfying chosen parameters:	2443163								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
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	Maximum Match 100%								
	Listing first 1000 summaries								
Database :	A_Geneseq_21.*								
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	7: Geneseqp2003bs.*								
	8: Geneseqp2004s.*								
	9: Geneseqp2005s.*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
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2	71	100.0	122	2	AAW23432		Aaw23432 rW12 heav		
3	71	100.0	122	2	AAW23437		Aaw23437 Modified		
4	71	100.0	122	2	AAW23441		Aaw23441 hW12 heav		
5	71	100.0	122	2	AAW23438		Aaw23438 Modified		
6	43	60.6	17	7	ADM07759		Adm07759 Canine im		
7	43	60.6	134	7	ADM07290		Adm07290 Canine im		
8	43	60.6	237	8	ADY11275		Ady11275 Plant ful		
9	43	60.6	241	4	AB50360		Ab50360 Maize ZnG		
10	43	60.6	262	8	ADY11626		Ady11626 Plant ful		
11	43	60.6	262	8	ADX96652		Adx96652 Plant ful		
12	43	60.6	362	8	ADS23337		Ads23337 Bacterial		
13	43	60.6	450	5	ABU48510		Abu48510 Protein e		
14	42	59.2	351	5	AB92490		Ab92490 Herbicide		
15	42	59.2	408	5	AB92275		Ab92275 Herbicide		
16	42	59.2	463	8	ADZ25621		Adz25621 Aspergill		
17	41	57.7	410	6	ABU29699		Abu29699 Protein e		
18	41	57.7	416	7	ADC95924		Adc95924 E. faeciu		
19	41	57.7	2247	2	AAW27126		Aaw27126 Equine rh		
20	40	56.3	42	7	AD544856		Ad544856 Neisseria		
21	40	56.3	42	8	ADR06405		Adr06405 Neisseria		
22	40	56.3	42	8	ADU03722		Adu03722 Bacterici		
23	40	56.3	183	6	ADK48317		Adk48317 Streptoco		
24	40	56.3	225	6	ABP98002		Abp98002 Protein 7		

Abp98001	Protein 7
Abp97998	Protein 7
Abp97996	Protein 7
Abm67642	Phototrab
Adp70282	Truncated
Aae10027	Neisseria
Ado07117	Neisseria
Adp70281	Truncated
Adr23253	Neisseria
Adr00574	N. mening
Adz27278	741 polyP
Adz44758	Neisseria
Adz44748	Neisseria
Adz44752	Neisseria
Adz44754	Neisseria
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Adz44646	Neisseria
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Adz44734	Neisseria
Adz44694	Neisseria
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Adp70235	Neisseria
Adp70234	Neisseria
Adr23261	Neisseria
Adu03774	Bacterici
Adz27286	741 varia
Adz44672	Neisseria
Adz44702	Neisseria
Adz44714	Neisseria
Adz44720	Neisseria
Adz44764	Neisseria
Adz44654	Neisseria
Adz44660	Neisseria
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98	40	56.3	255	7	ADe44770	ADe44770 Neisseria	171	40	56.3	274	8	ADP70328	ADP70328 Neisseria
99	40	56.3	255	7	ADe44760	ADe44760 Neisseria	172	40	56.3	274	8	ADP70327	ADP70327 Neisseria
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105	40	56.3	255	7	ADe44772	ADe44772 Neisseria	178	40	56.3	274	8	ADP70329	ADP70329 Neisseria
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107	40	56.3	255	7	ADe44738	ADe44738 Neisseria	180	40	56.3	274	8	ADP70326	ADP70326 Neisseria
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109	40	56.3	255	7	ADe44802	ADe44802 Neisseria	182	40	56.3	276	6	ABP81301	ABP81301 Streptoco
110	40	56.3	255	7	ADe44648	ADe44648 Neisseria	183	40	56.3	279	6	ABP98009	ABP98009 Protein 7
111	40	56.3	255	7	ADe44590	ADe44590 Neisseria	184	40	56.3	279	6	ABP97997	ABP97997 Protein 7
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114	40	56.3	255	7	ADe44778	ADe44778 Neisseria	187	40	56.3	279	8	ADP70222	ADP70222 Neisseria
115	40	56.3	255	7	ADe44678	ADe44678 Neisseria	188	40	56.3	279	8	ADP70206	ADP70206 Neisseria
116	40	56.3	255	7	ADe44708	ADe44708 Neisseria	189	40	56.3	280	6	ABP98000	ABP98000 Protein 7
117	40	56.3	255	8	ADU007123	ADU007123 Neisseria	190	40	56.3	280	6	ABP98003	ABP98003 Protein 7
118	40	56.3	255	8	ADP70226	ADP70226 Neisseria	191	40	56.3	281	8	ADP70220	ADP70220 Neisseria
119	40	56.3	255	8	ADP70227	ADP70227 Neisseria	192	40	56.3	281	8	ADP70221	ADP70221 Neisseria
120	40	56.3	255	8	ADP70233	ADP70233 Neisseria	193	40	56.3	282	8	ADP70341	ADP70341 Neisseria
121	40	56.3	255	8	ADP70225	ADP70225 Neisseria	194	40	56.3	320	8	ADL16112	ADL16112 Neisseria
122	40	56.3	255	8	ADP70228	ADP70228 Neisseria	195	40	56.3	433	8	ADP70293	ADP70293 Hybrid NM
123	40	56.3	255	8	ADU06423	ADU06423 N meningi	196	40	56.3	434	8	ADU007121	ADU007121 Neisseria
124	40	56.3	255	8	ADU23260	ADU23260 Neisseria	197	40	56.3	434	8	ADP23258	ADP23258 Neisseria
125	40	56.3	255	8	ADU03766	ADU03766 Bacterici	198	40	56.3	434	9	ADZ35999	ADZ35999 Neisseria
126	40	56.3	255	8	ADU03771	ADU03771 Bacterici	199	40	56.3	434	9	ADZ27283	ADZ27283 Chimeric
127	40	56.3	255	8	ADU03773	ADU03773 Bacterici	200	40	56.3	440	8	ADP70292	ADP70292 Hybrid NM
128	40	56.3	255	8	ADU03770	ADU03770 Bacterici	201	40	56.3	456	6	ABP98017	ABP98017 Amino aci
129	40	56.3	255	8	ADU03734	ADU03734 Bacterici	202	40	56.3	501	8	ADP70283	ADP70283 Tandem NM
130	40	56.3	255	8	ADU03768	ADU03768 Bacterici	203	40	56.3	504	8	ADP70286	ADP70286 Tandem NM
131	40	56.3	255	9	ADZ27285	ADZ27285 741 varia	204	40	56.3	508	8	ADP70280	ADP70280 Tandem NM
132	40	56.3	256	6	ABP97992	ABP97992 Protein 7	205	40	56.3	511	8	ADP70284	ADP70284 Tandem NM
133	40	56.3	256	7	ADe44762	ADe44762 Neisseria	206	40	56.3	514	8	ADP70289	ADP70289 Tandem NM
134	40	56.3	256	7	ADe44798	ADe44798 Neisseria	207	40	56.3	514	8	ADP70291	ADP70291 Tandem NM
135	40	56.3	256	7	ADe44768	ADe44768 Neisseria	208	40	56.3	521	8	ADP70290	ADP70290 Tandem NM
136	40	56.3	256	7	ADe44810	ADe44810 Neisseria	209	40	56.3	521	8	ADP70288	ADP70288 Tandem NM
137	40	56.3	256	7	ADe44774	ADe44774 Neisseria	210	40	56.3	590	4	AAE10039	AAE10039 N. mening
138	40	56.3	256	7	ADe44792	ADe44792 Neisseria	211	40	56.3	590	4	AAU27604	AAU27604 Neisseria
139	40	56.3	256	7	ADe44804	ADe44804 Neisseria	212	40	56.3	590	8	ADS00598	ADS00598 N. mening
140	40	56.3	256	7	ADe44780	ADe44780 Neisseria	213	40	56.3	593	4	AAE10029	AAE10029 N. mening
141	40	56.3	257	7	ADe44634	ADe44634 Neisseria	214	40	56.3	593	4	AAU27580	AAU27580 Neisseria
142	40	56.3	257	7	ADe44638	ADe44638 Neisseria	215	40	56.3	593	8	ADS00578	ADS00578 N. mening
143	40	56.3	258	7	ADe44636	ADe44636 Neisseria	216	40	56.3	612	4	AAE10042	AAE10042 N. mening
144	40	56.3	260	7	ADe44814	ADe44814 Neisseria	217	40	56.3	612	4	AAU27607	AAU27607 Neisseria
145	40	56.3	260	7	ADe44818	ADe44818 Neisseria	218	40	56.3	612	8	ADS00604	ADS00604 N. mening
146	40	56.3	260	8	ADP70245	ADP70245 Neisseria	219	40	56.3	645	4	AAE10036	AAE10036 N. mening
147	40	56.3	260	8	ADP70229	ADP70229 Neisseria	220	40	56.3	645	4	AAU27601	AAU27601 Neisseria
148	40	56.3	261	7	ADe44626	ADe44626 Neisseria	221	40	56.3	645	8	ADS00592	ADS00592 N. mening
149	40	56.3	261	7	ADe44622	ADe44622 Neisseria	222	40	56.3	648	4	AAE10028	AAE10028 N. mening
150	40	56.3	261	7	ADe44620	ADe44620 Neisseria	223	40	56.3	648	4	AAU27579	AAU27579 Neisseria
151	40	56.3	261	7	ADe44816	ADe44816 Neisseria	224	40	56.3	648	8	ADS00576	ADS00576 N. mening
152	40	56.3	261	7	ADe44616	ADe44616 Neisseria	225	40	56.3	672	4	AAE10032	AAE10032 N. mening
153	40	56.3	262	7	ADe44624	ADe44624 Neisseria	226	40	56.3	672	4	AAU27597	AAU27597 Neisseria
154	40	56.3	262	7	ADe44618	ADe44618 Neisseria	227	40	56.3	672	8	ADS00584	ADS00584 N. mening
155	40	56.3	262	8	ADP70243	ADP70243 Neisseria	228	40	56.3	675	4	AAE10031	AAE10031 N. mening
156	40	56.3	262	8	ADP70244	ADP70244 Neisseria	229	40	56.3	675	4	AAU27582	AAU27582 Neisseria
157	40	56.3	273	8	ADP70336	ADP70336 Neisseria	230	40	56.3	675	8	ADS00582	ADS00582 N. mening
158	40	56.3	273	8	ADP70212	ADP70212 Neisseria	231	40	56.3	700	8	ADS42591	ADS42591 Bacterial
159	40	56.3	273	8	ADP70211	ADP70211 Neisseria	232	40	56.3	757	8	ADP70343	ADP70343 Triple ta
160	40	56.3	273	8	ADP70335	ADP70335 Neisseria	233	40	56.3	1312	4	AAE10023	AAE10023 N. mening
161	40	56.3	273	8	ADP70332	ADP70332 Neisseria	234	40	56.3	1312	4	AAE10030	AAE10030 N. mening
162	40	56.3	273	8	ADP70334	ADP70334 Neisseria	235	40	56.3	1312	4	AAU27581	AAU27581 Neisseria
163	40	56.3	273	8	ADP70337	ADP70337 Neisseria	236	40	56.3	1312	4	AAU27576	AAU27576 Neisseria
164	40	56.3	273	8	ADP70333	ADP70333 Neisseria	237	40	56.3	1312	8	ADS00580	ADS00580 N. mening
165	40	56.3	274	3	AAU75531	AAU75531 Neisseria	238	40	56.3	1312	8	ADS00568	ADS00568 N. mening
166	40	56.3	274	4	AAE10026	AAE10026 Neisseria	239	39	54.9	26	3	AAU19606	AAU19606 Human CC
167	40	56.3	274	4	AAU27567	AAU27567 Neisseria	240	39	54.9	26	6	ABG73068	ABG73068 Human G-p
168	40	56.3	274	8	ADP70202	ADP70202 Neisseria	241	39	54.9	26	9	AEC20943	AEC20943 Human CC
169	40	56.3	274	8	ADP70203	ADP70203 Neisseria	242	39	54.9	37	4	AAG80061	AAG80061 Chemokine
170	40	56.3	274	8	ADP70210	ADP70210 Neisseria	243	39	54.9	49	4	AAG80060	AAG80060 Chemokine

244	39	54.9	129	4	AAE10558	Aae10558 HPL inhib	317	37.5	52.8	865	6	ABP55626	Abp55626 Human dpp
245	39	54.9	227	4	AAE75051	Aab75051 TRO005 Hu	318	37.5	52.8	865	7	ADE58041	Ades58041 Human Pro
246	39	54.9	356	5	AAE20597	Aae20597 HOMO sapi	319	37.5	52.8	865	7	ADE58037	Ades58037 Human Pro
247	39	54.9	357	3	AAE19605	Aab19605 Human CC	320	37.5	52.8	865	9	ADX26259	Adx26259 Novel cel
248	39	54.9	357	3	AAE90615	Aay90615 Human G p	321	37	52.1	823	123	AAW13531	Aaw13531 Anti-mela
249	39	54.9	357	3	AAE90649	Aay90649 Human mut	322	37	52.1	139	3	AAW16314	Aaw16314 Pinus rad
250	39	54.9	357	3	AAE80117	Aag80117 Human CCR	323	37	52.1	165	4	AAW00053	Aam00053 Sucrose s
251	39	54.9	357	6	AAE81878	Abp81878 Human C-C	324	37	52.1	288	4	AAE62520	Aar62520 Isoform 1
252	39	54.9	357	6	ABG73067	Abg73067 Human CC	325	37	52.1	442	2	AAE27802	Aar27802 EPSP synt
253	39	54.9	357	6	ADC22695	Adc22695 Human G p	326	37	52.1	444	2	AAE23065	Aar23065 Modified
254	39	54.9	357	7	ADC22543	Adc22543 Human G p	327	37	52.1	444	2	AAE27302	Aaw27302 Maize 5-e
255	39	54.9	357	7	ADC22543	Adc22543 Human G p	328	37	52.1	444	2	AAE27301	Aaw27301 Maize 5-e
256	39	54.9	357	7	ADH14016	Adh14016 Human GPR	329	37	52.1	444	2	AAE28462	Aaw28462 Maize 5-e
257	39	54.9	357	7	ADH14168	Adh14168 Mutated h	330	37	52.1	444	2	AAE28463	Aaw28463 Maize 5-e
258	39	54.9	357	8	ADF47692	Adf47692 Human che	331	37	52.1	444	2	AAE28461	Aaw28461 Maize 5-e
259	39	54.9	357	8	ADO29235	Ado29235 Human GPC	332	37	52.1	444	2	AAE44825	Aaw44825 Mutant ma
260	39	54.9	357	9	AEC20942	Aec20942 Human G-p	333	37	52.1	444	2	AAE44824	Aaw44824 Mutant ma
261	39	54.9	369	4	AAE80116	Aag80116 Human CCR	334	37	52.1	444	4	AAE67871	ABE67871 S-enolpyr
262	39	54.9	369	4	ABE56344	ABE56344 Non-endog	335	37	52.1	444	4	ABE67918	ABE67918 Wild type
263	39	54.9	369	8	ADR03498	Adr03498 Cytokine	336	37	52.1	444	8	ADR67921	ADR67921 Wild type
264	39	54.9	1726	2	AAW00385	Aaw00385 Truncated	337	37	52.1	444	8	AAE09792	AAE09792 Eleusine
265	39	54.9	2229	8	ADN24083	Adn24083 Bacterial	338	37	52.1	445	4	ABP27387	ABP27387 Streptoco
266	39	54.9	2913	2	AAW00384	Aaw00384 Plasmidii	339	37	52.1	483	5	ABP27387	ABP27387 Streptoco
267	38	53.5	17	5	ABG70452	Abg70452 CDR2 regi	340	37	52.1	506	8	ABU46697	ABU46697 Protein e
268	38	53.5	132	3	AAE00750	Aag00750 Human sec	341	37	52.1	511	8	ADQ37121	ADQ37121 Cell prol
269	38	53.5	132	3	AAE00747	Aag00747 Human sec	342	37	52.1	511	8	ADQ15707	ADQ15707 Rice stre
270	38	53.5	220	2	AAE76638	Aay76638 Human ova	343	37	52.1	515	8	ADJ79594	ADJ79594 Rice EPSP
271	38	53.5	223	5	AAE27023	Aae27023 Human gen	344	37	52.1	519	6	ABP76735	ABP76735 Streptomy
272	38	53.5	223	5	AAE27161	Aae27161 Human gen	345	37	52.1	523	6	ADM99121	ADM99121 Bacterial
273	38	53.5	223	6	ABU65034	ABU65034 Human sec	346	37	52.1	527	8	ADY06582	ADY06582 Plant ful
274	38	53.5	223	8	ADG89843	ADG89843 Human sec	347	37	52.1	528	8	ADX79052	ADX79052 Plant ful
275	38	53.5	285	3	AAE70322	Aay70322 Human RNA	348	37	52.1	541	8	ADX87496	ADX87496 Plant ful
276	38	53.5	346	7	ADJ70008	Adj70008 Human hea	349	37	52.1	570	2	AAW70529	AAW70529 Mutant ma
277	38	53.5	346	8	ABM81141	ABM81141 Tumour-as	350	37	52.1	570	2	ADX91627	ADX91627 Plant ful
278	38	53.5	346	9	ADW08721	Adw08721 Human pro	351	37	52.1	593	8	ADX87445	ADX87445 Plant ful
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280	38	53.5	373	6	ABU19527	ABU19527 Protein e	353	37	52.1	619	8	ADY12306	ADY12306 Plant ful
281	38	53.5	431	5	ABE90809	ABE90809 Herbicida	354	37	52.1	639	8	ADX95786	ADX95786 Plant ful
282	38	53.5	516	1	AAE70194	Aap70194 Sequence	355	37	52.1	651	8	ADX80545	ADX80545 Plant ful
283	38	53.5	539	6	ABU40194	ABU40194 Protein e	356	37	52.1	652	8	ADX77316	ADX77316 Plant ful
284	38	53.5	552	6	ABU21526	ABU21526 Protein e	357	37	52.1	670	8	ADX80503	ADX80503 Plant ful
285	38	53.5	552	6	ABU22677	ABU22677 Protein e	358	37	52.1	683	8	ADY12569	ADY12569 Plant ful
286	38	53.5	558	6	ABU23421	ABU23421 Protein e	359	37	52.1	749	8	ADX93532	ADX93532 Plant ful
287	38	53.5	663	2	AAW49872	Aaw49872 Thermotog	360	37	52.1	766	2	AAE66222	AAE66222 Sucrose-s
288	38	53.5	663	7	ADC26952	Adc26952 Thermotog	361	37	52.1	771	3	AAE85666	AAE85666 pSS3 prot
289	38	53.5	663	7	ADP93848	Adp93848 T. mariti	362	37	52.1	773	5	AAE28503	AAE28503 Maize suc
290	38	53.5	666	2	AAW34392	AAW34392 Thermotog	363	37	52.1	777	7	ADC08297	ADC08297 Rice prot
291	38	53.5	677	8	ADS30047	ADS30047 Bacterial	364	37	52.1	777	7	ADC07858	ADC07858 Rice prot
292	38	53.5	680	2	AAW34564	AAW34564 Thermotog	365	37	52.1	786	7	ADC07862	ADC07862 Rice prot
293	38	53.5	680	2	AAW35005	AAW35005 Thermotog	366	37	52.1	797	6	ABR39586	ABR39586 A. thalia
294	38	53.5	680	2	AAW49868	Aaw49868 Thermotog	367	37	52.1	798	7	ADC07860	ADC07860 Rice prot
295	38	53.5	680	2	ADC26916	Adc26916 Thermotog	368	37	52.1	802	5	AAE28499	AAE28499 Corn suc
296	38	53.5	680	7	ADP93812	Adp93812 T. mariti	369	37	52.1	802	5	AAE28500	AAE28500 Corn suc
297	38	53.5	802	6	ADB11480	ADB11480 Allolococ	370	37	52.1	802	8	ADY57502	ADY57502 Plant pol
298	38	53.5	806	8	AAW53103	AAW53103 Anabaena	371	37	52.1	803	9	ADY61067	ADY61067 Abiotic s
299	38	53.5	806	8	ADC30754	ADC30754 Bacterial	372	37	52.1	805	3	AAE16282	AAE16282 Eucalyptu
300	38	53.5	865	6	ADB11478	ADB11478 Allolococ	373	37	52.1	805	3	AAE16336	AAE16336 Eucalyptu
301	38	53.5	2703	2	AAE70236	Aar70236 P. falcip	374	37	52.1	805	3	AAE28141	AAE28141 Sucrose s
302	38	53.5	2710	2	AAW22482	AAW22482 Plasmidii	375	37	52.1	805	5	ABE93752	ABE93752 Herbicida
303	38	53.5	2710	3	AAE77904	Aay77904 P. falcip	376	37	52.1	805	5	AAU080759	AAU080759 Eucalyptu
304	38	53.5	3060	2	AAW22475	AAW22475 Plasmidii	377	37	52.1	805	6	ABR39585	ABR39585 A. thalia
305	38	53.5	3060	3	AAE77905	Aay77905 Plasmidii	378	37	52.1	805	9	ADH75493	ADH75493 Eucalyptu
306	38	53.5	6629	8	ABY03157	AbY03157 Avian inf	379	37	52.1	805	9	ADW80527	ADW80527 E. grandis
307	37.5	52.8	180	8	ADR08512	ADR08512 Human pro	380	37	52.1	805	9	ASE21245	ASE21245 Potato su
308	37.5	52.8	183	8	ADQ67817	ADQ67817 Novel hum	381	37	52.1	805	5	AAU97898	AAU97898 Cotton su
309	37.5	52.8	518	7	ABM86267	ABM86267 Rice abio	382	37	52.1	806	8	ADX91633	ADX91633 Plant ful
310	37.5	52.8	803	6	ABR58662	ABR58662 Human can	383	37	52.1	807	8	ADX95176	ADX95176 Rice suc
311	37.5	52.8	803	7	ADP79818	Adp79818 Human dipep	384	37	52.1	808	3	AAE85664	AAE85664 Rice suc
312	37.5	52.8	804	6	ABP55627	ABP55627 Human dpp	385	37	52.1	808	5	ABE92501	ABE92501 Herbicida
313	37.5	52.8	804	9	ADX26329	ADX26329 Novel cel	386	37	52.1	808	5	ABE93562	ABE93562 Herbicida
314	37.5	52.8	859	7	ADSE8039	Adse8039 Rat prote	387	37	52.1	808	5	ABG69063	ABG69063 Amino aci
315	37.5	52.8	859	7	ADSE8035	Adse8035 Rat prote	388	37	52.1	808	7	ADC68365	ADC68365 S. arundi
316	37.5	52.8	859	9	ADX26403	ADX26403 Novel cel	389	37	52.1	808	7	ADC68459	ADC68459 Lolium pe

390	37	52.1	808	7	ADC68364	Adc68364	Lolium pe	463	36	50.7	267	2	AAW85688	AAW85688 Humanised
391	37	52.1	808	9	AEb03162	Aeb03162	Fructan b	464	36	50.7	287	8	ADY23411	ADY23411 Plant ful
392	37	52.1	808	9	AEb03067	Aeb03067	Fructan b	465	36	50.7	305	2	AAW16476	AAW16476 Streptoco
393	37	52.1	808	9	AEb03068	Aeb03068	Fructan b	466	36	50.7	305	8	ADR57983	ADR57983 Streptoco
394	37	52.1	809	5	ABb92810	Abb92810	Herbicida	467	36	50.7	335	8	ADM25592	ADM25592 Hyperther
395	37	52.1	809	5	AAE28502	Aae28502	Corn Sus3	468	36	50.7	335	8	ADO62037	ADO62037 Transcrip
396	37	52.1	811	8	ADx87512	Adx87512	Plant ful	469	36	50.7	343	9	AEA27055	AEA27055 Stress to
397	37	52.1	811	8	ADx92520	Adx92520	Plant ful	470	36	50.7	397	8	ADN18360	ADN18360 Bacterial
398	37	52.1	811	8	ADx91301	Adx91301	Plant ful	471	36	50.7	423	7	ADD46100	ADD46100 Human Pro
399	37	52.1	814	7	ADC68366	Adc68366	Lolium pe	472	36	50.7	423	7	ADBE1666	ADBE1666 Human Pro
400	37	52.1	814	8	ABO84536	AbO84536	Mouse can	473	36	50.7	429	2	AAI34771	AAI34771 Chlamydia
401	37	52.1	814	9	ABE03069	Abe03069	Fructan b	474	36	50.7	429	5	ABB90639	ABB90639 Chlamydia
402	37	52.1	815	7	ADC68460	Adc68460	Lolium pe	475	36	50.7	429	6	ABU26926	ABU26926 Protein e
403	37	52.1	815	8	ADT60478	Adt60478	Plant pol	476	36	50.7	440	2	AAW57104	AAW57104 Brevibact
404	37	52.1	815	9	ABE03163	Abe03163	Fructan b	477	36	50.7	440	2	AAW57104	AAW57104 Brevibact
405	37	52.1	815	9	ABE03163	Abe03163	Fructan b	478	36	50.7	440	6	ABU25716	ABU25716 Protein e
406	37	52.1	816	5	AAE28501	Aae28501	Corn suc	479	36	50.7	443	8	ADJ66558	ADJ66558 KIAA0087
407	37	52.1	816	7	ADC07856	Adc07856	Rice prot	480	36	50.7	443	8	ABU26926	ABU26926 Protein e
408	37	52.1	816	7	ADC08209	Adc08209	Rice prot	481	36	50.7	445	3	AAW15553	AAW15553 Apoptosis
409	37	52.1	816	7	ADC68367	Adc68367	S. arundi	482	36	50.7	445	3	AAW84903	AAW84903 A human p
410	37	52.1	816	9	ABE03070	Abe03070	Fructan b	483	36	50.7	445	3	AAW29633	AAW29633 Human pol
411	37	52.1	823	8	ADx94032	Adx94032	Plant ful	484	36	50.7	445	4	AAW39113	AAW39113 Human pol
412	37	52.1	823	8	ADx94475	Adx94475	Plant ful	485	36	50.7	445	5	ABP66221	ABP66221 Bifidobac
413	37	52.1	823	8	ADY25029	Ady25029	Plant ful	486	36	50.7	445	8	ADT88052	ADT88052 Human pro
414	37	52.1	823	8	ADx90632	Adx90632	Plant ful	487	36	50.7	447	6	ADA35069	ADA35069 Acinetoba
415	37	52.1	824	8	ADx76568	Adx76568	Plant ful	488	36	50.7	449	4	AAW40899	AAW40899 Human pol
416	37	52.1	841	9	ABC21244	Aec21244	Recombina	489	36	50.7	460	8	ADN23643	ADN23643 Bacterial
417	37	52.1	841	9	ABC21236	Aec21236	Recombina	490	36	50.7	465	4	AAU30316	AAU30316 Novel hum
418	37	52.1	843	5	ABB93633	Abb93633	Herbicida	491	36	50.7	468	2	AAW85689	AAW85689 D9D10 hea
419	37	52.1	942	5	ABB91573	Abb91573	Herbicida	492	36	50.7	470	4	ABB60697	ABB60697 Drosophil
420	37	52.1	972	5	ABB92750	Abb92750	Herbicida	493	36	50.7	473	4	AAU56201	AAU56201 Propionib
421	37	52.1	4904	6	ABB62249	Abb62249	Drosophil	494	36	50.7	476	6	ABM52720	ABM52720 Propionib
422	36.5	51.4	1938	6	ABP76678	Abp76678	Streptomy	495	36	50.7	476	7	ADG33824	ADG33824 Actinomyc
423	36.5	51.4	21	8	ADR41095	Adr41095	Cyclic KD	496	36	50.7	479	4	ABG04915	ABG04915 Novel hum
424	36.5	51.4	21	8	ADU40138	Adu40138	Kinase do	497	36	50.7	521	6	ABM445514	ABM445514 Propionib
425	36.5	51.4	21	8	ADU40138	Adu40138	Kinase do	498	36	50.7	521	6	ABM445514	ABM445514 Propionib
426	36	50.7	145	6	ADA54389	Ada54389	Human pro	499	36	50.7	531	8	ADN20810	ADN20810 Bacterial
427	36	50.7	17	7	ADM07763	Adm07763	Canine im	500	36	50.7	547	4	AAW85691	AAW85691 MotAbi an
428	36	50.7	17	7	ADM07773	Adm07773	Canine im	501	36	50.7	547	4	AAU51151	AAU51151 Propionib
429	36	50.7	18	2	AAW63100	Aaw63100	Acetylcho	502	36	50.7	547	6	ABM65154	ABM65154 Propionib
430	36	50.7	18	3	AAW15075	Aab15075	Acetylcho	503	36	50.7	557	6	ABU22824	ABU22824 Protein e
431	36	50.7	18	3	AAW84773	Aay84773	Amino aci	504	36	50.7	557	6	ABU20076	ABU20076 Protein e
432	36	50.7	19	8	ADT77356	Adt77356	Human car	505	36	50.7	583	6	ABU19626	ABU19626 Protein e
433	36	50.7	19	8	ADT61255	Adt61255	Human ant	506	36	50.7	686	5	AD117259	AD117259 Human NOV
434	36	50.7	19	8	ADU14956	Adu14956	Human Car	507	36	50.7	711	2	AAW85692	AAW85692 MotAbi f
435	36	50.7	19	8	ADU15089	Adu15089	Human Car	508	36	50.7	720	3	AAW62325	AAW62325 Amino aci
436	36	50.7	19	8	ADU74239	Adu74239	Human car	509	36	50.7	720	4	ADY52025	ADY52025 Synchocy
437	36	50.7	19	9	ADU09033	Adv09033	Human car	510	36	50.7	720	4	ADY52025	ADY52025 Synchocy
438	36	50.7	21	8	ADR51176	Adr51176	Cyclic KD	511	36	50.7	720	8	ADN20195	ADN20195 Bacterial
439	36	50.7	21	8	ADR51176	Adr51176	Cyclic KD	512	36	50.7	753	8	ADR86279	ADR86279 Aspergill
440	36	50.7	21	8	ADU40171	Adu40171	Kinase do	513	36	50.7	786	6	ABU229875	ABU229875 Protein e
441	36	50.7	67	5	ABP63709	Abp63709	Human ORF	514	36	50.7	786	9	ADV16669	ADV16669 E. faeciu
442	36	50.7	76	5	ABW77398	Abw77398	Fungal me	515	36	50.7	789	9	ADC97107	ADC97107 E. faeciu
443	36	50.7	88	4	ABG02708	Abg02708	Novel hum	516	36	50.7	1321	7	ADT71057	ADT71057 Astrotact
444	36	50.7	93	4	AAW65911	Aaw65911	Novel hum	517	36	50.7	1359	4	ABG09585	ABG09585 Novel hum
445	36	50.7	93	6	ABM62430	Abm62430	Propionib	518	35	50.0	415	4	ABB64727	ABB64727 Drosophil
446	36	50.7	110	4	AAU49118	Aau49118	Propionib	519	35	49.3	17	9	AEA40582	AEA40582 Anti-VBGF
447	36	50.7	110	6	ABM45637	Abm45637	Propionib	520	35	49.3	21	5	AAU73494	AAU73494 Vascular
448	36	50.7	121	8	AD036343	Ad036343	Intracell	521	35	49.3	21	5	ABM70810	ABM70810 Staphyloc
449	36	50.7	123	4	ABG62748	Abg62748	Human HIV	522	35	49.3	51	9	ADY65200	ADY65200 S. mansoni
450	36	50.7	123	4	ABG00025	Abg00025	Novel hum	523	35	49.3	115	3	AAW90823	AAW90823 520C9 hyb
451	36	50.7	123	7	ADL91316	Adl91316	VH chain	524	35	49.3	118	3	AAW90823	AAW90823 520C9 hyb
452	36	50.7	147	9	ADY33975	Ady33975	Anti-Tie	525	35	49.3	120	5	ABW53893	ABW53893 Arabidops
453	36	50.7	193	4	AAU30314	Aau30314	Novel hum	526	35	49.3	121	2	AAW60626	AAW60626 Lactococc
454	36	50.7	206	9	ADJ68579	Adj68579	Human hea	527	35	49.3	123	6	ABR55795	ABR55795 Heavy cha
455	36	50.7	206	9	ADV09027	Adv09027	Human car	528	35	49.3	123	9	AEA40527	AEA40527 Anti-VBGF
456	36	50.7	215	3	ABW58127	Abw58127	Lung canc	529	35	49.3	124	8	ADO25833	ADO25833 Camelidae
457	36	50.7	215	5	ABP41372	Abp41372	Human ova	530	35	49.3	129	3	AAW23033	AAW23033 Arabidops
458	36	50.7	230	2	AAW85695	Aaw85695	Anti-IFNG	531	35	49.3	140	3	AAW23032	AAW23032 Arabidops
459	36	50.7	235	2	AAW85694	Aaw85694	Anti-IFNG	532	35	49.3	198	4	ABG21551	ABG21551 Novel hum
460	36	50.7	240	2	AAW85693	Aaw85693	Anti-IFNG	533	35	49.3	211	8	ADH44566	ADH44566 Prion pro
461	36	50.7	257	9	ABM91939	Abm91939	M. xanthu	534	35	49.3	235	8	ADH44567	ADH44567 Giraffe p
462	36	50.7	261	4	ABB67927	Abb67927	Drosophil	535	35	49.3	243	2	AAW02280	AAW02280 520C9 ant

536	35	49.3	243	2	AAW53170	AAW53170	520C9 ant	609	35	49.3	1573	8	ADN24214	Adn24214 Bacterial
537	35	49.3	243	2	AAW80424	AAW80424	520C9 8FV	610	35	49.3	1576	6	ABP56835	ABP56835 Human MEG
538	35	49.3	243	7	ABW00716	ABW00716	520C9 8FV	611	35	49.3	1576	8	ADN04594	Adn04594 Antipeori
539	35	49.3	243	9	ADY60808	ADY60808	520C9 8FV	612	35	49.3	1576	8	ADQ20313	Adq20313 Human sof
540	35	49.3	246	2	AAK39569	AAK39569	Sequence	613	35	49.3	1576	9	ADY70342	Ady70342 Human bet
541	35	49.3	248	6	ABU38676	ABU38676	Protein e	614	35	49.3	1596	4	AAU28354	AAU28354 Novel hum
542	35	49.3	249	6	ABU31296	ABU31296	Protein e	615	35	49.3	1630	6	AAE30206	AAE30206 Human LP2
543	35	49.3	256	4	AAW72363	AAW72363	Antelope	616	35	49.3	1632	7	ADM26542	Adm26542 Hyperther
544	35	49.3	256	6	ABP57902	ABP57902	White tai	617	35	49.3	1637	4	AAU28166	AAU28166 Novel hum
545	35	49.3	256	6	ABP57903	ABP57903	Mule deer	618	35	49.3	1852	5	ADH48776	Adh48776 NOV25 pro
546	35	49.3	256	6	ABP57904	ABP57904	Elk BSE-r	619	35	49.3	1905	7	AAE29923	AAE29923 Human LP2
547	35	49.3	256	6	ADY24191	ADY24191	White-tai	620	35	49.3	1905	7	ADH73026	Adh73026 Human MEG
548	35	49.3	256	7	ADD24189	ADD24189	Elk prion	621	35	49.3	1906	7	ADD93399	Add93399 Human lip
549	35	49.3	256	8	ADH44565	ADH44565	Mule deer	622	35	49.3	2214	8	ADN24084	Adn24084 Bacterial
550	35	49.3	256	8	ADH44565	ADH44565	Elk prion	623	35	49.3	5071	8	ADM68814	Adm68814 Nematode
551	35	49.3	256	9	ADY50407	ADY50407	Elk prion	624	35	49.3	5107	8	ADN23724	Adn23724 Bacterial
552	35	49.3	256	9	ADY50406	ADY50406	Deer prion	625	34	47.9	12	9	AEA53674	AEA53674 Novel hum
553	35	49.3	256	9	ADY50408	ADY50408	Muledeer	626	34	47.9	20	8	ADR84179	Adr84179 S. pyogen
554	35	49.3	256	9	ADY62821	ADY62821	Elk prion	627	34	47.9	21	8	ADR41049	Adr41049 Cyclic KD
555	35	49.3	256	9	ADY62824	ADY62824	White-tai	628	34	47.9	21	8	ADR41074	Adr41074 Cyclic KD
556	35	49.3	256	9	ADY62823	ADY62823	Mule deer	629	34	47.9	21	8	ADR41102	Adr41102 Cyclic KD
557	35	49.3	256	9	ADY62822	ADY62822	Fallow de	630	34	47.9	21	8	ADR51150	Adr51150 Duo bindi
558	35	49.3	258	7	ABO79408	ABO79408	Pseudomon	631	34	47.9	21	8	ADR51122	Adr51122 Duo bindi
559	35	49.3	263	6	AAE30320	AAE30320	Human LP2	632	34	47.9	21	8	ADR51097	Adr51097 Duo bindi
560	35	49.3	267	4	AAU04944	AAU04944	Humanised	633	34	47.9	21	8	ADU40145	Adu40145 Kinase do
561	35	49.3	278	2	AAE62519	AAE62519	Isoform 1	634	34	47.9	21	8	ADU40092	Adu40092 Kinase do
562	35	49.3	294	7	ABO66778	ABO66778	Klebsiell	635	34	47.9	21	8	ADU40117	Adu40117 Kinase do
563	35	49.3	318	8	ADX79663	ADX79663	Plant ful	636	34	47.9	33	8	ADM68875	Adm68875 Insect ep
564	35	49.3	323	9	ABM96020	ABM96020	M. xanthu	637	34	47.9	35	9	AEA54134	AEA54134 Novel hum
565	35	49.3	356	6	ABU25612	ABU25612	Protein e	638	34	47.9	40	6	ABJ25314	Abj25314 SAC isola
566	35	49.3	363	6	ABU50514	ABU50514	Protein e	639	34	47.9	43	3	AAAB18937	AAAB18937 Peptide d
567	35	49.3	380	7	ADC94238	ADC94238	E. faeciu	640	34	47.9	49	2	AAW72882	AAW72882 Helicobac
568	35	49.3	402	8	ADS42987	ADS42987	Bacterial	641	34	47.9	57	9	ADW48397	Adw48397 Anti-epit
569	35	49.3	403	4	AAAB1564	AAAB1564	Arginyl t	642	34	47.9	68	8	ADK01836	Adk01836 Hepatitis
570	35	49.3	406	8	ADT58182	ADT58182	Plant pol	643	34	47.9	79	2	AAW27958	AAW27958 Staphyloc
571	35	49.3	409	4	AAU04945	AAU04945	Humanised	644	34	47.9	80	3	AAAB10746	AAAB10746 Arabidops
572	35	49.3	438	6	ABU36016	ABU36016	Protein e	645	34	47.9	84	3	AAAB18938	AAAB18938 Peptide d
573	35	49.3	441	6	ABU36521	ABU36521	Protein e	646	34	47.9	103	3	AAAG10745	AAAG10745 Arabidops
574	35	49.3	441	6	ABU34566	ABU34566	Protein e	647	34	47.9	112	8	ADP96602	ADP96602 Anti-RAS
575	35	49.3	446	7	ABM89892	ABM89892	Rice abio	648	34	47.9	115	8	ADP96608	ADP96608 Anti-RAS
576	35	49.3	446	5	ABB93325	ABB93325	Herbicida	649	34	47.9	115	8	ADP96610	ADP96610 Anti-RAS
577	35	49.3	453	6	ABU33893	ABU33893	Protein e	650	34	47.9	115	8	ADP96607	ADP96607 Anti-RAS
578	35	49.3	455	8	ADO61855	ADO61855	Transcrip	651	34	47.9	115	8	ADP96611	ADP96611 Anti-RAS
579	35	49.3	459	8	ADN23642	ADN23642	Bacterial	652	34	47.9	115	8	ADP96603	ADP96603 Anti-RAS
580	35	49.3	494	8	ADN23638	ADN23638	Bacterial	653	34	47.9	115	8	ADP96604	ADP96604 Anti-RAS
581	35	49.3	516	6	ABR52592	ABR52592	Protein s	654	34	47.9	115	8	ADP96609	ADP96609 Anti-RAS
582	35	49.3	516	7	ADK62574	ADK62574	Disease t	655	34	47.9	115	8	ADP96605	ADP96605 Anti-RAS
583	35	49.3	516	8	ADS43498	ADS43498	Bacterial	656	34	47.9	119	8	ADU97907	Adu97907 Amino aci
584	35	49.3	534	2	AAK39571	AAK39571	Sequence	657	34	47.9	119	8	ADU97939	Adu97939 Amino aci
585	35	49.3	537	8	ADK16465	ADK16465	Nanoarcha	658	34	47.9	119	9	ABEB26565	ABEB26565 HuAIP13 m
586	35	49.3	558	8	ADN23640	ADN23640	Bacterial	659	34	47.9	119	9	ABEB26597	ABEB26597 Human ant
587	35	49.3	593	9	AEA81558	AEA81558	Undefined	660	34	47.9	119	9	ABEB26630	ABEB26630 HuAIP12 h
588	35	49.3	617	9	AEA81555	AEA81555	Kale BORS	661	34	47.9	119	9	ABEB26631	ABEB26631 HuAIP12 h
589	35	49.3	636	4	ABM50659	ABM50659	C. elegan	662	34	47.9	126	3	AAAB21359	AAAB21359 Rat antib
590	35	49.3	638	5	ABP65622	ABP65622	Bifidobac	663	34	47.9	126	8	ADP96606	ADP96606 Anti-RAS
591	35	49.3	638	6	ABU24463	ABU24463	Protein e	664	34	47.9	131	9	AEA53332	AEA53332 Novel hum
592	35	49.3	648	5	ABR92839	ABR92839	Herbicida	665	34	47.9	133	3	AAAG15138	AAAG15138 Arabidops
593	35	49.3	666	8	ABD93108	ABD93108	Bacterial	666	34	47.9	134	2	AAW16478	AAW16478 Streptoco
594	35	49.3	682	8	ADR89433	ADR89433	cry19Ba.	667	34	47.9	136	9	ABEB26572	ABEB26572 HuAIP13 v
595	35	49.3	700	8	ADU221109	ADU221109	Bacterial	668	34	47.9	138	8	ADU97914	Adu97914 Humanized
596	35	49.3	716	4	ABEB68317	ABEB68317	Drosophil	669	34	47.9	138	8	ADU97944	Adu97944 Humanized
597	35	49.3	785	3	AAK80096	AAK80096	TonB depe	670	34	47.9	138	8	ABEB26602	ABEB26602 HuAIP12 V
598	35	49.3	914	3	AAK49883	AAK49883	Arabidops	671	34	47.9	153	7	ADC87051	Adc87051 Human GPC
599	35	49.3	924	3	AAK49882	AAK49882	Arabidops	672	34	47.9	159	8	ADK93868	Adk93868 Plant ful
600	35	49.3	1000	4	ABE62399	ABE62399	Drosophil	673	34	47.9	174	3	AAAB18939	AAAB18939 Peptide d
601	35	49.3	1136	7	ADH73023	ADH73023	Human MEG	674	34	47.9	176	9	ABM95653	ABM95653 M. xanthu
602	35	49.3	1144	4	AAAB50658	AAAB50658	C. elegan	675	34	47.9	178	9	ABM94295	ABM94295 M. xanthu
603	35	49.3	1176	3	AAK49881	AAK49881	Arabidops	676	34	47.9	186	3	AAAB18940	AAAB18940 Peptide d
604	35	49.3	1231	6	ABU49875	ABU49875	Protein e	677	34	47.9	191	8	ADK94667	Adk94667 Plant ful
605	35	49.3	1235	7	ADI60124	ADI60124	Secreted	678	34	47.9	207	8	ADT60791	Adt60791 Plant pol
606	35	49.3	1252	7	ADI39108	ADI39108	Rhodobact	679	34	47.9	208	8	ADT60074	Adt60074 Plant pol
607	35	49.3	1553	5	AAE26419	AAE26419	Human tra	680	34	47.9	220	7	ABO76050	ABO76050 Pseudomon
608	35	49.3	1573	8	ADN24215	ADN24215	Bacterial	681	34	47.9	222	4	AAE00164	AAE00164 Bacillus

682	34	47.9	223	3	AAB26764	Aab26764 Human Nrf	755	34	47.9	456	2	AAR06255	Aar06255 Mouse ace
683	34	47.9	247	8	ADN20100	Adn20100 Bacterial	756	34	47.9	456	2	AAR06254	Aar06254 Human ace
684	34	47.9	249	8	ADN19910	Adn19910 Bacterial	757	34	47.9	456	2	AAR06256	Aar06256 Calf acet
685	34	47.9	251	8	ADM25654	Adm25654 Hyperther	758	34	47.9	463	6	ABR53777	AbR53777 Protein s
686	34	47.9	252	8	ADA42066	Ada42066 Bacterial	759	34	47.9	463	7	ADK63840	AdK63840 Disease t
687	34	47.9	255	7	ADE44788	Ade44788 Neisseria	760	34	47.9	463	7	ADL23150	AdL23150 Mouse/hum
688	34	47.9	255	7	ADB44746	Adb44746 Neisseria	761	34	47.9	465	9	ADW48338	AdW48338 Anti-epit
689	34	47.9	255	7	ADB44784	Adb44784 Neisseria	762	34	47.9	469	7	ADG33806	AdG33806 Actinomyc
690	34	47.9	255	7	ADB44742	Adb44742 Neisseria	763	34	47.9	472	4	ABB69894	AbB69894 Drosophil
691	34	47.9	255	8	ADP70231	Adp70231 Neisseria	764	34	47.9	472	5	ADIL17260	AdiL17260 Human NOV
692	34	47.9	255	8	ADP70232	Adp70232 Neisseria	765	34	47.9	516	2	AAR32774	Aar32774 Petunia E
693	34	47.9	255	8	ADP70230	Adp70230 Neisseria	766	34	47.9	516	2	AAW85136	Aaw85136 A Petunia
694	34	47.9	255	8	ADU03767	Adu03767 Bacterici	767	34	47.9	516	4	ABAB67870	AbA67870 5-enolpyr
695	34	47.9	255	8	ADU03772	Adu03772 Bacterici	768	34	47.9	539	8	ADN17319	AdN17319 D. destru
696	34	47.9	255	8	ADU03769	Adu03769 Bacterici	769	34	47.9	539	8	ADN17317	AdN17317 D. destru
697	34	47.9	256	5	ABP43498	Abp43498 Human sec	770	34	47.9	552	4	ABB61667	AbB61667 Drosophil
698	34	47.9	256	5	ABP44896	Abp44896 Human Bly	771	34	47.9	589	3	AAB26762	Aab26762 Human Nrf
699	34	47.9	256	7	ADE44744	Ade44744 Neisseria	772	34	47.9	589	5	ABG60312	ABg60312 Human lym
700	34	47.9	256	7	ADB44786	Adb44786 Neisseria	773	34	47.9	589	8	ADM79407	AdM79407 Human lym
701	34	47.9	256	7	ADG95723	Adg95723 Single ch	774	34	47.9	589	8	ADS23253	AdS23253 Bacterial
702	34	47.9	257	8	ADS25168	AdS25168 Bacterial	775	34	47.9	589	9	ADX08170	AdX08170 Cyclin-de
703	34	47.9	257	8	ADS22761	AdS22761 Bacterial	776	34	47.9	600	5	ABP41798	AbP41798 Human ova
704	34	47.9	257	8	ADS25497	AdS25497 Bacterial	777	34	47.9	605	7	ADE61143	Ade61143 Human Pro
705	34	47.9	257	8	ADS26015	AdS26015 Bacterial	778	34	47.9	605	7	ADD45999	AdD45999 Human Pro
706	34	47.9	258	3	AAG20580	Aag20580 Arabidops	779	34	47.9	605	7	ADDE61147	AdE61147 Human Pro
707	34	47.9	258	3	AG45769	Ag45769 Arabidops	780	34	47.9	605	8	ADJ64371	AdJ64371 Cartilage
708	34	47.9	261	9	ADW73644	Adw73644 Novel emi	781	34	47.9	605	8	ADL82953	AdL82953 Human PRO
709	34	47.9	261	9	ADW08601	Adw08601 Construct	782	34	47.9	605	8	ADRI14071	AdRI14071 Human NF-
710	34	47.9	262	4	ABH66342	Abh66342 Drosophil	783	34	47.9	605	9	ADY19908	AdY19908 PRO polyp
711	34	47.9	265	8	ADX66282	Adx66282 Plant ful	784	34	47.9	634	6	ABU24146	ABu24146 Protein e
712	34	47.9	268	9	ADW73647	Adw73647 Novel emi	785	34	47.9	638	6	ABU50502	ABu50502 Protein e
713	34	47.9	268	9	ADW08604	Adw08604 Construct	786	34	47.9	658	3	AAV68010	AAv68010 Epstein-B
714	34	47.9	274	3	AAV75532	AAv75532 Neisseria	787	34	47.9	677	8	ADOI6832	AdOI6832 Amylase e
715	34	47.9	274	8	ADP70207	Adp70207 Neisseria	788	34	47.9	680	8	ADJ49398	AdJ49398 Oll-assoc
716	34	47.9	274	8	ADP70209	Adp70209 Neisseria	789	34	47.9	681	6	ABU43733	ABu43733 Protein e
717	34	47.9	274	8	ADP70324	Adp70324 Neisseria	790	34	47.9	686	6	ABU07633	ABu07633 Amino aci
718	34	47.9	274	8	ADP70208	Adp70208 Neisseria	791	34	47.9	696	7	ABM90150	ABm90150 Rice abio
719	34	47.9	280	2	AAW72879	Aaw72879 Helicobac	792	34	47.9	764	8	ADX96260	AdX96260 Plant ful
720	34	47.9	280	6	ABP98006	Abp98006 Protein 7	793	34	47.9	821	5	ABB91742	AbB91742 Herbicida
721	34	47.9	282	2	AAW16477	Aaw16477 Streptoco	794	34	47.9	882	6	ABU19350	ABu19350 Protein e
722	34	47.9	282	3	AAW16477	Aaw16477 Streptoco	795	34	47.9	907	1	AAP50073	AAp50073 Epstein-B
723	34	47.9	283	3	AAG20579	Aag20579 Arabidops	796	34	47.9	907	1	AAW71136	AAw71136 Herpes S1
724	34	47.9	283	3	AG45768	Ag45768 Arabidops	797	34	47.9	907	2	AAR80144	AAr80144 EBV gp350
725	34	47.9	283	7	ABO71325	AbO71325 Pseudomon	798	34	47.9	907	3	AAV68009	AAv68009 Epstein-B
726	34	47.9	287	4	ABE66343	AbE66343 Drosophil	799	34	47.9	1024	3	AG47319	Ag47319 Arabidops
727	34	47.9	290	3	AAG45767	AAg45767 Arabidops	800	34	47.9	1036	5	ABB91984	AbB91984 Herbicida
728	34	47.9	290	3	AAG20578	AAg20578 Arabidops	801	34	47.9	1155	6	ABU25495	ABu25495 Protein e
729	34	47.9	304	8	ADX79636	Adx79636 Plant ful	802	34	47.9	1301	4	ABB64704	ABb64704 Drosophil
730	34	47.9	308	5	ABP29570	Abp29570 Streptoco	803	34	47.9	1813	6	AAE14917	AAe14917 C. elegan
731	34	47.9	308	8	ADR83968	Adr83968 S. pyogen	804	34	47.9	1813	6	AAE14924	AAe14924 C. elegan
732	34	47.9	322	8	ADS22783	AdS22783 Bacterial	805	34	47.9	1859	8	ADQ89710	AdQ89710 Antagonis
733	34	47.9	322	8	ADS22236	AdS22236 Bacterial	806	34	47.9	1966	5	ABP65538	ABp65538 Bifidobac
734	34	47.9	339	2	AAW98829	Aaw98829 H. pylori	807	34	47.9	4868	8	ADM68813	AdM68813 Mosquito
735	34	47.9	339	8	ADY24876	Ady24876 Plant ful	808	34	47.9	5100	8	ADM68902	AdM68902 Heliothis
736	34	47.9	339	8	ADX93191	Adx93191 Plant ful	809	34	47.9	5101	8	ADM68760	AdM68760 Myzus per
737	34	47.9	355	6	ABW73087	Abw73087 Staphyloc	810	34	47.9	5104	8	ADM68762	AdM68762 Periplane
738	34	47.9	356	5	AAW47339	AAw47339 Vibrio vu	811	34	47.9	5107	4	ABB65257	AbB65257 Drosophil
739	34	47.9	357	5	AAO17551	AAo17551 Human tra	812	34	47.9	5109	8	ADM68766	AdM68766 Drosophil
740	34	47.9	367	6	ABM68917	ABm68917 Photorhab	813	34	47.9	5112	8	ADM68881	AdM68881 Drosophil
741	34	47.9	393	8	ADT59904	Adt59904 Plant pol	814	34	47.9	5112	8	ADM68882	AdM68882 Drosophil
742	34	47.9	399	4	ABB65138	AbB65138 Drosophil	815	34	47.9	5113	8	ADM68877	AdM68877 Drosophil
743	34	47.9	415	4	AAE00417	AAe00417 Lycopersi	816	34	47.9	5126	8	ADM68879	AdM68879 Drosophil
744	34	47.9	415	6	ABM68675	ABm68675 Photorhab	817	34	47.9	5126	8	ADM68880	AdM68880 Drosophil
745	34	47.9	422	6	ABU25637	ABu25637 Protein e	818	34	47.9	5127	8	ADM68878	AdM68878 Drosophil
746	34	47.9	422	8	ADT58137	Adt58137 Plant pol	819	34	47.9	5127	8	ADM68764	AdM68764 Pterogrinnu
747	34	47.9	425	8	ADN18461	Adn18461 Bacterial	820	34	47.9	5127	8	ADM68876	AdM68876 Drosophil
748	34	47.9	439	9	ABM91485	ABm91485 M. xanthu	821	34	47.9	5127	8	ADM68879	AdM68879 Drosophil
749	34	47.9	440	2	AAW27799	AAw27799 EPSP synt	822	34	47.9	5128	8	ADM68884	AdM68884 Heliothis
750	34	47.9	443	2	AAW27798	AAw27798 EPSP synt	823	34	47.9	5134	8	ADM68886	AdM68886 Heliothis
751	34	47.9	444	2	AAW23061	AAw23061 Modified	824	34	47.9	5142	8	ADM68758	AdM68758 Heliothis
752	34	47.9	444	2	AAW23062	AAw23062 Modified	825	34	47.9	5142	8	ADM68900	AdM68900 Heliothis
753	34	47.9	447	8	ADX87540	Adx87540 Plant ful	826	33.5	47.2	241	6	ABP55595	ABp55595 DPp10 hom
754	34	47.9	448	8	ADR67919	Adr67919 Wild type	827	33.5	47.2	355	2	AAW52829	AAw52829 Alcaligen

828	33.5	47.2	497	6	ABP76773	Abp76773 N. gonorr	901	33	46.5	198	5	ABB90424	Abb90424 Human pol
829	33.5	47.2	523	6	ABP78692	Abp78692 N. gonorr	902	33	46.5	207	3	AGL1581	Aag11581 Arabidops
830	33.5	47.2	533	6	ABU23299	Abu23299 Protein e	903	33	46.5	207	8	ADT50392	Adt50392 Human CCA
831	33.5	47.2	1436	10	ABE65946	Abbe65946 Drosophil	904	33	46.5	217	3	AG25435	Ag25435 Arabidops
832	33	46.5	10	7	ADB44853	Adbe44853 Neisseria	905	33	46.5	220	8	ADI10195	Adi10195 Interrupt
833	33	46.5	10	8	ADU06402	Adro6402 N meningi	906	33	46.5	221	4	AAE00187	Aae00187 Bacillus
834	33	46.5	10	8	ADU03719	Aduo3719 Bacterici	907	33	46.5	222	2	AAR14159	Aar14159 Serine pr
835	33	46.5	10	9	AEA53765	Aea53765 Novel hum	908	33	46.5	222	2	AAR26467	Aar26467 Sequence
836	33	46.5	10	9	AEA46156	Aea46156 Apolipop	909	33	46.5	222	4	AAE00039	Aae00039 Bacillus
837	33	46.5	14	9	AEA22670	Aea22670 Synthetic	910	33	46.5	222	4	AAE00076	Aae00076 Bacillus
838	33	46.5	17	4	ABG61399	Abg61399 Enhanced	911	33	46.5	222	4	AAE00107	Aae00107 Bacillus
839	33	46.5	17	7	ADM07758	Adm07758 Canine im	912	33	46.5	222	4	AAE00181	Aae00181 Bacillus
840	33	46.5	17	9	AEA40584	Aea40584 Anti-VEGF	913	33	46.5	222	4	AAE00067	Aae00067 Bacillus
841	33	46.5	29	2	AAR27564	Aar27564 Insert D	914	33	46.5	222	4	AAE00072	Aae00072 Bacillus
842	33	46.5	32	4	ABB39664	Abb39664 Peptide #	915	33	46.5	222	4	AAE00074	Aae00074 Bacillus
843	33	46.5	32	4	AAE00074	Aae00074 Peptide #	916	33	46.5	222	4	AAE00079	Aae00079 Bacillus
844	33	46.5	32	4	ABB24336	Abb24336 Protein #	917	33	46.5	222	4	AAE00152	Aae00152 Bacillus
845	33	46.5	32	4	AAE00152	Aae00152 Human bon	918	33	46.5	222	4	AAE00156	Aae00156 Bacillus
846	33	46.5	32	4	AAE00156	Aae00156 Human bra	919	33	46.5	222	4	AAE00161	Aae00161 Bacillus
847	33	46.5	32	4	ABG54727	Abg54727 Human liv	920	33	46.5	222	4	AAE00179	Aae00179 Bacillus
848	33	46.5	32	5	ABG42855	Abg42855 Human pep	921	33	46.5	222	4	AAE00048	Aae00048 Bacillus
849	33	46.5	35	2	AAW32146	Aaw32146 Porphyrom	922	33	46.5	222	4	AAE00065	Aae00065 Bacillus
850	33	46.5	44	6	ABU45616	Abu45616 Protein e	923	33	46.5	222	4	AAE00068	Aae00068 Bacillus
851	33	46.5	47	2	AAE00176	Aae00176 Protein e	924	33	46.5	222	4	AAE00082	Aae00082 Bacillus
852	33	46.5	50	4	AAE00176	Aae00176 Human dig	925	33	46.5	222	4	AAE00084	Aae00084 Bacillus
853	33	46.5	51	6	ABU56843	Abu56843 BONT/A Hc	926	33	46.5	222	4	AAE00094	Aae00094 Bacillus
854	33	46.5	59	4	ABG26066	Abg26066 Novel hum	927	33	46.5	222	4	AAE00090	Aae00090 Bacillus
855	33	46.5	71	6	ABO00872	Ab000872 Polypteti	928	33	46.5	222	4	AAE00098	Aae00098 B. lichen
856	33	46.5	95	3	AG25177	Ag25177 Arabidops	929	33	46.5	222	4	AAE00118	Aae00118 Bacillus
857	33	46.5	109	3	AG51638	Ag51638 Arabidops	930	33	46.5	222	4	AAE00124	Aae00124 Bacillus
858	33	46.5	117	2	AAW76003	Aaw76003 LM609 ant	931	33	46.5	222	4	AAE00125	Aae00125 Bacillus
859	33	46.5	117	2	AAW76001	Aaw76001 Vitaxin a	932	33	46.5	222	4	AAE00126	Aae00126 Bacillus
860	33	46.5	117	2	AAE01361	Aae01361 Murine mo	933	33	46.5	222	4	AAE00177	Aae00177 Bacillus
861	33	46.5	117	4	AAE01361	Aae01361 Antibody	934	33	46.5	222	4	AAE00031	Aae00031 Bacillus
862	33	46.5	117	4	AAE01359	Aae01359 Vitaxin h	935	33	46.5	222	4	AAE00036	Aae00036 Bacillus
863	33	46.5	117	4	AAE03589	Aae03589 A heavy c	936	33	46.5	222	4	AAE00042	Aae00042 Bacillus
864	33	46.5	117	4	AAE03587	Aae03587 A heavy c	937	33	46.5	222	4	AAE00062	Aae00062 Bacillus
865	33	46.5	117	6	ABO19797	Ab019797 Vitaxin h	938	33	46.5	222	4	AAE00066	Aae00066 Bacillus
866	33	46.5	117	6	ABO19799	Ab019799 LM609 hea	939	33	46.5	222	4	AAE00073	Aae00073 Bacillus
867	33	46.5	117	7	ADG71776	Adg71776 Vitaxin h	940	33	46.5	222	4	AAE00077	Aae00077 Bacillus
868	33	46.5	117	7	ADG71780	Adg71780 Mab LM609	941	33	46.5	222	4	AAE00080	Aae00080 Bacillus
869	33	46.5	117	8	ADJ57961	Adj57961 Murine LM	942	33	46.5	222	4	AAE00081	Aae00081 Bacillus
870	33	46.5	117	8	ADJ57957	Adj57957 Vitaxin h	943	33	46.5	222	4	AAE00086	Aae00086 Bacillus
871	33	46.5	117	9	ADY92978	Ady92978 Mouse LM6	944	33	46.5	222	4	AAE00097	Aae00097 B. lichen
872	33	46.5	117	9	ADY92974	Ady92974 LM609 gra	945	33	46.5	222	4	AAE00102	Aae00102 Bacillus
873	33	46.5	120	9	AAV13948	Aav13948 VH chain	946	33	46.5	222	4	AAE00151	Aae00151 Bacillus
874	33	46.5	122	9	AEA53939	Aea53939 Novel hum	947	33	46.5	222	4	AAE00166	Aae00166 Bacillus
875	33	46.5	122	9	AEA53342	Aea53342 Novel hum	948	33	46.5	222	4	AAE00168	Aae00168 Bacillus
876	33	46.5	123	9	AEA40525	Aea40525 Anti-VEGF	949	33	46.5	222	4	AAE00176	Aae00176 Bacillus
877	33	46.5	125	8	ADR38646	Adr38646 Mouse hea	950	33	46.5	222	4	AAE00053	Aae00053 Bacillus
878	33	46.5	126	3	AAE00176	Aae00176 Arabidops	951	33	46.5	222	4	AAE00058	Aae00058 Bacillus
879	33	46.5	129	2	AAV15402	Aav15402 Protein e	952	33	46.5	222	4	AAE00060	Aae00060 Bacillus
880	33	46.5	130	2	AAV06379	Aav06379 Murine mo	953	33	46.5	222	4	AAE00093	Aae00093 Bacillus
881	33	46.5	131	6	ABU21898	Abu21898 Protein e	954	33	46.5	222	4	AAE00103	Aae00103 Bacillus
882	33	46.5	141	6	ABP71175	Abp71175 Xenopus p	955	33	46.5	222	4	AAE00104	Aae00104 Bacillus
883	33	46.5	142	4	AAE00416	Aae00416 A. actino	956	33	46.5	222	4	AAE00167	Aae00167 Bacillus
884	33	46.5	142	7	ADP60715	Adp60715 Polypepti	957	33	46.5	222	4	AAE00173	Aae00173 Bacillus
885	33	46.5	142	8	ADO57776	Ado57776 Actinobac	958	33	46.5	222	4	AAE00174	Aae00174 Bacillus
886	33	46.5	143	6	ADA43059	Ada43059 Human ant	959	33	46.5	222	4	AAE00186	Aae00186 Bacillus
887	33	46.5	148	4	ABG12883	Abg12883 Novel hum	960	33	46.5	222	4	AAE00192	Aae00192 Bacillus
888	33	46.5	166	3	AGL1582	Agl1582 Arabidops	961	33	46.5	222	4	AAE00038	Aae00038 Bacillus
889	33	46.5	167	3	AGG1637	Agg1637 Arabidops	962	33	46.5	222	4	AAE00055	Aae00055 Bacillus
890	33	46.5	170	8	AD327569	Ad327569 Bacterial	963	33	46.5	222	4	AAE00083	Aae00083 Bacillus
891	33	46.5	173	3	AG25437	Ag25437 Arabidops	964	33	46.5	222	4	AAE00100	Aae00100 Bacillus
892	33	46.5	173	4	ABE2452	Abbe2452 Drosophil	965	33	46.5	222	4	AAE00108	Aae00108 Bacillus
893	33	46.5	178	3	AG25436	Ag25436 Arabidops	966	33	46.5	222	4	AAE00115	Aae00115 Bacillus
894	33	46.5	195	6	AE30035	Aae30035 Arabidops	967	33	46.5	222	4	AAE00148	Aae00148 Bacillus
895	33	46.5	195	6	ADB23090	Adb23090 Environme	968	33	46.5	222	4	AAE00172	Aae00172 Bacillus
896	33	46.5	195	7	ADB31789	Adb31789 Plant (A.	969	33	46.5	222	4	AAE00044	Aae00044 Bacillus
897	33	46.5	195	7	ADC46665	Adc46665 Thalecres	970	33	46.5	222	4	AAE00045	Aae00045 Bacillus
898	33	46.5	195	7	ADD30528	Add30528 Plant yie	971	33	46.5	222	4	AAE00054	Aae00054 Bacillus
899	33	46.5	195	8	ADI43975	Adi43975 Plant tra	972	33	46.5	222	4	AAE00085	Aae00085 Bacillus
900	33	46.5	195	9	AEA26671	Aea26671 Stress to	973	33	46.5	222	4	AAE00113	Aae00113 Bacillus

CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The CAB is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample
 XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 71; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
 |||||
 DB 99 DDYGGQSTYVMDA 111

RESULT 3

AAW23437

ID AAW23437 standard; protein; 122 AA.

XX AC AAW23437;

XX 23-APR-1998 (first entry)

XX Modified heavy chain variable region KOLWI2VH-1.

XX Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.

XX Synthetic.

OS Rattus sp.

XX Key Location/Qualifiers

FT Misc-difference 10 /note= "D to G mutation"

FT Misc-difference 11 /note= "L to V mutation"

FT Misc-difference 19 /note= "K to R mutation"

FT Misc-difference 23 /note= "V to S mutation"

FT Misc-difference 24 /note= "A to S mutation"

FT Region 31. .35

FT Misc-difference 43 /note= "complementarity determining region-1"

FT Region 50. .66

FT Misc-difference 77 /note= "complementarity determining region-2"

FT Misc-difference 80 /note= "S to N mutation"

FT Misc-difference 84 /note= "Y to P mutation"

FT Misc-difference 92 /note= "N to D mutation"

FT Misc-difference 93 /note= "A to G mutation"

FT Region 99. .111

FT Misc-difference 116 /note= "complementarity determining region-3"

FT Misc-difference 117 /note= "S to T mutation"

FT Misc-difference 117 /note= "S to P mutation"

XX WO9734636-A1.

PN

PD 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Losman MJ, Hansen H;

XX WPI; 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.

XX Claim 7; Fig 1; 46pp; English.

CC This sequence represents a modified version of the rat rW12 heavy chain
 CC variable region, designated KOLWI2VH-1. This sequence is used in an
 CC antibody of the invention. The antibody of the invention is a chimeric or
 CC humanised anti-idiotype antibodies (cAb and hAb, respectively) or a
 CC fragment which specifically binds to the idiotype region of an anti-
 CC carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light
 CC (L) and heavy (H) chain variable regions, or silent mutations; and (ii)
 CC hAb comprises rW12 complementarity determining regions (CDR) and
 CC humanised framework (FR) regions. The hAb is used as a vaccine to
 CC stimulate an immune response in a patient against cancers expressing CEA.
 CC The hAb, can be used to clear non-targeted antibody in a method of
 CC diagnosis or treatment of a patient where a CEA antibody is used as a
 CC (pre-)targeting or therapy agent. The CAB is used to detect the presence
 CC of an antibody that specifically binds to CEA in a sample
 XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 71; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
 |||||
 DB 99 DDYGGQSTYVMDA 111

RESULT 4

AAW23441

ID AAW23441 standard; protein; 122 AA.

XX AC AAW23441;

XX 23-APR-1998 (first entry)

XX hW12 heavy chain.

XX Antibody; complementarity determining region; heavy chain; human; CEA;
 KW hW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 31. .35 /note= "complementarity determining region-1"

FT Region 50. .66 /note= "complementarity determining region-2"

FT Region 99. .111 /note= "complementarity determining region-3"

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.
 XX (IMMU-) IMMUNOMEDICS INC.
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX N-PSDB; ANT86299.
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 FT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 FT stimulate immune response against cancer.
 XX Disclosure; Fig 3; 46pp; English.
 XX This sequence represents the human hW12 heavy chain. This sequence is
 CC used in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotypic antibodies (cAb and hAb,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb
 CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cAb is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample
 XX Sequence 122 AA;
 SQ Query Match 100.0%; Score 71; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DDYGGQSTYVMDA 13
 Db 99 DDYGGQSTYVMDA 111
 RESULT 5
 ID AAW23438
 XX AAW23438 standard; protein; 122 AA.
 XX AAW23438;
 XX 23-APR-1998 (first entry)
 XX Modified heavy chain variable region KOLW12VH-2.
 XX Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.
 XX Synthetic.
 OS Rattus sp.
 XX Key Location/Qualifiers
 FH Misc-difference 5 /note= "Q to V mutation"
 FT Misc-difference 10 /note= "D to G mutation"
 FT Misc-difference 11 /note= "L to V mutation"
 FT Misc-difference 19 /note= "K to R mutation"
 FT Misc-difference 23 /note= "V to S mutation"
 FT Misc-difference 24 /note= "A to S mutation"
 FT Region 31. .35 /note= "complementarity determining region-1"

FT Misc-difference 43 /note= "E to K mutation"
 FT Region 50. .66 /note= "complementarity determining region-2"
 FT Misc-difference 77 /note= "S to N mutation"
 FT Misc-difference 80 /note= "Y to F mutation"
 FT Misc-difference 84 /note= "N to D mutation"
 FT Misc-difference 92 /note= "A to G mutation"
 FT Misc-difference 93 /note= "T to V mutation"
 FT Region 99. .111 /note= "complementarity determining region-3"
 FT Misc-difference 116 /note= "S to T mutation"
 FT Misc-difference 117 /note= "S to P mutation"
 XX W09734636-A1.
 XX 25-SEP-1997.
 XX 19-MAR-1997; 97WO-US004696.
 XX 20-MAR-1996; 96US-0013708P.
 XX (IMMU-) IMMUNOMEDICS INC.
 XX Leung S, Losman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 FT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 FT stimulate immune response against cancer.
 XX Claim 7; Fig 1; 46pp; English.
 XX This sequence represents a modified version of the rat rW12 heavy chain
 CC variable region, designated KOLW12VH-2. This sequence is used in an
 CC antibody of the invention. The antibody of the invention is a chimeric or
 CC humanised anti-idiotypic antibodies (cAb and hAb, respectively) or a
 CC fragment which specifically binds to the idiotype region of an anti-
 CC carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light
 CC (L) and heavy (H) chain variable regions, or silent mutations; and (ii)
 CC hAb comprises rW12 complementarity determining regions (CDR) and
 CC humanised framework (FR) regions. The hAb is used as a vaccine to
 CC stimulate an immune response in a patient against cancers expressing CEA.
 CC The hAb, can be used to clear non-targeted antibody in a method of
 CC diagnosis or treatment of a patient where a CEA antibody is used as a
 CC (pre-)targeting or therapy agent. The cAb is used to detect the presence
 CC of an antibody that specifically binds to CEA in a sample
 XX Sequence 122 AA;
 SQ Query Match 100.0%; Score 71; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DDYGGQSTYVMDA 13
 Db 99 DDYGGQSTYVMDA 111
 RESULT 6
 ADM07759
 ID ADM07759 standard; peptide; 17 AA.
 XX ADM07759;
 AC ADM07759;
 XX

DT 20-MAY-2004 (first entry)
XX Canine immunoglobulin heavy chain variable domain CDR2 peptide 3.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgE; gene therapy;
KW complementarity determining region; CDR2.
XX
XX Canis familiaris.
OS
XX WO2003060080-A2.
PN
XX 24-JUL-2003.
PD
XX 20-DEC-2002; 2002WO-US041362.
PF
XX 21-DEC-2001; 2001US-0344874P.
PR
XX (IDEX-) IDEXX LAB INC.
PA
XX Krah ER, Guo H, Aiyappa A, Lawton R;
PI
XX WPI; 2003-598521/56.
DR
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Claim 16; Page 95; 130pp; English.
PS
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin heavy chain variable domain complementarity determining
CC region (CDR) peptide of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 60.6%; Score 43; DB 7; Length 17;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 YGGQSTYYVMDA 13
DB 4 YGGSSTYYADA 14
RESULT 7
ADM07290
ID ADM07290 standard; protein; 134 AA.
XX
XX ADM07290;
AC
XX 20-MAY-2004 (first entry)
DT
XX Canine immunoglobulin heavy chain variable domain protein 7.
DE
XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgE; gene therapy.
KW
XX Canis familiaris.
OS
XX WO2003060080-A2.
PN
XX 24-JUL-2003.
PD
XX 20-DEC-2002; 2002WO-US041362.
PF
XX 21-DEC-2001; 2001US-0344874P.
PR
XX (IDEX-) IDEXX LAB INC.
PA
XX Krah ER, Guo H, Aiyappa A, Lawton R;
PI

XX WPI; 2003-598521/56.
DR N-PSDB; ADM07289.
XX
XX New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
XX Example 8; Page 58; 130pp; English.
PS
XX The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin heavy chain variable domain protein of the invention.
XX
XX Sequence 134 AA;
SQ
Query Match 60.6%; Score 43; DB 7; Length 134;
Best Local Similarity 72.7%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 YGGQSTYYVMDA 13
DB 72 YGGSSTYYADA 82
RESULT 8
ADV11275
ID ADV11275 standard; protein; 237 AA.
XX
XX ADV11275;
AC
XX 21-APR-2005 (first entry)
DT
XX Plant full length insert polypeptide seqid 67090.
DE
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
XX Unidentified.
OS
XX US2004034888-A1.
PN
XX 19-FEB-2004.
PD
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
PR
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX WPI; 2004-180133/17.
DR
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 67090; 15pp; English.
PS

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 237 AA;

Query Match 60.6%; Score 43; DB 8; Length 237;
 Best Local Similarity 70.0%; Pred. No. 57;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
 Db 45 DDFGGQKAYV 54
 ||:|||||

RESULT 9
 AAB50360
 ID AAB50360 standard; protein; 241 AA.
 AC AAB50360;
 DT 09-MAR-2001 (first entry)
 XX Maize ZmGnsN4 glucanase.
 DE
 XX Maize; ZmGnsN4; glucanase; plant growth; disease resistance;
 KW transgenic plant; mutation detection; expression analysis.
 KW
 XX Zea mays.
 OS
 XX WO200073470-A2.
 FN
 XX 07-DEC-2000.
 PD
 XX 08-JUN-1999; 99WO-US012761.
 PF
 XX 26-MAY-1999; 99US-00320076.
 PR
 XX (PION-) PIONEER HI-BRED INT INC.
 PA
 XX Simmons CR;
 PI
 XX WPI; 2001-061547/07.
 DR
 XX N-PSDB; AAC89729.
 DR
 XX New exo- and endo-glucanase polypeptides and polynucleotides useful in
 PT e.g. cell wall elongation or expansion, enhancing silage or forage crop
 PT digestibility, improving plant defense against pathogens and stress.
 PT
 XX Claim 9; Page 69; 108pp; English.
 PS
 XX The present sequence is one of a number of glucanase polypeptides
 CC isolated from Zea mays. The nucleic acids encoding for glucanases are
 CC useful for improving cell wall elongation or expansion and altering the
 CC growth of a plant or improving kernel growth rates, enhancing silage or
 CC forage crop digestibility, plant defense against pathogens and stress,
 CC flowering, fruit and seed maturation, abscission and senescence, and

CC tissue differentiation. The nucleic acids may also be used as probes or
 CC amplification primers in the detection, quantitation or isolation of gene
 CC transcripts, and for detecting deficiencies in mRNA levels in screening
 CC for a desired transgenic plant. They can also be used for detecting gene
 CC mutations, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, and for detection of any
 CC number of allelic variants of the gene, as molecular markers in plant
 CC breeding programmes. The nucleic acids can be used for recombinant
 CC expression of exo- or endo-glucanase polypeptides, and as immunogens in
 CC preparing or screening antibodies. The proteins may also be used in
 CC assays for enzyme agonists or antagonists, or as immunogens or antigens
 CC to obtain antibodies immunoreactive with the protein

XX SQ Sequence 241 AA;

Query Match 60.6%; Score 43; DB 4; Length 241;
 Best Local Similarity 70.0%; Pred. No. 58;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
 Db 24 DDFGGQKAYV 33
 ||:|||||

RESULT 10
 ADY11626
 ID ADY11626 standard; protein; 262 AA.
 XX ADY11626;
 AC
 XX 21-APR-2005 (first entry)
 DT
 XX Plant full length insert polypeptide seqid 67441.
 DE
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 XX US2004034888-A1.
 FN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985678.
 PR
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PT
 XX Claim 1; SEQ ID NO 67441; 15pp; English.
 PS
 XX The invention describes a recombinant DNA construct comprising a

CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 262 AA;
 Query Match 60.6%; Score 43; DB 8; Length 262;
 Best Local Similarity 70.0%; Pred. No. 64;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTTV 10
 Db 45 DDFGGQKAYV 54
 ||:|||| ||
 RESULT 11
 ADX96652
 ID ADX96652 standard; protein; 262 AA.
 AC ADX96652;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 59316.
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX Unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.
 XX Claim 1; SEQ ID NO 59316; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 262 AA;
 Query Match 60.6%; Score 43; DB 8; Length 262;
 Best Local Similarity 70.0%; Pred. No. 64;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTTV 10
 Db 45 DDFGGQKAYV 54
 ||:|||| ||
 RESULT 12
 ADS23337
 ID ADS23337 standard; protein; 362 AA.
 AC ADS23337;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #12370.
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 XX Claim 1; SEQ ID NO 12370; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 362 AA;

Query Match 60.6%; Score 43; DB 8; Length 362;
 Best Local Similarity 70.0%; Pred. No. 90;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
 |||||
 Db 88 DDYGGMSAYL 97

RESULT 13
 ABU48510
 ID ABU48510 standard; protein; 450 AA.

XX AC ABU48510;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #34037.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Treponema pallidum.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 26-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PF Wang L, Zamudio C, Malone C, Haselbeck R, Ohleen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX PR WPI; 2003-029926/02.

DR N-PSDB; ACA52380.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 76434; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 450 AA;

Query Match 60.6%; Score 43; DB 6; Length 450;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YGGQSTYV 10
 |||||
 Db 253 YGGQSTYI 260

RESULT 14

ABB92490
 ID ABB92490 standard; protein; 351 AA.

XX AC ABB92490;

XX DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 1701.

XX KW Herbicidal; plant; agriculture; herbicide.

XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.

XX PD 07-FEB-2002.

XX PF 28-AUG-2001; 2001WO-EP009892.

XX PR 28-AUG-2001; 2001WO-EP009892.

XX

PA (FARB) BAYER AG.
 XX Tietjen K, Weidler M;
 XX WPI; 2002-269010/31.
 XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.
 XX Claim 5; SEQ ID NO 1701; 261pp + Sequence Listing; English.
 XX The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 XX Sequence 351 AA;
 SQ

Query Match 59.2%; Score 42; DB 5; Length 351;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTYV 10
 Db 118 DDYGGKKQYV 127
 |||||: ||

RESULT 15
 ABB92275
 ID ABB92275 standard; protein; 408 AA.
 AC ABB92275;
 XX 31-MAY-2002 (first entry)
 DT Herbicidally active polypeptide SEQ ID NO 1486.
 DE Herbicidal; plant; agriculture; herbicide.
 XX Arabidopsis thaliana.
 OS WO200210210-A2.
 PN 07-FEB-2002.
 PD 28-AUG-2001; 2001WO-EP009892.
 PF 28-AUG-2001; 2001WO-EP009892.
 PR (FARB) BAYER AG.
 PA Tietjen K, Weidler M;
 PI WPI; 2002-269010/31.
 XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.
 XX Claim 5; SEQ ID NO 1486; 261pp + Sequence Listing; English.
 XX The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search

CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 XX Sequence 408 AA;
 SQ

Query Match 59.2%; Score 42; DB 5; Length 408;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTYV 10
 Db 134 DDYGGKKQYV 143
 |||||: ||

RESULT 16
 ADZ25621
 ID ADZ25621 standard; protein; 463 AA.
 XX AC ADZ25621;
 XX 16-JUN-2005 (first entry)
 DT Aspergillus oryzae mannanase SEQ ID NO:2.
 DE mannan endo-1 4-b-mannosidase; mannanase; food; EC 3.2.1.78.
 XX Aspergillus oryzae.
 OS JP2003164286-A.
 PN 10-JUN-2003.
 PD 30-NOV-2001; 2001JP-00365829.
 PF 30-NOV-2001; 2001JP-00365829.
 PR (NODA) ZH NODA SANGYO KAGAKU KENKYUSHO.
 PA (KIKK) KIKKOWAN CORP.
 XX WPI; 2004-112444/12.
 DR N-PSDB; ADZ25620.
 XX Novel protein derived from Aspergillus oryzae having mannanase activity,
 PT useful in food processing.
 XX Claim 1; SEQ ID NO 2; 10pp; Japanese.
 XX The invention relates to a mannanase protein (I) having the 463 amino
 CC acid sequence of ADZ25621, or sequence which has one or more amino acid
 CC deletions, substitutions or additions in ADZ25621, or a sequence which
 CC has 70% or more homology to ADZ25621 or its fragment. Also described: (1)
 CC mannanase gene (II) encoding (I); (2) a recombinant vector (III)
 CC containing (II); (3) a transformed organism (IV) containing (III); and
 CC (4) producing (V) mannanase, which involves culturing (IV) and extracting
 CC the mannanase protein from the culture. (I) is useful in food processing.
 XX The present sequence represents Aspergillus oryzae mannanase.
 XX Sequence 463 AA;
 SQ

Query Match 59.2%; Score 42; DB 8; Length 463;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTYV 10
 Db 232 DDYGGYNAYV 241
 |||||: ||

RESULT 17
 ABU29699

ID ABU29699 standard; protein; 410 AA.
 AC ABU29699;
 XX 19-JUN-2003 (first entry)
 DT Protein encoded by Prokaryotic essential gene #15226.
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Enterococcus faecium.
 OS WO200277183-A2.
 XX 03-OCT-2002.
 PD 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 FI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA33569.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 57623; 1766pp; English.
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 410 AA;
 SQ Query Match 57.7%; Score 41; DB 6; Length 410;

Best Local Similarity 53.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 DDYGGQSTYVMDA 13
 Db :|||:|:|:
 97 ENTYDGEITVLDA 109
 RESULT 18
 ADC95924
 ID ADC95924 standard; protein; 416 AA.
 XX AC ADC95924;
 XX 01-JAN-2004 (first entry)
 DT E. faecium protein sequence SEQ ID 5551.
 DE Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 XX Enterococcus faecium.
 OS US6583275-B1.
 XX 24-JUN-2003.
 PD 30-JUN-1998; 98US-00107532.
 XX 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Doucette-Stamm LA, Bush D;
 FI WPI; 2003-799836/75.
 DR N-PSDB; ADC92270.
 XX New isolated nucleic acid derived from *Enterococcus faecium* encoding an
 PT *Enterococcus faecium* polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 XX Example 1; SEQ ID NO 5551; 243pp; English.
 PS The invention relates to an isolated nucleic acid derived from
 XX *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC a transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids are useful for diagnosing pathological conditions
 CC resulting from *E. faecium* bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of *Candida albicans* -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating *Enterococcus faecium* infections. The present sequence represents
 CC one if the disclosed *E. faecium* proteins.
 XX Sequence 416 AA;
 SQ Query Match 57.7%; Score 41; DB 7; Length 416;
 Best Local Similarity 53.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 DDYGGQSTYVMDA 13
 Db :|||:|:|:

DR	WFI; 1997-341692/31.
DR	N-PSDB; AAT85178.
XX	
PT	Genomic sequence of equine rhinovirus 1 - and derived proteins or virus-

XX Claim 4; SEQ ID NO 290; 480pp; English.
 PS This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a peptide derived from a *Neisseria*
 CC meningitidis 2086 subfamily B protein which can be used to create the
 CC composition of the invention.

XX Sequence 42 AA;

Query Match 56.3%; Score 40; DB 7; Length 42;
 Best Local Similarity 58.3%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDVGQSTYVMD 12
 ||||: ||:
 Db 11 DDAGGKLYTID 22

RESULT 21

ADR06405
 ID ADR06405 standard; protein; 42 AA.

XX AC ADR06405;

XX DT 21-OCT-2004 (first entry)

XX DE N meningitidis ORF2086 protein fragment SeqID65.

XX KW expression level; PorA protein; host cell; antibacterial; vaccine;
 ORF2086; immunogenic composition.

XX OS *Neisseria meningitidis* serogroup B.

XX PN WO2004065603-A2.

XX PD 05-AUG-2004.

XX PF 13-JAN-2004; 2004WO-US000800.

XX PR 15-JAN-2003; 2003US-0440244P.

XX PA (AMHP) WYETH HOLDINGS CORP.

XX PI Farley JE, Hoiseth SK;

XX DR WPI; 2004-593483/57.

XX Increasing the expression levels of a *Neisseria* PorA protein or
 PT polypeptide in a host cell comprises infecting, transfecting or
 PT transforming a host cell with an expression vector.

XX Claim 103; SEQ ID NO 65; 161pp; English.

XX This invention relates to a novel method of increasing the expression
 CC levels of a *Neisseria* PorA protein or polypeptide in a host cell which
 CC comprises infecting, transfecting or transforming a host cell with an
 CC expression vector, where codon 18 of the PorA gene is a codon other than
 CC an ATC. The invention may be useful for the production of compounds with
 CC an antibacterial activity or a vaccine. The method is useful for

CC increasing the expression levels of a *Neisseria* PorA protein or
 CC polypeptide in a host cell. The polypeptide or polynucleotide and
 CC composition are useful for immunising against *Neisseria*. The present
 CC sequence is that of a fragment of the *Neisseria meningitidis* ORF2086
 CC protein which may be used in combination with the PorA peptides and
 CC proteins of the invention to form immunogenic compositions.

XX SQ Sequence 42 AA;

Query Match 56.3%; Score 40; DB 8; Length 42;
 Best Local Similarity 58.3%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDVGQSTYVMD 12
 ||||: ||:
 Db 11 DDAGGKLYTID 22

RESULT 22

ADU03722
 ID ADU03722 standard; peptide; 42 AA.

XX AC ADU03722;

XX DT 27-JAN-2005 (first entry)

XX DE Bactericidal 2086 protein associated peptide seqid 290.

XX KW vaccine; meningococcal disease; immunogenic; immune response;
 bactericidal; 2086 protein; subfamily B.

XX OS *Neisseria*.

XX PN WO2004094596-A2.

XX PD 04-NOV-2004.

XX PF 16-APR-2004; 2004WO-US011901.

XX PR 16-APR-2003; 2003US-0463161P.

XX PA (AMHP) WYETH HOLDINGS CORP.

XX PI Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 Metcalf BJ;

XX DR WPI; 2004-775919/76.

XX New immunogenic compositions useful in the preparation of a medicament
 PT for inducing an immune response in a mammal, particularly in preventing,
 PT diagnosing and/or treating meningococcal infection.

XX PS Claim 92; SEQ ID NO 290; 160pp; English.

XX The invention describes a composition for the prevention and treatment of
 CC meningococcal disease. The composition comprises: a protein comprising 10
 CC -14 amino acids (SEQ ID NO: 444-452), or one of 56 odd numbered sequences
 CC from SEQ ID NO: 331-443, not given in the specification; a protein
 CC encoded by a polynucleotide that hybridises to one of the polynucleotides
 CC that encode SEQ ID NO: 444-452, or one of 56 even numbered sequences from
 CC SEQ ID NO: 330-442; an immunogenic portion of (a) or (b); or a biological
 CC equivalent of (a) or (b), or an immunogenic portion of (c). The
 CC compositions are used in preparing a medicament for inducing an immune
 CC response in a mammal, where the medicament is effective against bacterial
 CC meningitis in a mammal. The compositions can be used in preventing,
 CC diagnosing and/or treating meningococcal infection. This is the amino
 CC acid sequence of a bactericidal protein 2086 subfamily B associated
 CC peptide.

XX SQ Sequence 42 AA;

Query Match 56.3%; Score 40; DB 8; Length 42;
 Best Local Similarity 58.3%; Pred. No. 29;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
 || ||: ||: ||
 Db 11 DDAGGKLTVTID 22

RESULT 23
 ADK48317
 ID ADK48317 standard; protein; 183 AA.
 XX AC
 XX ADK48317;
 XX DT 20-MAY-2004 (first entry)
 XX DE Streptococcus pneumoniae protein, Seq ID No 4832.
 XX KW Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
 XX OS Streptococcus pneumoniae.
 XX PN US6699703-B1.
 XX PD 02-MAR-2004.
 XX PF 26-MAY-2000; 2000US-00583110.
 XX PR 02-JUL-1997; 97US-0051553P.
 XX PR 12-MAY-1998; 98US-0085131P.
 XX PR 30-JUN-1998; 98US-00107433.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Doucette-Stamm L, Bush D, Zeng Q, Opperman T, Housewears CE;
 XX DR WPI: 2004-212399/20.
 XX DR N-PSDB; ADK45656.
 XX PT New nucleic acid molecules and polypeptides useful for diagnosing,
 PT preventing and treating pathological conditions resulting from bacterial
 PT infection, e.g. Streptococcus pneumoniae infection, and in drug
 PT screening.
 XX PS Disclosure; SEQ ID NO 4832; 301pp; English.
 XX CC The invention relates to isolated Streptococcus pneumoniae nucleic acids
 CC and polypeptides. The nucleic acids and proteins are useful for
 CC diagnosing, preventing and treating pathological conditions resulting
 CC from bacterial infection, such as S. pneumoniae infection. These may also
 CC be used for drug screening procedures. The present sequence represents a
 CC Streptococcus pneumoniae polypeptide of the invention. Note: The sequence
 CC data for this patent did not appear in the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX SQ Sequence 183 AA;

Query Match 56.3%; Score 40; DB 8; Length 183;
 Best Local Similarity 61.5%; Pred. No. 1.4e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
 || ||: ||: ||
 Db 48 DDIGGKSTEVQA 60

RESULT 24
 ABP98002
 ID ABP98002 standard; protein; 225 AA.
 XX AC ABP98002;
 XX DT 11-AUG-2003 (first entry)

XX DE Protein 741 from Neisseria strain 72/00.
 XX KW Hybrid protein; Neisseria gonorrhoeae; Neisseria meningitidis; orf1;
 KW orf4; orf25; orf40; orf46.1; orf83; NMB1343; 230; 233; 287; 292; 594;
 KW 687; 736; 741; 907; 919; 936; 953; 961; 983; meningitis disease;
 KW Neisseria septicaemia; vaccine; immune response.
 XX OS Neisseria sp.
 XX PN WO2003020756-A2.
 XX PD 13-MAR-2003.
 XX PF 06-SEP-2002; 2002WO-IB003904.
 XX PR 06-SEP-2001; 2001GB-00021591.
 XX PA (CHIR-) CHIRON SPA.
 XX PI Pizza M;
 XX WPI: 2003-300862/29.
 XX PT Novel hybrid protein derived from Neisseria gonorrhoeae, preferably
 PT Neisseria meningitidis, useful for treating a patient with meningitis and
 PT for preparing a medicament for raising an immune response in a mammal.
 XX PS Claim 13; Page 41; 43pp; English.
 XX CC The specification describes a hybrid protein which is derived from
 CC Neisseria gonorrhoeae or N. meningitidis. The hybrid protein is of a
 CC formula given in the specification, and comprises open reading frame
 CC (orf) 1, orf4, orf25, orf40, orf46.1, orf83, NMB1343, 230, 233, 287, 292,
 CC 594, 687, 736, 741, 907, 919, 936, 953, 961 or 983 proteins. Compositions
 CC comprising the hybrid protein are useful as a medicament, and for
 CC treating a patient with meningitis disease caused by N. meningitidis, or
 CC with a disease caused by N. septicaemia or N. gonorrhoeae. The medicament
 CC is preferably a vaccine, and is useful for raising an immune response in
 CC a mammal. Hybrid proteins of the invention are also useful as diagnostic
 CC agents for detecting the presence of Neisseria bacteria or of antibodies
 CC raised against bacteria, and as reagents for raising antibodies against
 CC Neisseria. ABP97991-ABP98012 represent 741 proteins from different
 CC Neisseria strains. These proteins may be used to produce hybrid proteins
 CC of the invention
 XX SQ Sequence 225 AA;

Query Match 56.3%; Score 40; DB 6; Length 225;
 Best Local Similarity 58.3%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
 || ||: ||: ||
 Db 130 DDAGGKLTVTID 141

RESULT 25
 ABP98001
 ID ABP98001 standard; protein; 225 AA.
 XX AC ABP98001;
 XX DT 11-AUG-2003 (first entry)
 XX DE Protein 741 from Neisseria strain B2169.
 XX KW Hybrid protein; Neisseria gonorrhoeae; Neisseria meningitidis; orf1;
 KW orf4; orf25; orf40; orf46.1; orf83; NMB1343; 230; 233; 287; 292; 594;
 KW 687; 736; 741; 907; 919; 936; 953; 961; 983; meningitis disease;
 KW Neisseria septicaemia; vaccine; immune response.
 XX OS Neisseria sp.

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XX WO2003020756-A2.
XX
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XX 13-MAR-2003.
XX
XX
XX 06-SEP-2002; 2002WO-IB003904.
XX
XX 06-SEP-2001; 2001GB-00021591.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M;
XX
XX WPI; 2003-300862/29.
XX
XX Novel hybrid protein derived from Neisseria gonorrhoeae, preferably
PT Neisseria meningitidis, useful for treating a patient with meningitis and
PT for preparing a medicament for raising an immune response in a mammal.
XX
XX Claim 13; Page 41; 43pp; English.
XX
XX The specification describes a hybrid protein which is derived from
CC Neisseria gonorrhoeae or N. meningitidis. The hybrid protein is of a
CC formula given in the specification, and comprises open reading frame
CC (orf) 1, orf4, orf25, orf40, orf46.1, orf83, NMB1343, 230, 233, 287, 292,
CC 594, 687, 736, 741, 907, 919, 936, 953, 961 or 983 proteins. Compositions
CC comprising the hybrid protein are useful as a medicament, and for
CC treating a patient with meningitis disease caused by N. meningitidis, or
CC with a disease caused by N. septicaemia or N. gonorrhoeae. The medicament
CC is preferably a vaccine, and is useful for raising an immune response in
CC a mammal. Hybrid proteins of the invention are also useful as diagnostic
CC agents for detecting the presence of Neisserial bacteria or of antibodies
CC raised against bacteria, and as reagents for raising antibodies against
CC Neisseria. ABP97991-ABP98012 represent 741 proteins from different
CC Neisseria strains. These proteins may be used to produce hybrid proteins
XX of the invention
XX
XX Sequence 225 AA;
XX
XX Query Match 56.3%; Score 40; DB 6; Length 225;
XX Best Local Similarity 58.3%; Pred. NO. 1.7e+02;
XX Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1 DDYGGQSTYVMD 12
XX |||||: ||
XX Db 130 DDAGGKLYTID 141
XX
XX RESULT 26
XX ABP97998
XX ID ABP97998 standard; protein; 228 AA.
XX
XX AC ABP97998;
XX
XX DT 11-AUG-2003 (first entry)
XX
XX DE Protein 741 from Neisseria strain 39/99.
XX
XX Hybrid protein; Neisseria gonorrhoeae; Neisseria meningitidis; orf1;
XX orf4; orf25; orf40; orf46.1; orf83; NMB1343; 230; 233; 287; 292; 594;
XX 687; 736; 741; 907; 919; 936; 953; 961; 983; meningitis disease;
XX Neisseria septicaemia; vaccine; immune response.
XX
XX OS Neisseria sp.
XX
XX PN WO2003020756-A2.
XX
XX PD 13-MAR-2003.
XX
XX PF 06-SEP-2002; 2002WO-IB003904.
XX
XX PR 06-SEP-2001; 2001GB-00021591.
XX
XX PT

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PA (CHIR-) CHIRON SPA.
XX
XX Pizza M;
XX
XX WPI; 2003-300862/29.
XX
XX Novel hybrid protein derived from Neisseria gonorrhoeae, preferably
PT Neisseria meningitidis, useful for treating a patient with meningitis and
PT for preparing a medicament for raising an immune response in a mammal.
XX
XX Claim 13; Page 40; 43pp; English.
XX
XX The specification describes a hybrid protein which is derived from
CC Neisseria gonorrhoeae or N. meningitidis. The hybrid protein is of a
CC formula given in the specification, and comprises open reading frame
CC (orf) 1, orf4, orf25, orf40, orf46.1, orf83, NMB1343, 230, 233, 287, 292,
CC 594, 687, 736, 741, 907, 919, 936, 953, 961 or 983 proteins. Compositions
CC comprising the hybrid protein are useful as a medicament, and for
CC treating a patient with meningitis disease caused by N. meningitidis, or
CC with a disease caused by N. septicaemia or N. gonorrhoeae. The medicament
CC is preferably a vaccine, and is useful for raising an immune response in
CC a mammal. Hybrid proteins of the invention are also useful as diagnostic
CC agents for detecting the presence of Neisserial bacteria or of antibodies
CC raised against bacteria, and as reagents for raising antibodies against
CC Neisseria. ABP97991-ABP98012 represent 741 proteins from different
CC Neisseria strains. These proteins may be used to produce hybrid proteins
XX of the invention
XX
XX Sequence 228 AA;
XX
XX Query Match 56.3%; Score 40; DB 6; Length 228;
XX Best Local Similarity 58.3%; Pred. No. 1.8e+02;
XX Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1 DDYGGQSTYVMD 12
XX |||||: ||
XX Db 133 DDAGGKLYTID 144
XX
XX RESULT 27
XX ABP97996
XX ID ABP97996 standard; protein; 229 AA.
XX
XX AC ABP97996;
XX
XX DT 11-AUG-2003 (first entry)
XX
XX DE Protein 741 from Neisseria strain 30/00.
XX
XX Hybrid protein; Neisseria gonorrhoeae; Neisseria meningitidis; orf1;
XX orf4; orf25; orf40; orf46.1; orf83; NMB1343; 230; 233; 287; 292; 594;
XX 687; 736; 741; 907; 919; 936; 953; 961; 983; meningitis disease;
XX Neisseria septicaemia; vaccine; immune response.
XX
XX OS Neisseria sp.
XX
XX PN WO2003020756-A2.
XX
XX PD 13-MAR-2003.
XX
XX PF 06-SEP-2002; 2002WO-IB003904.
XX
XX PR 06-SEP-2001; 2001GB-00021591.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M;
XX
XX WPI; 2003-300862/29.
XX
XX Novel hybrid protein derived from Neisseria gonorrhoeae, preferably
PT Neisseria meningitidis, useful for treating a patient with meningitis and
PT for preparing a medicament for raising an immune response in a mammal.
PT

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XX PS Claim 13; Page 40; 43pp; English.

XX CC The specification describes a hybrid protein which is derived from

CC CC *Neisseria gonorrhoeae* or *N. meningitidis*. The hybrid protein is of a

CC CC formula given in the specification, and comprises open reading frame

CC CC (orf) 1, orf4, orf25, orf40, orf46.1, orf83, NMB1343, 230, 233, 287, 292,

CC CC 594, 687, 736, 741, 907, 919, 936, 953, 961 or 983 proteins. Compositions

CC CC comprising the hybrid protein are useful as a medicament, and for

CC CC treating a patient with meningitis disease caused by *N. meningitidis*, or

CC CC with a disease caused by *N. septicaemia* or *N. gonorrhoeae*. The medicament

CC CC is preferably a vaccine, and is useful for raising an immune response in

CC CC a mammal. Hybrid proteins of the invention are also useful as diagnostic

CC CC agents for detecting the presence of *Neisseria* bacteria or of antibodies

CC CC raised against bacteria, and as reagents for raising antibodies against

CC CC *Neisseria*. ABP97991-ABP98012 represent 741 proteins from different

CC CC *Neisseria* strains. These proteins may be used to produce hybrid proteins

CC CC of the invention

XX SQ Sequence 229 AA;

Query Match 56.3%; Score 40; DB 6; Length 229;

Best Local Similarity 58.3%; Pred. No. 1.8e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTVMD 12

DB 134 DDAGGKLTVID 145

RESULT 28

ABM67642

ID ABM67642 standard; protein; 243 AA.

XX AC ABM67642;

XX DT 20-NOV-2003 (first entry)

XX DE Photorhabdus luminescens protein sequence #739.

XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

XX KW detection; food; gene expression; plant; animal; microorganism; toxin;

XX KW antibiotic; biopesticide; virulence factor; disease model; plague;

XX KW whooping cough.

XX OS Photorhabdus luminescens.

XX PN WO200294867-A2.

XX PD 28-NOV-2002.

XX PF 07-FEB-2002; 2002WO-IB003040.

XX PR 07-FEB-2001; 2001FR-00001659.

XX PS (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst P, Danchin A;

PI Buchrieser C;

XX WPI; 2003-148459/14.

XX PT Genomic sequence of *Photorhabdus luminescens* and encoded polypeptides,

PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX PS Claim 2; SEQ ID NO 739; 1205pp; French.

XX CC The invention relates to the isolation of genes and their encoded

CC CC proteins from *Photorhabdus luminescens*. The isolated sequences are

CC CC sources of probes and primers for detecting the genome of *P. luminescens*

CC CC and related species; to study polymorphisms; for gene analysis and for

CC CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification

CC of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that

CC carry a gene-containing vector are used to select compounds that

CC modulate, regulate, induce or inhibit expression of the genes in plants,

CC animals or microorganisms other than *P. luminescens* and are able to alter

CC response or sensitivity to toxins and antibiotics produced by *P.*

CC *luminescens*. Cells transformed to express the genes are useful for

CC recombinant production of the proteins, particularly toxins and

CC antibacterials useful as insecticides, bactericides and fungicides. The

CC genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that

CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as

CC biopesticides. Other uses of the genes and the proteins are as virulence

CC factors and for identifying targets of human diseases for which *P.*

CC *luminescens* is a model (particularly plague and whooping cough). This

CC sequence represents one of the isolated *P. luminescens* proteins

XX SQ Sequence 243 AA;

Query Match 56.3%; Score 40; DB 6; Length 243;

Best Local Similarity 56.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9

DB 229 NDFGGESTY 237

RESULT 29

ADP70282

ID ADP70282 standard; protein; 247 AA.

XX AC ADP70282;

XX DT 26-AUG-2004 (first entry)

XX DE Truncated NMB1870 protein, SEQ ID 81.

XX KW Antibacterial; Antiinflammatory; Vaccine; meningococcal protein; NMB1870;

XX KW antigen; bactericide; meningitis; bacteraemia; *Neisseria* infection;

XX KW lipoprotein.

XX OS *Neisseria meningitidis*.

XX OS Synthetic.

XX PN WO2004048404-A2.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-IB006320.

XX PR 22-NOV-2002; 2002GB-00027346.

XX PS (CHTR) CHIRON SRL.

XX PI Comanducci M, Pizza M;

XX WPI; 2004-468293/44.

XX PT Composition for producing medicament for preventing *Neisseria* infection

PT in mammal, comprising multiple variant of meningococcal protein NMB1870,

PT as antigen.

XX PS Claim 11; SEQ ID NO 81; 77pp; English.

XX CC The present invention relates to composition (I) comprising at least two

CC multiple variants of meningococcal protein NMB1870 (ADP70202-ADP70246,

CC ADP70278, ADP70280-ADP70286, ADP70288-ADP70295, ADP70324-ADP70343) as

CC antigen, (I) elicit a bactericidal response effective against each of

CC serogroup B *Neisseria meningitidis* strains MC58, 961-5945 and M1239, and

CC also elicit an antibody response which is bactericidal against *N.*

CC *meningitidis* strains in at least 2 of hypervirulent lineages ET-37, ET-5,

CC cluster A4, lineage 3, subgroup I, subgroup III, and subgroup IV-1. In

CC NMB1870 is a lipoprotein. In (I) at least one of the proteins does not
 CC include the amino acid sequence ADP70271 or ADP70272 within 10 amino
 CC acids of its N-terminus or at least one of the proteins does not include
 CC the amino acid sequences ADP70273 within 10 amino acids of its N-terminus
 CC or at least one of the proteins includes the amino acid sequence
 CC ADP70274. ADP70271-ADP70274 are sequence motifs for retention or omission
 CC from the NMB1870 proteins. (I) or (II) is efficiently elicits systemic
 CC and/or mucosal immunity and thereby prevents/treat meningitis and
 CC bacteremia. (I) is useful as medicament and for raising an antibody
 CC response in a mammal for protecting a mammal against a Neisserial
 CC infection.

XX SQ Sequence 247 AA;

Query Match 56.3%; Score 40; DB 8; Length 247;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYYVMD 12
 ||||: ||: ||
 Db 152 DDAGGKLTYYTID 163

RESULT 30
 AAEL10027
 ID AAEL10027 standard; protein; 248 AA.

XX AC AAEL10027;

XX DT 11-SEP-2003 (revised)
 XX DT 29-NOV-2001 (first entry)

XX DE Neisseria meningitidis strain 2996 deltaG 741 protein.

XX KW Heterologous expression; Neisserial protein; deltaG 741 protein.

XX OS Neisseria meningitidis; 2996.

XX FN WO200164920-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-IB000420.

XX PR 28-FEB-2000; 2000GB-00004695.

XX PR 13-NOV-2000; 2000GB-00027675.

XX PA (CHIR-) CHIRON SPA.

XX PI Arico MB, Comanducci M, Galeotti C, Massignani V, Giuliani MM;
 XX PI Pizza M;

XX DR WPI; 2001-557776/62.

XX Heterologous expression for the expression of two or more Neisserial
 XX proteins in fused state.

XX PS Claim 12; Page 19; 52pp; English.

XX The present invention relates to a method for simultaneous heterologous
 CC expression of two or more Neisserial proteins which are in a fused state.
 CC The method is useful for simultaneous heterologous expression of two or
 CC more Neisserial proteins. A protein that may be unstable or poorly
 CC expressed on its own is assisted by adding a suitable hybrid partner and
 CC commercial manufacture is simplified-only one expression and purification
 CC need to be employed in order to produce two separately- useful proteins.
 CC The present sequence is Neisseria meningitidis (serogroup B, strain 2996)
 CC deltaG 741 protein. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 248 AA;

Query Match 56.3%; Score 40; DB 4; Length 248;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 DDYGGQSTYYVMD 12
 ||||: ||: ||: ||
 Db 153 DDAGGKLTYYTID 164

RESULT 31

ADO07117
 ID ADO07117 standard; protein; 248 AA.

XX AC ADO07117;

XX DT 15-JUL-2004 (first entry)

XX DE Neisseria meningitidis serogroup B deltaG-741 protein, useful in vaccine.

XX KW Vaccine; antigen; antibacterial; meningitis; 741 protein.

XX OS Neisseria meningitidis.

XX FN WO2004032958-A1.

XX PD 22-APR-2004.

XX PF 02-OCT-2003; 2003WO-IB004848.

XX PR 11-OCT-2002; 2002GB-00023741.

XX PR 13-MAR-2003; 2003GB-00005831.

XX PR 22-APR-2003; 2003GB-00009115.

XX PA (CHIR) CHIRON SRL.

XX PI Pizza M;

XX DR WPI; 2004-340823/31.

XX Composition useful for treating infection caused by hypervirulent
 XX lineages A4, ET-5 and lineage 3 of Neisseria meningitidis serogroup B,
 XX comprises five antigens NadA protein, 741 protein, 936 protein, 953
 XX protein and 287 protein.

XX PS Claim 29; SEQ ID NO 3; 53pp; English.

XX The present sequence is that of Neisseria meningitidis strain MC58
 CC (serogroup B) 741 protein from which the N-terminal region (amino acids 1
 CC -72) has been removed (deltaG-741 protein). This deletion can enhance
 CC recombinant expression and also removes the lipidation site. Protein 741
 CC is an extremely effective antigen for eliciting anti-meningococcal
 CC antibody responses, and is expressed across all meningococcal serogroups.
 CC The protein, and its variants, can be used in vaccine compositions of the
 CC invention. The invention is based on the discovery that a small number of
 CC defined antigens is able to provide broad protection against
 CC meningococcal infection. A composition is provided which is able induce
 CC an antibody response that is bactericidal against 2 or more of
 CC hypervirulent lineages A4, ET-5 and lineage 3 of N. meningitidis
 CC serogroup B. The preferred composition comprises a mixture of 10 or fewer
 CC purified antigens, and should not include complex or undefined mixtures
 CC of antigens such as outer membrane vesicles. The antigens are obtained by
 CC recombinant expression. A mixture of 5 defined protein antigens has been
 CC found to elicit a good protective immune response: a NadA protein, a 741
 CC protein, a 936 protein, a 953 protein, and a 287 protein. For maximum
 CC cross-strain efficacy, it is preferred that the composition should
 CC include more than one variant of protein 741; exemplary sequences are
 CC provided ADO071123-ADO07125.

XX SQ Sequence 248 AA;

Query Match 56.3%; Score 40; DB 8; Length 248;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYYVMD 12

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Db      153 DDAGGKLTYYTID 164
||| ||| : |||
ADP70281
ID ADP70281 standard; protein; 248 AA.
XX
AC ADP70281;
XX
DT 26-AUG-2004 (first entry)
XX
DE Truncated NMB1870 protein, SEQ ID 80.
XX
KW Antibacterial; Antiinflammatory; Vaccine; meningococcal protein; NMB1870;
KW antigen; bactericide; meningitis; bacteraemia; Neisserial infection;
KW lipoprotein.
XX
OS Neisseria meningitidis.
OS Synthetic.
XX
PN WO2004048404-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-IB006320.
XX
PR 22-NOV-2002; 2002GB-00027346.
XX
PA (CHIR ) CHIRON SRL.
XX
PI Comanducci M, Pizza M;
XX
PI WPI; 2004-468293/44.
XX
DR
XX
PT Composition for producing medicament for preventing Neisserial infection
PT in mammal, comprising multiple variant of meningococcal protein NMB1870,
PT as antigen.
XX
PS Claim 11; SEQ ID NO 80; 77pp; English.
XX
CC The present invention relates to composition (I) comprising at least two
CC multiple variants of meningococcal protein NMB1870 (ADP70202-ADP70246,
CC ADP70278, ADP70280-ADP70286, ADP70288-ADP70295, ADP70324-ADP70343) as
CC antigen. (I) elicit a bactericidal response effective against each of
CC serogroup B Neisseria meningitidis strains MC58, 961-5945 and M1239, and
CC also elicit an antibody response which is bactericidal against N.
CC meningitidis strains in at least 2 of hypervirulent lineages ET-37, ET-5,
CC cluster A4, lineage 3, subgroup I, subgroup III, and subgroup IV-1. In
CC NMB1870 is a lipoprotein. In (I) at least one of the proteins does not
CC include the amino acid sequence ADP70271 or ADP70272 within 10 amino
CC acids of its N-terminus or at least one of the proteins does not include
CC the amino acid sequences ADP70273 within 10 amino acids of its N-terminus
CC or at least one of the proteins includes the amino acid sequence
CC ADP70274. ADP70271-ADP70274 are sequence motifs for retention or omission
CC from the NMB1870 proteins. (I) or (II) is efficiently elicits systemic
CC and/or mucosal immunity and thereby prevents/treat meningitis and
CC bacteraemia. (I) is useful as medicament and for raising an antibody
CC response in a mammal for protecting a mammal against a Neisserial
CC infection.
XX
SQ Sequence 248 AA;
Query Match 56.3%; Score 40; DB 8; Length 248;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DDYGGQSTYVMD 12
||| ||| : |||
Db 153 DDAGGKLTYYTID 164
||| ||| : |||
RESULT 34
ADSO0574
ID ADS00574 standard; protein; 248 AA.
XX
AC ADS00574;
XX
XX
XX

```

ADR23253
ID ADR23253 standard; protein; 248 AA.
XX
AC ADR23253;
XX
DT 04-NOV-2004 (first entry)
XX
DE Neisseria meningitidis 741 protein (N-terminal deleted), vaccine antigen.
XX
KW Meningitis; vaccine; 741 protein; antibacterial.
XX
OS Neisseria meningitidis.
XX
PN WO2004067030-A2.
XX
PD 12-AUG-2004.
XX
PF 30-JAN-2004; 2004WO-IB000651.
XX
PR 30-JAN-2003; 2003GB-00002217.
PR 02-OCT-2003; 2003GB-00023101.
XX
PA (CHIR) CHIRON SRL.
XX
PI Costantino P;
XX
PI WPI; 2004-580857/56.
XX
DR
XX
PT New injectable immunogenic composition comprising saccharide antigens
PT from serogroup B Neisseria meningitidis, Hemophilus influenzae type B and
PT Streptococcus pneumoniae, useful in treating or preventing bacterial
PT meningitis.
XX
PS Disclosure; SEQ ID NO 3; 46pp; English.
XX
CC The present sequence is that of the 741 protein from Neisseria
CC meningitidis serogroup MenB strain MC58, minus the N-terminal poly-
CC glycine sequence. This deletion can enhance expression. Protein 741 is an
CC extremely effective antigen for eliciting anti-meningococcal antibody
CC responses, and it is expressed across all meningococcal serogroups. A
CC claimed injectable immunogenic composition comprises capsular saccharides
CC from at least 2 of serogroups A, C, W135 and Y of N. meningitidis, where
CC the capsular saccharides are conjugated to carrier protein(s) and/or are
CC oligosaccharides. The composition may further comprise an antigen from
CC one or more of serogroup B N. meningitidis, Haemophilus influenzae type
CC B, and/or Streptococcus pneumoniae. The serogroup B antigen is a NADa
CC protein in oligomeric form, a 741 protein, a 936 protein, a 953 protein
CC or a 287 protein. The immunogenic composition is useful in the
CC manufacture of an injectable medicament for the prevention and/or
CC treatment of bacterial meningitis (claimed). Preferred 741 protein
CC fragments for use in the compositions lack one or more amino acids from
CC the C-terminus and/or N-terminus of the present sequence, or comprise an
CC epitope of the polypeptide, or an allelic variant, homologue, mutant,
CC etc. For maximum cross-strain efficacy, preferred compositions include
CC more than one variant of protein 741 ADR23260-ADR23262.
XX
SQ Sequence 248 AA;
Query Match 56.3%; Score 40; DB 8; Length 248;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DDYGGQSTYVMD 12
||| ||| : |||
Db 153 DDAGGKLTYYTID 164
||| ||| : |||
RESULT 34
ADSO0574
ID ADS00574 standard; protein; 248 AA.
XX
AC ADS00574;
XX
XX
XX

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DT 04-NOV-2004 (first entry)
XX
DE N. meningitides 741 protein, deltaG741 mutant.
XX
KW ORF46; 287 protein; 741 protein; 919 protein; 953 protein; 961 protein;
KW 983 protein; bacterial infection; vaccine; fusion protein; bactericide;
KW mutant; mutein.
XX
OS Neisseria meningitidis; serogroup B, strain 2996.
OS Synthetic.
XX
PN AU2004201216-A1.
XX
XX 22-APR-2004.
XX
PF 15-MAR-2004; 2004AU-00201216.
XX
PR 09-MAR-2001; 2001AU-00239478.
XX
XX (CHIR-) CHIRON SPA.
XX
PI Giuliani MM, Maignani V, Galeotti C, Comanducci M, Arico MB;
DR WPI; 2004-616327/60.
XX
XX Method for simultaneous heterologous expression of two or more Neisserial
PT proteins, useful in producing antibodies with significant bactericidal
PT efficacy, involves fusing two or more Neisserial proteins.
XX
PS Example 4; Page 19; 54pp; English.
XX
CC The invention relates to a method (M1) for simultaneous heterologous
CC expression of two or more Neisserial proteins, involving fusing two or
CC more Neisserial proteins (chosen from chosen from orf1, orf4, orf25,
CC orf40, orf83, 233, 287, 292L, 564, 687, 741, 907, 919, 953, 961
CC and 983) including domain deletion variants (e.g. N-terminal deletions
CC where all N-terminal amino acids up to and including the poly-Gly region
CC are deleted, termed deltaG). Also included are a protein expressed by
CC (M1) and a hybrid protein (P1) of formula NH2-A-B-COOH, where A and B are
CC different Neisserial proteins. (M1) is useful for simultaneous
CC heterologous expression of two or more Neisserial proteins and for
CC producing hybrid Neisserial proteins. The hybrid proteins produced by
CC (M1) enable production of antibodies with significant bactericidal
CC efficacy. The present sequence is a deltaG mutant Neisserial protein
CC suitable for use in the hybrid constructs.
XX
SQ Sequence 248 AA;

Query Match 56.3%; Score 40; DB 8; Length 248;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 153 DDAGGKLTYYTID 164

RESULT 35
ADE44758
ID ADE44758 standard; protein; 248 AA.
XX
AC ADE44758;
XX
XX 29-JAN-2004 (first entry)
XX
DE Neisseria meningitidis ORF2086 protein SeqID192.
XX
KW ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
KW anti-inflammatory; immune response; bacterial meningitis;
KW Streptococcus pneumoniae infection; non-pathogenic;
KW immunogenic composition; 2086 protein.
XX
OS Neisseria meningitidis.
XX
XX WO2003063766-A2.
XX
PN 07-AUG-2003.
XX
PD 11-OCT-2002; 2002WO-US032369.
XX
PF 11-OCT-2001; 2001US-0328101P.
XX
PR 30-AUG-2002; 2002US-0406934P.
XX
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WO2005032583-A2.

14-APR-2005.

04-OCT-2004; 2004WO-IB003373.

02-OCT-2003; 2003GB-00023102.

28-MAY-2004; 2004GB-00012052.

(CHIR) CHIRON SRL.

Contorni M;

WPI; 2005-285336/29.

An aqueous immunogenic composition for immunizing against bacterial meningitis comprises conjugated capsular saccharides from meningococcal serogroups C, W135, Y, B and A.

Disclosure; SEQ ID NO 3; 47pp; English.

The invention relates to an aqueous immunogenic composition which induces an immune response that is bactericidal against serogroups B, C, W135 and Y of *Neisseria meningitidis*, when administered to a patient. The composition comprises a conjugated serogroup C capsular saccharide antigen, a conjugated serogroup W135 capsular saccharide antigen, a conjugated serogroup Y capsular saccharide antigen, and one or more polypeptide antigens from serogroup B. The conjugated saccharides are oligosaccharides. The saccharides are conjugated to a carrier protein selected from diphtheria toxoid, tetanus toxoid, *Haemophilus influenzae* protein D and CRM197. The composition or in manufacturing a medicament for raising an immune response in a mammal. The composition and method may be used for immunizing against bacterial meningitis. This sequence represents an N. meningitidis 741 polypeptide with a deletion.

Sequence 248 AA;

Query Match 56.3%; Score 40; DB 9; Length 248; Best Local Similarity 58.3%; Pred. No. 1.9e+02; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 153 DDAGGKLTYYTID 164

RESULT 36
ADE44758
ID ADE44758 standard; protein; 249 AA.
XX
AC ADE44758;
XX
XX 29-JAN-2004 (first entry)
XX
DE Neisseria meningitidis ORF2086 protein SeqID192.
XX
KW ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
KW anti-inflammatory; immune response; bacterial meningitis;
KW Streptococcus pneumoniae infection; non-pathogenic;
KW immunogenic composition; 2086 protein.
XX
OS Neisseria meningitidis.
XX
XX WO2003063766-A2.
XX
PN 07-AUG-2003.
XX
PD 11-OCT-2002; 2002WO-US032369.
XX
PF 11-OCT-2001; 2001US-0328101P.
XX
PR 30-AUG-2002; 2002US-0406934P.
XX

PA (AMHP) WYETH HOLDINGS CORP.
 XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;
 XX WPI; 2003-663416/62.
 DR N-PSDB; ADE44757.
 XX Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp.; that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.
 XX Claim 60; SEQ ID NO 192; 480pp; English.
 XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein which can be used to create the composition
 CC of the invention.
 XX SQ Sequence 249 AA;
 Query Match 56.3%; Score 40; DB 7; Length 249;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DDYGGQSTYVMD 12
 DB 160 DDAGGKLTITD 171
 ||| ||| :||
 RESULT 37
 ADE44748
 ID ADE44748 standard; protein; 249 AA.
 XX ADE44748;
 XX 29-JAN-2004 (first entry)
 XX *Neisseria meningitidis* ORF2086 protein SeqID182.
 XX ORF2086; *Neisseria meningitidis* serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW *Streptococcus pneumoniae* infection; non-pathogenic;
 KW immunogenic composition; 2086 protein.
 XX *Neisseria meningitidis*.
 XX WO2003063766-A2.
 XX 07-AUG-2003.
 XX 11-OCT-2002; 2002WO-US032369.
 XX 07-AUG-2003.
 XX 11-OCT-2002; 2002WO-US032369.
 XX 11-OCT-2001; 2001US-0328101P.
 PR 30-AUG-2002; 2002US-0406934P.
 XX (AMHP) WYETH HOLDINGS CORP.
 PA Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

XX WPI; 2003-663416/62.
 DR N-PSDB; ADE44747.
 XX Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp.; that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.
 XX Claim 60; SEQ ID NO 182; 480pp; English.
 XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein with a native leader sequence which can be
 CC used to create the composition of the invention.
 XX SQ Sequence 249 AA;
 Query Match 56.3%; Score 40; DB 7; Length 249;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DDYGGQSTYVMD 12
 DB 160 DDAGGKLTITD 171
 ||| ||| :||
 RESULT 38
 ADE44752
 ID ADE44752 standard; protein; 249 AA.
 XX ADE44752;
 XX 29-JAN-2004 (first entry)
 XX *Neisseria meningitidis* ORF2086 protein SeqID186.
 XX ORF2086; *Neisseria meningitidis* serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW *Streptococcus pneumoniae* infection; non-pathogenic;
 KW immunogenic composition; 2086 protein.
 XX *Neisseria meningitidis*.
 XX WO2003063766-A2.
 XX 07-AUG-2003.
 XX 11-OCT-2002; 2002WO-US032369.
 XX 11-OCT-2001; 2001US-0328101P.
 PR 30-AUG-2002; 2002US-0406934P.
 XX (AMHP) WYETH HOLDINGS CORP.
 PA Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;
 XX WPI; 2003-663416/62.
 DR N-PSDB; ADE44751.
 XX

PT Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

XX Claim 60; SEQ ID NO 186; 480pp; English.

PS This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein which can be used to create the composition
 CC of the invention.

XX Sequence 249 AA;

Query Match 56.3%; Score 40; DB 7; Length 249;
 Best Local Similarity 58.3%; Pred. NO. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12

Db 160 DDAGGKLYTID 171

RESULT 39

ADE44754

ID ADE44754 standard; protein; 249 AA.

XX AC ADE44754;

XX 29-JAN-2004 (first entry)

DE *Neisseria meningitidis* ORF2086 protein SeqID188.

XX ORF2086; *Neisseria meningitidis* serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW *Streptococcus pneumoniae* infection; non-pathogenic;
 KW immunogenic composition; 2086 protein.

XX *Neisseria meningitidis*.

XX WO2003063766-A2.

XX 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

XX 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

DR WPI; 2003-663416/62.

DR N-PSDB; ADE44753.

PT Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

PS Claim 60; SEQ ID NO 188; 480pp; English.

XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein with a native leader sequence which can be
 CC used to create the composition of the invention.

XX Sequence 249 AA;

Query Match 56.3%; Score 40; DB 7; Length 249;
 Best Local Similarity 58.3%; Pred. NO. 1.9e+02;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12

Db 160 DDAGGKLYTID 171

RESULT 40

ADE44756

ID ADE44756 standard; protein; 250 AA.

XX AC ADE44756;

XX 29-JAN-2004 (first entry)

XX *Neisseria meningitidis* ORF2086 protein SeqID190.

DE ORF2086; *Neisseria meningitidis* serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW *Streptococcus pneumoniae* infection; non-pathogenic;
 KW immunogenic composition; 2086 protein; P4 leader.

XX *Neisseria meningitidis*.

OS *Haemophilus influenzae*.

XX WO2003063766-A2.

XX 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

XX 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

DR WPI; 2003-663416/62.

DR N-PSDB; ADE44755.

PT Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

XX Claim 60; SEQ ID NO 190; 480pp; English.

XX This invention relates to a novel composition which comprises at least

CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein with a P4 leader sequence (derived from the
 CC *Haemophilus influenzae* P4 protein) which can be used to create the
 CC composition of the invention.

XX
 SQ Sequence 250 AA;

Query Match 56.3%; Score 40; DB 7; Length 250;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
 ||||: ||:
 Db 161 DDAGGKLTYYTD 172

RESULT 41

ADBE44750
 ID ABE44750 standard; protein; 250 AA.

AC ABE44750;

DT 29-JAN-2004 (first entry)

DE *Neisseria meningitidis* ORF2086 protein SeqID184.

XX ORF2086; *Neisseria meningitidis* serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW *Streptococcus pneumoniae* infection; non-pathogenic;
 KW immunogenic composition; 2086 protein; P4 leader.

XX *Neisseria meningitidis*.

OS *Haemophilus influenzae*.

XX WO2003063766-A2.

PN 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

PR 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

DR WPI; 2003-663416/62.

XX N-PSDB; ABE44749.

XX Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of *Neisseria* sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

PS Claim 60; SEQ ID NO 184; 480pp; English.

XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC *Neisseria* sp. (ORF2086), where the ORF encoding a crossreactive

CC immunogenic antigen provides immunogenicity against infection by
 CC *Neisseria meningitidis* serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of *Streptococcus pneumoniae* infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a *Neisseria meningitidis* strain-
 CC specific mature 2086 protein with a P4 leader sequence (derived from the
 CC *Haemophilus influenzae* P4 protein) which can be used to create the
 CC composition of the invention.

XX
 SQ Sequence 250 AA;

Query Match 56.3%; Score 40; DB 7; Length 250;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
 ||||: ||:
 Db 161 DDAGGKLTYYTD 172

RESULT 42

ADP70340
 ID ADP70340 standard; protein; 250 AA.

AC ADP70340;

XX 26-AUG-2004 (first entry)

XX *Neisseria meningitidis* NMB1870 protein, SEQ ID 139.

XX Antibacterial; Antiinflammatory; Vaccine; meningococcal protein; NMB1870;
 KW antigen; bactericide; meningitis; bacteraemia; *Neisseria* infection;
 KW lipoprotein.

XX *Neisseria meningitidis*; strain 220173i.

XX WO2004048404-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-IB006320.

XX 22-NOV-2002; 2002GB-00027346.

XX (CHIR) CHIRON SRL.

XX Comanducci M, Pizza M;

XX WPI; 2004-468293/44.

XX Composition for producing medicament for preventing *Neisseria* infection
 PT in mammal, comprising multiple variant of meningococcal protein NMB1870,
 PT as antigen.

XX Claim 11; SEQ ID NO 139; 77pp; English.

XX The present invention relates to composition (I) comprising at least two
 CC multiple variants of meningococcal protein NMB1870 (ADP70202-ADP70246,
 CC ADP70278, ADP70280-ADP70286, ADP70288-ADP70295, ADP70324-ADP70343) as
 CC antigen. (i) elicit a bactericidal response effective against each of
 CC serogroup B *Neisseria meningitidis* strains MC58, 961-5945 and M1239, and
 CC also elicit an antibody response which is bactericidal against N.
 CC meningitidis strains in at least 2 of hypervirulent lineages ET-37, ET-5,
 CC cluster A4, lineage 3, subgroup I, subgroup III, and subgroup IV-1. In
 CC NMB1870 is a lipoprotein. In (i) at least one of the proteins does not
 CC include the amino acid sequence ADP70271 or ADP70272 within 10 amino

CC acids of its N-terminus or at least one of the proteins does not include
 CC the amino acid sequences ADP70273 within 10 amino acids of its N-terminus
 CC or at least one of the proteins includes the amino acid sequence
 CC ADP70274. ADP70271-ADP70274 are sequence motifs for retention or omission
 CC from the NMB1870 proteins. (I) or (II) is efficiently elicits systemic
 CC and/or mucosal immunity and thereby prevents/treat meningitis and
 CC bacteraemia. (I) is useful as medicament and for raising an antibody
 CC response in a mammal for protecting a mammal against a Neisserial
 CC infection.
 CC
 CC SQ Sequence 250 AA;

Query Match 56.3%; Score 40; DB 8; Length 250;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
 || ||: ||: ||
 Db 179 DDAGGKLTYYTID 190

RESULT 43
 ADE44724
 ID ADE44724 standard; protein; 253 AA.

XX ADE44724;

XX 29-JAN-2004 (first entry)

XX Neisseria meningitidis ORF2086 protein SeqID158.

XX ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW Streptococcus pneumoniae infection; non-pathogenic;
 KW immunogenic composition; 2086 protein.

XX Neisseria meningitidis.

XX WO2003063766-A2.

XX 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

XX 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

XX WPI; 2003-663416/62.

XX N-PSDB; ADE44723.

XX Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

XX Claim 60; SEQ ID NO 158; 480pp; English.

XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC Neisseria meningitidis serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of Streptococcus pneumoniae infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.

CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
 CC specific mature 2086 protein with a native leader sequence which can be
 CC used to create the composition of the invention.

XX SQ Sequence 253 AA;

Query Match 56.3%; Score 40; DB 7; Length 253;
 Best Local Similarity 58.3%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
 || ||: ||: ||
 Db 158 DDAGGKLTYYTID 169

RESULT 44

ADE44728

ID ADE44728 standard; protein; 253 AA.

XX ADE44728;

XX 29-JAN-2004 (first entry)

XX Neisseria meningitidis ORF2086 protein SeqID162.

XX ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
 KW antiinflammatory; immune response; bacterial meningitis;
 KW Streptococcus pneumoniae infection; non-pathogenic;
 KW immunogenic composition; 2086 protein.

XX Neisseria meningitidis.

XX WO2003063766-A2.

XX 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

XX 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 PI Metcalf BJ;

XX WPI; 2003-663416/62.

XX N-PSDB; ADE44727.

XX Composition comprising crossreactive immunogenic antigen encoded by open
 PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
 PT meningitis, or its immunogenic portion or biological equivalent.

XX Claim 60; SEQ ID NO 162; 480pp; English.

XX This invention relates to a novel composition which comprises at least
 CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
 CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
 CC immunogenic antigen provides immunogenicity against infection by
 CC Neisseria meningitidis serogroup B in a subject. The composition of the
 CC invention may have antibacterial or antiinflammatory activity through the
 CC induction of the immune response. The invention may be useful for the
 CC treatment of bacterial meningitis in a mammal. One or more polypeptides
 CC or nucleic acids encoding such polypeptides are useful in a composition
 CC or as a part of the treatment regimen for the prevention of amelioration
 CC of Streptococcus pneumoniae infection. The composition of the invention
 CC is non-pathogenic and substantially free from any infectious impurities.
 CC The immunogenic compositions can be compounded with fewer components to
 CC elicit protection comparable to previously used agents. The present
 CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
 CC specific mature 2086 protein which can be used to create the composition

CC of the invention.
XX Sequence 253 AA;

Query Match 56.3%; Score 40; DB 7; Length 253;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DDYGGQSTYVMD 12
|||:|:|:
Db 158 DDAGGKLYTID 169

Query Match 56.3%; Score 40; DB 7; Length 253;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 45
ADE44668
ID ADE44668 standard; protein; 254 AA.

RESULT 46
ADE44700
ID ADE44700 standard; protein; 254 AA.

AC ADE44668;

AC ADE44700;

DT 29-JAN-2004 (first entry)

DT 29-JAN-2004 (first entry)

DE Neisseria meningitidis ORF2086 protein SeqID102.

DE Neisseria meningitidis ORF2086 protein SeqID134.

XX ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
KW antinflammatory; immune response; bacterial meningitis;
KW Streptococcus pneumoniae infection; non-pathogenic;
KW immunogenic composition; 2086 protein.

XX ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
KW antinflammatory; immune response; bacterial meningitis;
KW Streptococcus pneumoniae infection; non-pathogenic;
KW immunogenic composition; 2086 protein.

XX Neisseria meningitidis.

XX Neisseria meningitidis.

XX WO2003063766-A2.

XX WO2003063766-A2.

XX 07-AUG-2003.

XX 07-AUG-2003.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2002; 2002WO-US032369.

XX 11-OCT-2001; 2001US-0328101P.

XX 11-OCT-2001; 2001US-0328101P.

XX 30-AUG-2002; 2002US-0406934P.

XX 30-AUG-2002; 2002US-0406934P.

XX (AMHP) WYETH HOLDINGS CORP.

XX (AMHP) WYETH HOLDINGS CORP.

XX Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
PI Metcalf BJ;

PI Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
PI Metcalf BJ;

DR WPI; 2003-663416/62.

DR WPI; 2003-663416/62.

DR N-PSDB; ADE44667.

DR N-PSDB; ADE44699.

XX Composition comprising crossreactive immunogenic antigen encoded by open
PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
PT meningitis, or its immunogenic portion or biological equivalent.

PT Composition comprising crossreactive immunogenic antigen encoded by open
PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
PT meningitis, or its immunogenic portion or biological equivalent.

XX Claim 60; SEQ ID NO 102; 480pp; English.

XX Claim 60; SEQ ID NO 134; 480pp; English.

XX This invention relates to a novel composition which comprises at least
CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
CC immunogenic antigen provides immunogenicity against infection by
CC Neisseria meningitidis serogroup B in a subject. The composition of the
CC invention may have antibacterial or antinflammatory activity through the
CC induction of the immune response. The invention may be useful for the
CC treatment of bacterial meningitis in a mammal. One or more polypeptides
CC or nucleic acids encoding such polypeptides are useful in a composition
CC or as a part of the treatment regimen for the prevention of amelioration
CC of Streptococcus pneumoniae infection. The composition of the invention
CC is non-pathogenic and substantially free from any infectious impurities.
CC The immunogenic compositions can be compounded with fewer components to
CC elicit protection comparable to previously used agents. The present
CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
CC specific mature 2086 protein which can be used to create the composition
CC of the invention.

XX This invention relates to a novel composition which comprises at least
CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
CC immunogenic antigen provides immunogenicity against infection by
CC Neisseria meningitidis serogroup B in a subject. The composition of the
CC invention may have antibacterial or antinflammatory activity through the
CC induction of the immune response. The invention may be useful for the
CC treatment of bacterial meningitis in a mammal. One or more polypeptides
CC or nucleic acids encoding such polypeptides are useful in a composition
CC or as a part of the treatment regimen for the prevention of amelioration
CC of Streptococcus pneumoniae infection. The composition of the invention
CC is non-pathogenic and substantially free from any infectious impurities.
CC The immunogenic compositions can be compounded with fewer components to
CC elicit protection comparable to previously used agents. The present
CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
CC specific mature 2086 protein with a native leader sequence which can be
CC used to create the composition of the invention.

XX Sequence 254 AA;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. NO. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

XX Sequence 254 AA;

Qy 1 DDYGGQSTYVMD 12
 ||||: ||: |
 Db 159 DDAGGKLTYYTID 170

RESULT 47
 ADE44646
 ID ADE44646 standard; protein; 254 AA.
 AC ADE44646;
 XX

29-JAN-2004 (first entry)
 XX
 XX

Neisseria meningitidis ORF2086 protein SeqID80.

ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
 antiinflammatory; immune response; bacterial meningitis;
 Streptococcus pneumoniae infection; non-pathogenic;
 immunogenic composition; 2086 protein.

Neisseria meningitidis.

WO2003063766-A2.

07-AUG-2003.

11-OCT-2002; 2002WO-US032369.

11-OCT-2001; 2001US-0328101P.

30-AUG-2002; 2002US-0406934P.

(AMHP) WYETH HOLDINGS CORP.

Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 Metcalf BJ;

WPI; 2003-663416/62.
 N-PSDB; ADE44645.

Composition comprising crossreactive immunogenic antigen encoded by open
 reading frame 2086 of Neisseria sp., that provides immunogenicity against
 meningitis, or its immunogenic portion or biological equivalent.

Claim 60; SEQ ID NO 80; 480pp; English.

This invention relates to a novel composition which comprises at least
 one protein (or fragment of) encoded by an open reading frame (ORF) of a
 Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
 immunogenic antigen provides immunogenicity against infection by
 Neisseria meningitidis serogroup B in a subject. The composition of the
 invention may have antibacterial or antiinflammatory activity through the
 induction of the immune response. The invention may be useful for the
 treatment of bacterial meningitis in a mammal. One or more polypeptides
 or nucleic acids encoding such polypeptides are useful in a composition
 or as a part of the treatment regimen for the prevention of amelioration
 of Streptococcus pneumoniae infection. The composition of the invention
 is non-pathogenic and substantially free from any infectious impurities.
 The immunogenic compositions can be compounded with fewer components to
 elicit protection comparable to previously used agents. The present
 sequence is the amino acid sequence of a Neisseria meningitidis strain-
 specific mature 2086 protein with a native leader sequence which can be
 used to create the composition of the invention.

Seq Sequence 254 AA;

Query Match 56.3%; Score 40; DB 7; Length 254;
 Best Local Similarity 58.3%; Pred. NO. 2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
 ||||: ||: |
 Db 159 DDAGGKLTYYTID 170

RESULT 48

ADE44656
 ID ADE44656 standard; protein; 254 AA.

AC ADE44656;
 XX

29-JAN-2004 (first entry)
 XX
 XX

Neisseria meningitidis ORF2086 protein SeqID90.

ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
 antiinflammatory; immune response; bacterial meningitis;
 Streptococcus pneumoniae infection; non-pathogenic;
 immunogenic composition; 2086 protein.

Neisseria meningitidis.

WO2003063766-A2.

07-AUG-2003.

11-OCT-2002; 2002WO-US032369.

11-OCT-2001; 2001US-0328101P.

30-AUG-2002; 2002US-0406934P.

(AMHP) WYETH HOLDINGS CORP.

Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
 Metcalf BJ;

WPI; 2003-663416/62.

N-PSDB; ADE44655.

Composition comprising crossreactive immunogenic antigen encoded by open
 reading frame 2086 of Neisseria sp., that provides immunogenicity against
 meningitis, or its immunogenic portion or biological equivalent.

Claim 60; SEQ ID NO 90; 480pp; English.

This invention relates to a novel composition which comprises at least
 one protein (or fragment of) encoded by an open reading frame (ORF) of a
 Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
 immunogenic antigen provides immunogenicity against infection by
 Neisseria meningitidis serogroup B in a subject. The composition of the
 invention may have antibacterial or antiinflammatory activity through the
 induction of the immune response. The invention may be useful for the
 treatment of bacterial meningitis in a mammal. One or more polypeptides
 or nucleic acids encoding such polypeptides are useful in a composition
 or as a part of the treatment regimen for the prevention of amelioration
 of Streptococcus pneumoniae infection. The composition of the invention
 is non-pathogenic and substantially free from any infectious impurities.
 The immunogenic compositions can be compounded with fewer components to
 elicit protection comparable to previously used agents. The present
 sequence is the amino acid sequence of a Neisseria meningitidis strain-
 specific mature 2086 protein which can be used to create the composition
 of the invention.

Seq Sequence 254 AA;

Query Match 56.3%; Score 40; DB 7; Length 254;
 Best Local Similarity 58.3%; Pred. NO. 2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
 ||||: ||: |
 Db 159 DDAGGKLTYYTID 170

RESULT 49

ADE44706
 ID ADE44706 standard; protein; 254 AA.

```

XX AC ADE44706;
XX XX
XX DT 29-JAN-2004 (first entry)
XX XX
XX DE Neisseria meningitidis ORF2086 protein SeqID140.
XX XX
XX KW ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
XX KW antinflammatory; immune response; bacterial meningitis;
XX KW Streptococcus pneumoniae infection; non-pathogenic;
XX KW immunogenic composition; 2086 protein.
XX XX
XX OS Neisseria meningitidis.
XX XX
XX PN WO2003063766-A2.
XX XX
XX PD 07-AUG-2003.
XX XX
XX PF 11-OCT-2002; 2002WO-US032369.
XX XX
XX PD 11-OCT-2001; 2001US-0328101P.
XX PR 30-AUG-2002; 2002US-0406934P.
XX XX
XX PA (AMHP ) WYETH HOLDINGS CORP.
XX XX
XX PI Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
XX PI Metcalf BJ;
XX XX
XX DR WPI; 2003-663416/62.
XX DR N-PSDB; ADE44705.
XX XX
XX PT Composition comprising crossreactive immunogenic antigen encoded by open
XX PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
XX PT meningitis, or its immunogenic portion or biological equivalent.
XX XX
XX PS Claim 60; SEQ ID NO 140; 480pp; English.
XX XX
XX CC This invention relates to a novel composition which comprises at least
XX CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
XX CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
XX CC immunogenic antigen provides immunogenicity against infection by
XX CC Neisseria meningitidis serogroup B in a subject. The composition of the
XX CC invention may have antibacterial or antinflammatory activity through the
XX CC induction of the immune response. The invention may be useful for the
XX CC treatment of bacterial meningitis in a mammal. One or more polypeptides
XX CC or nucleic acids encoding such polypeptides are useful in a composition
XX CC or as a part of the treatment regimen for the prevention of amelioration
XX CC of Streptococcus pneumoniae infection. The composition of the invention
XX CC is non-pathogenic and substantially free from any infectious impurities.
XX CC The immunogenic compositions can be compounded with fewer components to
XX CC elicit protection comparable to previously used agents. The present
XX CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
XX CC specific mature 2086 protein with a native leader sequence which can be
XX CC used to create the composition of the invention.
XX SQ Sequence 254 AA;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:|
Db 159 DDAGGKLYTID 170

RESULT 50
ADE44658
ID ADE44658 standard; protein; 254 AA.
XX XX
AC ADE44658;
XX XX
XX DT 29-JAN-2004 (first entry)

```

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XX XX Neisseria meningitidis ORF2086 protein SeqID92.
XX DE
XX KW ORF2086; Neisseria meningitidis serogroup B infection; antibacterial;
XX KW antinflammatory; immune response; bacterial meningitis;
XX KW Streptococcus pneumoniae infection; non-pathogenic;
XX KW immunogenic composition; 2086 protein.
XX XX
XX OS Neisseria meningitidis.
XX XX
XX PN WO2003063766-A2.
XX XX
XX PD 07-AUG-2003.
XX XX
XX PF 11-OCT-2002; 2002WO-US032369.
XX XX
XX PR 11-OCT-2001; 2001US-0328101P.
XX PR 30-AUG-2002; 2002US-0406934P.
XX XX
XX PA (AMHP ) WYETH HOLDINGS CORP.
XX XX
XX PI Zlotnick GW, Fletcher LD, Farley J, Bernfield LA, Zagursky RJ;
XX PI Metcalf BJ;
XX XX
XX DR WPI; 2003-663416/62.
XX DR N-PSDB; ADE44657.
XX XX
XX PT Composition comprising crossreactive immunogenic antigen encoded by open
XX PT reading frame 2086 of Neisseria sp., that provides immunogenicity against
XX PT meningitis, or its immunogenic portion or biological equivalent.
XX XX
XX PS Claim 60; SEQ ID NO 92; 480pp; English.
XX XX
XX CC This invention relates to a novel composition which comprises at least
XX CC one protein (or fragment of) encoded by an open reading frame (ORF) of a
XX CC Neisseria sp. (ORF2086), where the ORF encoding a crossreactive
XX CC immunogenic antigen provides immunogenicity against infection by
XX CC Neisseria meningitidis serogroup B in a subject. The composition of the
XX CC invention may have antibacterial or antinflammatory activity through the
XX CC induction of the immune response. The invention may be useful for the
XX CC treatment of bacterial meningitis in a mammal. One or more polypeptides
XX CC or nucleic acids encoding such polypeptides are useful in a composition
XX CC or as a part of the treatment regimen for the prevention of amelioration
XX CC of Streptococcus pneumoniae infection. The composition of the invention
XX CC is non-pathogenic and substantially free from any infectious impurities.
XX CC The immunogenic compositions can be compounded with fewer components to
XX CC elicit protection comparable to previously used agents. The present
XX CC sequence is the amino acid sequence of a Neisseria meningitidis strain-
XX CC specific mature 2086 protein with a native leader sequence which can be
XX CC used to create the composition of the invention.
XX SQ Sequence 254 AA;

Query Match 56.3%; Score 40; DB 7; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:|
Db 159 DDAGGKLYTID 170

Search completed: May 11, 2006, 16:27:19
Job time : 144.197 secs

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GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 19.1803 Seconds
(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-3
Perfect score: 71
Sequence: 1 DDYGGQSTYVMDA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: Piri:*
2: Piri2:*
3: Piri3:*
4: Piri4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	60.6	450	2 F71351	probable preprotei
2	43	60.6	510	2 AH0366	probable sugar tra
3	41	57.7	909	2 T33749	hypothetical prote
4	40	56.3	276	2 A95017	ABC transporter, s
5	40	56.3	276	2 B97890	hypothetical prote
6	40	56.3	320	2 D81032	hypothetical prote
7	39	54.9	1729	2 T18396	erythrocyte membra
8	39	54.9	2229	2 T16199	hypothetical prote
9	39	54.9	2924	2 T18378	variant-specific s
10	38	53.5	137	2 S34152	Ig mu chain - axol
11	38	53.5	196	2 AE2876	conserved hypother
12	38	53.5	198	2 G97652	hypothetical prote
13	38	53.5	215	2 T17207	hypothetical prote
14	38	53.5	223	1 E64411	flagellin B3 precu
15	38	53.5	295	2 D96648	hypothetical prote
16	38	53.5	354	2 T44109	conserved hypother
17	38	53.5	411	2 D86153	hypothetical prote
18	38	53.5	567	2 H87370	major facilitator
19	38	53.5	614	2 A12882	MFS permease [auga
20	38	53.5	620	2 A70525	hypothetical prote
21	38	53.5	632	2 AE3560	proline/betaine tr
22	38	53.5	657	2 G97658	hypothetical prote
23	38	53.5	669	2 D72278	endo-1,4-beta-mann
24	38	53.5	806	2 A12428	sucrose synthase [
25	38	53.5	1251	2 B86194	hypothetical prote
26	38	53.5	1635	2 T32452	hypothetical prote
27	38	53.5	3078	2 T28432	variant-specific s
28	38	53.5	3951	1 VFIH81	F1 protein - avian
29	37.5	52.8	803	2 I68600	dipeptidyl aminope

30	37.5	52.8	865	2 I54331	dipeptidyl aminope
31	37	52.1	118	2 A49026	Ig heavy chain V r
32	37	52.1	178	2 S18459	gamma-crystallin m
33	37	52.1	437	2 S50006	preprotein translo
34	37	52.1	437	2 JC5115	preprotein translo
35	37	52.1	437	2 JC4288	preprotein translo
36	37	52.1	586	2 S4966	sucrose synthase (
37	37	52.1	677	2 T02951	probable mitogen a
38	37	52.1	801	2 T14338	sucrose synthase (
39	37	52.1	802	1 YUZMS	sucrose synthase (
40	37	52.1	805	1 YUPOS	sucrose synthase (
41	37	52.1	806	2 S31479	sucrose synthase (
42	37	52.1	807	2 S29242	sucrose synthase (
43	37	52.1	808	2 S37560	sucrose synthase (
44	37	52.1	808	2 S23543	sucrose synthase (
45	37	52.1	808	2 T49233	sucrose synthase-1
46	37	52.1	808	2 T01420	sucrose synthase (
47	37	52.1	809	2 B85029	probable sucrose s
48	37	52.1	809	2 T06497	probable sucrose s
49	37	52.1	816	2 S32451	sucrose synthase (
50	37	52.1	816	2 S19139	sucrose synthase (
51	37	52.1	822	2 S71493	sucrose synthase (
52	37	52.1	942	2 C96760	probable sucrose s
53	37	52.1	972	2 T47922	anthranilate phosph
54	36	50.7	105	2 A56897	glutamate-5-semial
55	36	50.7	119	1 A1HUBR	Ig heavy chain V-I
56	36	50.7	136	2 S35759	BHD9D10 protein -
57	36	50.7	160	2 PL0105	anti-PR2 erythrocy
58	36	50.7	206	2 JC2070	flavin reductase (
59	36	50.7	247	2 AF0869	probable fibrial
60	36	50.7	301	2 T25388	hypothetical prote
61	36	50.7	311	2 AE2277	hypothetical prote
62	36	50.7	397	2 B69378	probable acyl-CoA
63	36	50.7	408	1 F70090	probable formaldeh
64	36	50.7	429	2 B72109	GMP synthase CP059
65	36	50.7	429	2 C86532	GMP synthase limpo
66	36	50.7	440	2 I40340	preprotein translo
67	36	50.7	446	2 AC2812	conserved hypother
68	36	50.7	446	2 D97590	hypothetical prote
69	36	50.7	453	2 P90327	cytosine permease
70	36	50.7	460	2 T29946	hypothetical prote
71	36	50.7	492	2 T21934	hypothetical prote
72	36	50.7	496	2 A10907	probable sialic ac
73	36	50.7	506	2 D85986	sialic acid transp
74	36	50.7	506	2 A91141	sialic acid transp
75	36	50.7	506	2 B65114	probable sialic ac
76	36	50.7	543	2 B84398	hypothetical prote
77	36	50.7	547	2 S12025	celloextrinase -
78	36	50.7	699	2 A70300	translation elonga
79	36	50.7	700	2 S38928	translation elonga
80	36	50.7	720	2 S75935	hypothetical prote
81	36	50.7	725	2 JC1300	endo-beta-1,4-gluc
82	36	50.7	1321	2 T00382	hypothetical prote
83	35.5	50.0	803	2 A41793	dipeptidyl aminope
84	35.5	50.0	958	2 S41013	hypothetical prote
85	35.5	50.0	1032	2 T23164	hypothetical prote
86	35.5	50.0	1035	2 T23165	hypothetical prote
87	35.5	50.0	1040	2 D88568	protein ZK757_3 li
88	35	49.3	40	2 A05301	hemoglobin alpha-2
89	35	49.3	72	2 C73263	Ig heavy chain V r
90	35	49.3	96	2 S38916	hypothetical prote
91	35	49.3	120	2 G86697	hypothetical prote
92	35	49.3	160	2 C69976	YrK8 protein - Bac
93	35	49.3	172	2 T17377	hypothetical prote
94	35	49.3	178	1 CYCAG1	gamma-crystallin m
95	35	49.3	201	2 C97074	terg family protei
96	35	49.3	248	2 B83134	probable pill assem
97	35	49.3	278	2 A49505	lectin light chain
98	35	49.3	288	2 A48452	galactose-inhibita
99	35	49.3	304	2 C70978	probable rmlD prot
100	35	49.3	311	2 H87002	probable dTDP-rham
101	35	49.3	362	2 H84175	hypothetical prote
102	35	49.3	363	2 AC0244	conserved hypother

103	35	49.3	366	2	B58729	probable outer mem	176	34	47.9	342	2	D98155	hypothetical prote
104	35	49.3	366	2	D90888	putative outer memb	177	34	47.9	342	2	AD3132	conserved hypotet
105	35	49.3	378	1	A59139	outer membrane por	178	34	47.9	342	2	D95874	probable proline r
106	35	49.3	378	1	MNEBC	outer membrane por	179	34	47.9	342	2	AD3450	proline racemase (
107	35	49.3	378	2	A10789	outer membrane pro	180	34	47.9	342	2	B89768	conserved hypotet
108	35	49.3	402	2	D69530	probable acyl-CoA	181	34	47.9	390	2	T10742	chalcone synthase
109	35	49.3	431	2	H72247	preprotein translo	182	34	47.9	400	2	B70806	tryptophan synthas
110	35	49.3	438	2	T45389	SacY, preprotein t	183	34	47.9	423	1	B36044	translational initia
111	35	49.3	440	2	E95352	Probable MtBA prot	184	34	47.9	425	1	H69124	coat protein A - p
112	35	49.3	441	2	G70822	Probable secY prot	185	34	47.9	434	1	Z3BPIK	conserved hypotet
113	35	49.3	448	2	T48214	endo-1,4-beta-mann	186	34	47.9	438	2	F75290	hypothetical prote
114	35	49.3	455	2	C86393	TIK7.2 protein - A	187	34	47.9	446	2	AG2361	glycosyltransferas
115	35	49.3	459	2	T29945	hypothetical prote	188	34	47.9	454	2	AG2657	hypothetical prote
116	35	49.3	460	2	C84750	probable tyrosyl-t	189	34	47.9	454	2	D97439	transcription regu
117	35	49.3	479	2	B69764	transcription regu	190	34	47.9	462	2	G83986	hypothetical prote
118	35	49.3	494	2	T28984	hypothetical prote	191	34	47.9	463	2	S64119	hypothetical prote
119	35	49.3	497	2	H87555	amidase family pro	192	34	47.9	507	2	T35677	probable hydrolase
120	35	49.3	510	2	F75260	glutamyl-tRNA(Gln)	193	34	47.9	508	2	B49131	ryanodine receptor
121	35	49.3	513	2	E72741	hypothetical prote	194	34	47.9	510	2	JS0724	cytochrome P450 AL
122	35	49.3	516	2	S64120	TATA box-binding p	195	34	47.9	516	1	XUPJVS	3-phosphoshikimate
123	35	49.3	518	2	G70471	flagellin - Aquife	196	34	47.9	518	2	S18353	3-phosphoshikimate
124	35	49.3	549	2	H96944	arginine degradati	197	34	47.9	520	1	XUOVVS	3-phosphoshikimate
125	35	49.3	558	2	C98996	protein C17B7.8 [i	198	34	47.9	567	1	ACFFAI	nicotinic acetylch
126	35	49.3	601	1	T50052	probable phosphoe	199	34	47.9	589	2	I59340	transcription fact
127	35	49.3	648	2	H85056	probable receptor-	200	34	47.9	634	2	F97199	alkaline phosphata
128	35	49.3	652	2	S09133	NADH2 dehydrogenas	201	34	47.9	638	2	AB0446	membrane exported
129	35	49.3	666	1	D69103	DNA helicase (EC 3	202	34	47.9	710	1	QOBE22	membrane antigen g
130	35	49.3	696	2	A12849	GGDEF family prote	203	34	47.9	712	2	AB2776	DNA gyrase subunit
131	35	49.3	696	2	G97626	hypothetical prote	204	34	47.9	712	2	H97555	DNA gyrase chain b
132	35	49.3	827	2	F64512	hypothetical prote	205	34	47.9	715	2	S10843	NADH2 dehydrogenas
133	35	49.3	884	2	G96787	protein T4O12.9 [i	206	34	47.9	821	2	S64929	hypothetical prote
134	35	49.3	899	2	A84421	probable ATP-depen	207	34	47.9	882	2	B84509	hypothetical Na/H anti
135	35	49.3	900	2	AC1852	hypothetical prote	208	34	47.9	882	2	H70199	translational initia
136	35	49.3	1231	2	AB0453	5-methyltetrahydro	209	34	47.9	886	2	S29605	glycoprotein 350/2
137	35	49.3	1242	2	T20739	hypothetical prote	210	34	47.9	907	1	QOBE21	membrane antigen g
138	35	49.3	1329	2	T29074	hypothetical prote	211	34	47.9	1036	2	D84741	probable cellulose
139	35	49.3	1573	2	T21219	hypothetical prote	212	34	47.9	1128	2	T04922	hypothetical prote
140	35	49.3	1770	2	S56221	hypothetical prote	213	34	47.9	1261	2	AI3471	5-methyltetrahydro
141	35	49.3	2214	2	T16305	hypothetical prote	214	34	47.9	1603	2	T24098	hypothetical prote
142	35	49.3	5107	2	T29144	partial CDS - Caen	215	34	47.9	1734	2	A41101	phorbol ester-bind
143	34.5	48.6	268	2	D33465	lic-1 protein D -	216	34	47.9	1813	2	T19295	hypothetical prote
144	34	47.9	15	2	I67525	CD33 antigen homol	217	34	47.9	5126	2	S40450	ryanodine receptor
145	34	47.9	119	2	D97173	chemotaxis signal	218	33	46.5	81	2	T17555	hypothetical prote
146	34	47.9	123	2	T49794	hypothetical prote	219	33	46.5	87	2	B69948	phage-related prot
147	34	47.9	133	2	B69279	conserved hypotet	220	33	46.5	88	2	A69733	phsx prophage ORF
148	34	47.9	169	2	S54745	cytochrome-c biosy	221	33	46.5	94	2	G32513	Ig heavy chain V r
149	34	47.9	171	2	F90267	hypothetical prote	222	33	46.5	97	1	FEPRR	ferredoxin [2Fe-2S
150	34	47.9	177	2	AC3305	gamma-crystallin M	223	33	46.5	114	2	PH1027	Ig heavy chain V r
151	34	47.9	198	2	AC3305	hypothetical prote	224	33	46.5	114	2	S09752	hypothetical prote
152	34	47.9	202	1	E43255	Ni, Fe-Hydrogenase	225	33	46.5	138	2	B56701	Ig heavy chain V r
153	34	47.9	202	2	AC0676	hydrogenase 1 matu	226	33	46.5	142	1	HAXL2	hemoglobin alpha c
154	34	47.9	203	2	T37404	IWV membrane prote	227	33	46.5	150	2	T29726	hypothetical prote
155	34	47.9	203	2	A42519	A17L protein - vac	228	33	46.5	160	2	AG0689	alternative bacter
156	34	47.9	203	2	T28559	hypothetical prote	229	33	46.5	167	2	H84812	hypothetical prote
157	34	47.9	203	2	G72165	A18L protein - var	230	33	46.5	178	2	JC2353	gamma-crystallin M
158	34	47.9	203	2	I36849	A17L protein - var	231	33	46.5	178	2	JC2355	gamma-crystallin M
159	34	47.9	232	2	S75699	cAMP receptor prot	232	33	46.5	178	2	I50601	hypothetical prote
160	34	47.9	249	2	T59503	hypothetical prote	233	33	46.5	195	2	A96779	transcription regu
161	34	47.9	249	2	T40182	conserved hypotet	234	33	46.5	231	2	AI3632	hypothetical prote
162	34	47.9	263	2	H87296	aminomethyltransfe	235	33	46.5	241	2	B84068	rod shape-determin
163	34	47.9	268	2	AC2594	enoyl - (acyl)-carrie	236	33	46.5	248	2	D64691	hypothetical prote
164	34	47.9	270	2	H97376	enoyl - (acyl)-carrie	237	33	46.5	254	2	B89780	hypothetical prote
165	34	47.9	280	2	G81977	Probable lipoprote	238	33	46.5	254	2	T05076	membrane intrinsic
166	34	47.9	295	2	A43663	host-inducible pro	239	33	46.5	309	2	T14889	probable major hea
167	34	47.9	309	2	H84869	hypothetical prote	240	33	46.5	315	2	F91250	endopeptidase (EC
168	34	47.9	310	2	T45873	hypothetical prote	241	33	46.5	316	2	A45134	hypothetical prote
169	34	47.9	320	1	JC1286	porphobilinogen sy	242	33	46.5	321	2	A37842	suas protein [lmpo
170	34	47.9	334	2	B96810	unknown protein T1	243	33	46.5	323	2	AB3443	hypothetical prote
171	34	47.9	336	2	A23366	delta-aminolevulin	244	33	46.5	323	2	JQ0935	coat protein - ric
172	34	47.9	338	2	S18354	3-phosphoshikimate	245	33	46.5	332	2	B95978	probable 6-aminohe
173	34	47.9	339	2	B71951	aliphatic amidase	246	33	46.5	334	2	T26711	hypothetical prote
174	34	47.9	339	2	F64556	aliphatic amidase	247	33	46.5	337	2	AG0802	probable semialdeh
175	34	47.9	342	2	T25766	hypothetical prote	248	33	46.5	344	2	C70208	conserved hypotet

249	33	46.5	345	2	S12788	transcription fact	322	33	46.5	3351	2	T13812	lipophorin - fruit
250	33	46.5	345	2	B83260	probable transcrip	323	33	46.5	3498	2	T22330	hypothetical prote
251	33	46.5	345	2	D88108	protein C46E10.4 [324	32.5	45.8	256	2	B97099	probable glycosyl
252	33	46.5	349	2	AF2130	iron(III) dicitrat	325	32.5	45.8	2032	2	T34433	hypothetical prote
253	33	46.5	365	2	C83512	conserved hypothet	326	32.5	45.8	2232	2	T34433	hypothetical prote
254	33	46.5	384	2	A81987	hypothetical prote	327	32	45.1	55	2	A24932	ferredoxin 2[4Fe-4
255	33	46.5	387	2	S11985	serine proteinase	328	32	45.1	62	2	AG1905	hypothetical prote
256	33	46.5	394	2	C64185	cell division prot	329	32	45.1	83	2	D90776	hypothetical prote
257	33	46.5	397	2	E90167	hypothetical prote	330	32	45.1	91	2	A82553	phage-related base
258	33	46.5	406	1	T34839	probable hexosyltr	331	32	45.1	97	2	S26935	ig heavy chain v r
259	33	46.5	422	1	JGAGLR	lactose-binding pr	332	32	45.1	97	2	S46462	ig heavy chain v r
260	33	46.5	424	2	S09884	hypothetical prote	333	32	45.1	104	2	PH1665	ig heavy chain v r
261	33	46.5	425	2	D81728	conserved hypothet	334	32	45.1	106	2	AI0133	probable DNA-bindi
262	33	46.5	427	2	T02381	hypothetical prote	335	32	45.1	113	2	PH1018	ig heavy chain v r
263	33	46.5	427	2	B71466	hypothetical prote	336	32	45.1	116	2	B28966	ig heavy chain pre
264	33	46.5	428	2	E95906	probable solute-bi	337	32	45.1	116	2	S31110	ig heavy chain - h
265	33	46.5	431	2	B87285	phosphate ABC tran	338	32	45.1	118	2	P84263	transcription repr
266	33	46.5	433	2	T47750	N2,N2-dimethylguan	339	32	45.1	147	2	A47017	orf 5' of sigB - A
267	33	46.5	444	2	T01782	GDP dissociation i	340	32	45.1	149	2	G90364	hypothetical prote
268	33	46.5	445	2	F75389	Rab GDP dissociati	341	32	45.1	168	2	G83068	hypothetical prote
269	33	46.5	445	1	C42022	transcription fact	342	32	45.1	169	2	S28732	hypothetical prote
270	33	46.5	445	2	T00690	GDP dissociation i	343	32	45.1	173	2	S45017	gamma-crystallin S
271	33	46.5	459	2	F75389	probable carboxyl-	344	32	45.1	176	2	S45015	gamma-crystallin M
272	33	46.5	459	1	G89005	multidrug transpor	345	32	45.1	180	2	B83460	cytochrome C bioge
273	33	46.5	464	2	T33249	hypothetical prote	346	32	45.1	184	2	B82124	probable 16S rRNA
274	33	46.5	487	2	I64033	hypothetical prote	347	32	45.1	188	2	G75326	hypothetical prote
275	33	46.5	491	1	S19458	hypothetical prote	348	32	45.1	210	2	G96832	SSU ribosomal prot
276	33	46.5	498	2	A47286	3',5'-cyclic-AMP p	349	32	45.1	211	2	H69539	ATP-phosphoribosyl
277	33	46.5	516	2	S12744	3-phosphohikimate	350	32	45.1	211	2	B83089	conserved hypothet
278	33	46.5	520	1	XUMU5	3-phosphohikimate	351	32	45.1	219	2	E84335	anther-specific pr
279	33	46.5	520	2	H84888	hypothetical prote	352	32	45.1	222	2	S26252	hypothetical prote
280	33	46.5	520	2	T21666	hypothetical prote	353	32	45.1	228	2	AE2541	hypothetical prote
281	33	46.5	521	2	D86526	hypothetical prote	354	32	45.1	228	2	F72520	hypothetical prote
282	33	46.5	523	2	T05692	hypothetical prote	355	32	45.1	230	2	E87578	hypothetical prote
283	33	46.5	549	2	T11688	phosphoinositide-s	356	32	45.1	243	2	JC5723	capsular polysacch
284	33	46.5	551	2	T06777	phosphoinositide-s	357	32	45.1	244	2	S36245	chaperone-like pro
285	33	46.5	553	2	T06771	phosphoinositide-s	358	32	45.1	250	2	C69952	ABC transporter (A
286	33	46.5	560	2	F84341	hypothetical prote	359	32	45.1	253	1	UUHU	major prion protei
287	33	46.5	571	2	S83356	pept protein - Sta	360	32	45.1	254	2	S28362	coat protein - bee
288	33	46.5	577	2	T22460	hypothetical prote	361	32	45.1	257	2	AH0859	periplasmic fibrin
289	33	46.5	581	1	S71170	phosphoinositide-s	362	32	45.1	258	2	S51828	alpha-amylase inhi
290	33	46.5	581	2	T50841	phosphoinositide-s	363	32	45.1	259	2	AD3082	short-chain dehydr
291	33	46.5	581	2	T33737	phosphoinositide-s	364	32	45.1	259	2	D98204	probable short-cha
292	33	46.5	594	2	T06467	phosphoinositide-s	365	32	45.1	260	1	A30202	transcription init
293	33	46.5	596	2	T07421	phosphoinositide-s	366	32	45.1	260	2	B87668	2-deoxy-D-gluconat
294	33	46.5	600	2	T06775	phosphoinositide-s	367	32	45.1	261	2	B83969	RNA polymerase spo
295	33	46.5	600	2	T06420	phosphoinositide-s	368	32	45.1	263	2	B75361	WD-repeat family p
296	33	46.5	619	2	T48557	hypothetical prote	369	32	45.1	263	2	S53488	water-stress-induc
297	33	46.5	720	2	J01676	ABI3 protein - Ara	370	32	45.1	265	2	AH2252	ATP-binding protei
298	33	46.5	724	2	B71404	hypothetical prote	371	32	45.1	277	2	G75505	hypothetical prote
299	33	46.5	729	2	T35028	probable glycosyl	372	32	45.1	291	2	F71416	hypothetical prote
300	33	46.5	747	2	T08531	probable DNA relax	373	32	45.1	291	2	A86681	hypothetical prote
301	33	46.5	747	2	S22994	traI protein - Esc	374	32	45.1	291	2	AI3071	conserved hypothet
302	33	46.5	849	2	C87740	protein H26D21.2 [375	32	45.1	291	2	H98214	aldose epimerase f
303	33	46.5	875	2	A49608	outer membrane ush	376	32	45.1	292	1	A26952	electron transfer
304	33	46.5	884	2	A44839	glutamate receptor	377	32	45.1	292	2	G95317	FixA electron tran
305	33	46.5	899	2	H87513	hypothetical prote	378	32	45.1	294	2	B83698	hypothetical prote
306	33	46.5	902	2	D40170	glutamate receptor	379	32	45.1	294	2	C86802	hypothetical prote
307	33	46.5	910	2	A32560	outer membrane pro	380	32	45.1	301	2	C64633	hook assembly prot
308	33	46.5	982	1	S16292	nitrate reductase	381	32	45.1	304	1	S74557	acetylpolysamine am
309	33	46.5	1000	2	F70368	cation efflux (Acr	382	32	45.1	308	2	AB1253	glycine betaine/ca
310	33	46.5	1006	2	T36770	hypothetical prote	383	32	45.1	318	2	AH1615	glycine betaine/ca
311	33	46.5	1015	2	B83627	probable RND efflu	384	32	45.1	319	2	S71877	carbonate dehydrat
312	33	46.5	1026	2	T18220	chitin synthase (E	385	32	45.1	323	2	T04826	hypothetical prote
313	33	46.5	1067	2	A80260	probable phage hos	386	32	45.1	324	2	A86839	conserved hypothet
314	33	46.5	1125	2	E90598	membrane nuclease,	387	32	45.1	326	2	F83338	hypothetical prote
315	33	46.5	1209	1	DNBECA	DNA-binding protei	388	32	45.1	327	2	C84374	tyrosyl-tRNA synth
316	33	46.5	1252	2	A47213	beta-fodrin - huma	389	32	45.1	327	2	S58305	hypothetical prote
317	33	46.5	1617	2	T28153	complement C4 - ch	390	32	45.1	332	2	F82140	C4-dicarboxylate-b
318	33	46.5	1876	2	S50235	1,3-beta-glucan sy	391	32	45.1	344	2	B83488	hypothetical prote
319	33	46.5	2157	1	GNN11B	genome polyprotein	392	32	45.1	357	2	S75666	3-chlorobenzoate-3
320	33	46.5	2364	1	A44159	spectrin beta-G ch	393	32	45.1	363	2	F71881	probable flagellar
321	33	46.5	3135	2	A48584	transmission block	394	32	45.1	380	2	F98299	probable acyl-CoA

395	32	45.1	380	2	A12983	acyl-CoA dehydroge	468	32	45.1	815	2	AC0394	probable acyl-CoA
396	32	45.1	380	2	T00792	hypothetical prote	469	32	45.1	838	2	A96557	probable receptor
397	32	45.1	387	2	B72292	hypothetical prote	470	32	45.1	873	2	B86471	hypothetical prote
398	32	45.1	388	1	S22387	cuticle-degrading	471	32	45.1	888	2	C40170	glutamate receptor
399	32	45.1	393	2	H84272	cystathionine alph	472	32	45.1	894	2	S49460	glutamate receptor
400	32	45.1	393	2	S69537	hypothetical prote	473	32	45.1	894	2	S50128	glutamate receptor
401	32	45.1	408	2	AB0710	succinylornithine	474	32	45.1	894	2	S53696	hypothetical prote
402	32	45.1	414	2	T16466	hypothetical prote	475	32	45.1	910	2	T29935	hypothetical prote
403	32	45.1	422	2	AH2352	hypothetical prote	476	32	45.1	916	2	F71962	hypothetical prote
404	32	45.1	428	2	C37432	probable oxidoredu	477	32	45.1	933	2	S53609	DNA mismatch repai
405	32	45.1	428	2	A02650	oxidoreductase ord	478	32	45.1	933	2	JC6184	mismatch repair pr
406	32	45.1	429	2	A10029	conserved hypothet	479	32	45.1	934	2	T64819	DNA mismatch repai
407	32	45.1	429	2	AC2227	hypothetical prote	480	32	45.1	935	2	S53608	DNA mismatch repai
408	32	45.1	432	2	T00949	hypothetical prote	481	32	45.1	964	2	S57379	MSH2 protein - yea
409	32	45.1	449	2	A70568	probable dicarboxy	482	32	45.1	982	2	T43659	DNA mismatch repai
410	32	45.1	461	2	A70185	hypothetical prote	483	32	45.1	1045	2	S55253	sucrose-phosphate
411	32	45.1	466	2	B91186	probable permease	484	32	45.1	1047	2	T51800	sucrose-phosphate
412	32	45.1	466	2	A86033	probable permease	485	32	45.1	1049	2	JC4783	sucrose-phosphate
413	32	45.1	470	2	D69012	conserved hypothet	486	32	45.1	1053	2	S34172	sucrose-phosphate
414	32	45.1	477	2	G83205	probable lyase PA3	487	32	45.1	1054	2	T09833	sucrose-phosphate
415	32	45.1	482	2	S37845	transcription init	488	32	45.1	1056	2	JQ2277	sucrose-phosphate
416	32	45.1	503	2	AH3535	periplasmic dipept	489	32	45.1	1057	2	S72648	sucrose-phosphate
417	32	45.1	521	2	T27996	hypothetical prote	490	32	45.1	1059	2	T12195	sucrose-phosphate
418	32	45.1	522	2	E86453	CDS protein F911.	491	32	45.1	1064	2	F86182	hypothetical prote
419	32	45.1	525	2	T00459	hypothetical prote	492	32	45.1	1068	1	JQ1329	sucrose-phosphate
420	32	45.1	531	2	T18741	hypothetical prote	493	32	45.1	1081	2	T09837	sucrose-phosphate
421	32	45.1	539	2	E83181	probable MFS trans	494	32	45.1	1083	2	T04062	sucrose-phosphate
422	32	45.1	542	2	S62508	probable U4/U6 sma	495	32	45.1	1083	2	C88854	protein F1110.3 [
423	32	45.1	544	2	S41094	triacylglycerol li	496	32	45.1	1084	2	T04103	sucrose-phosphate
424	32	45.1	544	2	S41091	triacylglycerol li	497	32	45.1	1119	2	AD1822	leucine-rich-repea
425	32	45.1	544	2	S59958	triacylglycerol li	498	32	45.1	1146	2	A89922	conserved hypothet
426	32	45.1	544	2	S41090	triacylglycerol li	499	32	45.1	1181	2	B64516	hypothetical prote
427	32	45.1	544	2	S41092	triacylglycerol li	500	32	45.1	1206	2	E96507	hypothetical prote
428	32	45.1	544	2	S41095	triacylglycerol li	501	32	45.1	1245	1	VHVV82	structural polypro
429	32	45.1	544	2	S41096	triacylglycerol li	502	32	45.1	1245	1	VHVV82	structural polypro
430	32	45.1	544	2	S41093	triacylglycerol li	503	32	45.1	1280	2	T34357	hypothetical prote
431	32	45.1	549	2	T33517	hypothetical prote	504	32	45.1	1280	2	T34357	hypothetical prote
432	32	45.1	550	2	A87252	major facilitator	505	32	45.1	1413	2	D88844	protein ZK792.1 [i
433	32	45.1	559	2	T43071	activation/secreti	506	32	45.1	1562	2	T07323	DNA-directed RNA p
434	32	45.1	562	2	AF0852	secretory protein	507	32	45.1	1695	2	JE0084	voltage-gated sodi
435	32	45.1	563	1	AC0UGC	triacylglycerol li	508	32	45.1	1774	2	T17421	polyketide synthas
436	32	45.1	563	1	PG0493	triacylglycerol li	509	32	45.1	1883	2	T13944	chromodomain helic
437	32	45.1	563	2	S59957	triacylglycerol li	510	32	45.1	1946	2	JC6032	lactocepin [SC 3.4
438	32	45.1	563	2	S54420	invasion protein i	511	32	45.1	1999	2	AB2018	hypothetical prote
439	32	45.1	584	2	T49206	phosphoinositide-s	512	32	45.1	2052	2	C97038	phage-related prot
440	32	45.1	585	2	T18736	hypothetical prote	513	32	45.1	2182	2	T28634	variant-specific s
441	32	45.1	598	2	T40676	hypothetical prote	514	32	45.1	2336	2	S37077	genome polyprotein
442	32	45.1	601	2	T26062	hypothetical prote	515	32	45.1	2336	2	WMBEH6	U36 protein - hum
443	32	45.1	604	2	D90523	lipoprotein [impor	516	31.5	44.4	514	2	B87711	coenzyme A transfe
444	32	45.1	605	2	A89937	DNA primase [impor	517	31.5	44.4	1337	2	T13948	atypical CTRP - mal
445	32	45.1	611	2	T38908	probable gamma-glu	518	31.5	44.4	2098	2	T18397	protein CTRP - mal
446	32	45.1	616	2	S33804	male sterility pro	519	31	43.7	55	2	AG2572	hypothetical prote
447	32	45.1	616	2	T08096	male sterility pro	520	31	43.7	60	2	D97849	hypothetical prote
448	32	45.1	620	2	AD1659	exonuclease ABC c	521	31	43.7	86	2	D69774	hypothetical prote
449	32	45.1	628	2	S51422	probable membrane	522	31	43.7	106	2	PH1008	probable GDP diaso
450	32	45.1	637	2	A72532	probable DNA-direc	523	31	43.7	111	2	T05919	Ig heavy chain V r
451	32	45.1	655	2	T26061	hypothetical prote	524	31	43.7	118	2	D49590	Ig heavy chain V r
452	32	45.1	656	2	T73733	hypothetical prote	525	31	43.7	118	2	S00700	Ig heavy chain V r
453	32	45.1	665	2	E86775	ribonuclease [impo	526	31	43.7	118	2	A32530	Ig heavy chain V r
454	32	45.1	692	2	E36802	hypothetical prote	527	31	43.7	119	2	H45722	anti-glycoprotein
455	32	45.1	699	2	A89841	unknown protein [i	528	31	43.7	123	2	S31509	Ig heavy chain V r
456	32	45.1	708	2	J01148	killer toxin KHS p	529	31	43.7	123	2	S32186	Ig heavy chain V r
457	32	45.1	710	2	T20704	hypothetical prote	530	31	43.7	125	2	PH0100	Ig heavy chain V r
458	32	45.1	719	2	T49434	hypothetical prote	531	31	43.7	128	2	A97248	anti-glycoprotein
459	32	45.1	736	2	H75460	conserved hypothet	532	31	43.7	134	2	S21916	Ig heavy chain V r
460	32	45.1	742	2	C83061	probable TonB-depe	533	31	43.7	141	2	D25929	hemoglobin alpha-I
461	32	45.1	750	1	D69403	conserved hypothet	534	31	43.7	141	2	C25929	hemoglobin alpha-I
462	32	45.1	751	2	D98320	hypothetical prote	535	31	43.7	141	2	H83081	hypothetical prote
463	32	45.1	763	2	JC4376	beta-glucosidase (536	31	43.7	142	1	HAXL1	hemoglobin alpha c
464	32	45.1	776	2	T20738	hypothetical prote	537	31	43.7	142	2	H81898	hypothetical prote
465	32	45.1	786	2	S71091	acetyl-CoA carboxy	538	31	43.7	143	2	C81135	hypothetical prote
466	32	45.1	792	2	B71539	probable omp85 ana	539	31	43.7	144	2	T50649	elicitor-responsiv
467	32	45.1	792	2	H81693	outer membrane pro	540	31	43.7	145	2	S76758	hypothetical prote

541	31	43.7	147	2	B75275	hypothetical prote	614	31	43.7	287	2	AB2354	dihydropteroate sy
542	31	43.7	153	2	T12960	hypothetical prote	615	31	43.7	289	2	S75361	dihydropteroate sy
543	31	43.7	153	2	T27157	hypothetical prote	616	31	43.7	289	2	P96770	protein RNA-bindin
544	31	43.7	154	2	D75525	hypothetical prote	617	31	43.7	297	1	WJMS29	homeotic protein H
545	31	43.7	156	2	AC3636	hypothetical prote	618	31	43.7	301	2	T06151	hypothetical prote
546	31	43.7	159	2	S47251	gene 1 Sc2 protein	619	31	43.7	301	2	C70529	probable ABC trans
547	31	43.7	160	2	S47250	gene 1-Sc1 protein	620	31	43.7	304	1	SVSMFG	dtDP-dihydrostrept
548	31	43.7	167	2	T32353	hypothetical prote	621	31	43.7	306	2	AB1394	conserved hypothet
549	31	43.7	168	1	A70303	conserved hypothet	622	31	43.7	306	2	AH1769	conserved hypothet
550	31	43.7	169	1	S23478	probable benzoate	623	31	43.7	310	2	T29731	hypothetical prote
551	31	43.7	172	2	D69801	hypothetical prote	624	31	43.7	311	2	C95962	probable transcrip
552	31	43.7	175	2	T44347	hypoxanthine phosph	625	31	43.7	312	2	D69347	hypothetical prote
553	31	43.7	177	2	S62649	mannose-binding le	626	31	43.7	321	2	A85829	fucose synthetase
554	31	43.7	178	2	E70069	hypothetical prote	627	31	43.7	321	2	F90983	fucose synthetase
555	31	43.7	183	2	S62650	mannose-binding le	628	31	43.7	321	2	A71168	hypothetical prote
556	31	43.7	184	2	B72383	thymidine kinase (629	31	43.7	323	2	S38887	2S albumin - commo
557	31	43.7	190	2	G64065	probable methylate	630	31	43.7	323	2	F82212	conserved hypothet
558	31	43.7	190	2	E81109	lipoate-protein li	631	31	43.7	326	2	JG4124	pregnancy-specific
559	31	43.7	190	2	E81907	probable lipoate-p	632	31	43.7	333	2	G86237	protein P14N23.27
560	31	43.7	191	2	D90712	lipoate biosynthes	633	31	43.7	335	2	A12026	hypothetical prote
561	31	43.7	191	2	H85562	lipoate biosynthes	634	31	43.7	339	2	A42259	endo-beta-N-acetyl
562	31	43.7	191	2	D64797	lipoate-protein li	635	31	43.7	343	2	T31269	4-hydroxy-2-oxoval
563	31	43.7	191	2	AP0580	lipoate-protein li	636	31	43.7	345	2	S35223	4-hydroxy-2-oxoval
564	31	43.7	195	1	Q08CHD	hydrogenase 1 matu	637	31	43.7	345	2	AD3024	hypothetical prote
565	31	43.7	195	2	C90770	Ni,Fe-Hydrogenase	638	31	43.7	350	1	RGB011	GTP-binding regula
566	31	43.7	196	2	G85632	Ni,Fe-Hydrogenase	639	31	43.7	352	2	C55511	4-hydroxy-2-oxoval
567	31	43.7	196	1	TUBPA7	tail tubular prote	640	31	43.7	353	2	T51615	alternative respir
568	31	43.7	198	2	AG0721	hydrogenase-1 oper	641	31	43.7	355	1	RGRUGX	GTP-binding regula
569	31	43.7	200	2	AB0620	probable bacteriop	642	31	43.7	355	1	RGRUGX	GTP-binding regula
570	31	43.7	204	2	T51982	proteasome endopep	643	31	43.7	355	2	A11909	hypothetical prote
571	31	43.7	204	2	B72370	hypothetical prote	644	31	43.7	357	2	F83537	4-hydroxyphenylpyr
572	31	43.7	208	2	AG2742	conserved hypothet	645	31	43.7	359	2	B71566	probable translati
573	31	43.7	208	2	F97523	hypothetical prote	646	31	43.7	359	2	B98260	periplasmic bindin
574	31	43.7	209	2	AE1257	hypothetical prote	647	31	43.7	361	1	F64355	conserved hypothet
575	31	43.7	215	2	S74602	hypothetical prote	648	31	43.7	364	2	H97275	sugar kinase CAC30
576	31	43.7	215	2	A83146	lipoate-protein li	649	31	43.7	365	2	A75577	nicotinate-nucleot
577	31	43.7	219	1	A23128	myelin P0 protein	650	31	43.7	367	2	T35929	probable alcohol d
578	31	43.7	219	2	C82259	lipoate-protein li	651	31	43.7	369	2	C82211	probable NADH-depe
579	31	43.7	219	2	F87505	hypothetical prote	652	31	43.7	370	2	H75303	probable NADH-depe
580	31	43.7	229	2	D82701	lipoate biosynthes	653	31	43.7	370	2	AC2845	oxidoreductase Atu
581	31	43.7	230	2	JE0083	luza chaperon - Ph	654	31	43.7	370	2	E97622	gtm reductase (Y13
582	31	43.7	233	2	JA0151	NS-glycoprotein -	655	31	43.7	370	2	AC1275	aminopeptidase hom
583	31	43.7	233	2	AC0317	lipoate-protein li	656	31	43.7	370	2	AC1636	aminopeptidase hom
584	31	43.7	233	2	S38899	site-specific DNA-	657	31	43.7	373	2	F81438	probable periplasm
585	31	43.7	235	2	A22962	carbonate dehydrat	658	31	43.7	378	2	A55735	G protein-coupled
586	31	43.7	239	2	T01941	hypothetical prote	659	31	43.7	379	2	A84235	acyl-CoA dehydroge
587	31	43.7	239	2	S35723	spore coat polysac	660	31	43.7	380	2	F89811	cystathionine gamm
588	31	43.7	241	2	S25435	chlorophyll a/b-bi	661	31	43.7	385	2	T01332	hypothetical prote
589	31	43.7	241	2	F96631	hypothetical prote	662	31	43.7	387	2	T09086	sedoheptulose-bisp
590	31	43.7	243	2	D64300	(R)-2-hydroxygluta	663	31	43.7	393	2	S51838	sedoheptulose-bisp
591	31	43.7	245	2	S06329	chlorophyll a/b-bi	664	31	43.7	401	2	S06099	para protein - pha
592	31	43.7	245	2	S28827	chlorophyll a/b-bi	665	31	43.7	401	2	S21569	hypothetical prote
593	31	43.7	246	2	S00443	chlorophyll a/b-bi	666	31	43.7	409	2	S77262	hypothetical prote
594	31	43.7	251	2	AB2352	probable phosphopr	667	31	43.7	411	2	T34585	probable secreted
595	31	43.7	252	2	JG6175	prion protein - ra	668	31	43.7	411	2	T21758	hypothetical prote
596	31	43.7	252	2	T46661	beta 1,4 glucosylt	669	31	43.7	412	2	S37906	translation elonga
597	31	43.7	252	2	B81053	beta-1,4-glucosylt	670	31	43.7	415	2	S29345	translation elonga
598	31	43.7	254	2	D81824	beta-1,4-glucosylt	671	31	43.7	418	2	S38125	hypothetical prote
599	31	43.7	256	2	A80586	probable esterase/	672	31	43.7	419	2	B54312	pregnancy-specific
600	31	43.7	259	2	S30950	gene 2 protein - M	673	31	43.7	419	2	A36109	pregnancy-specific
601	31	43.7	260	1	CRH01D	carbonate dehydrat	674	31	43.7	423	2	F84307	succinyl-CoA synth
602	31	43.7	261	2	T38348	hypothetical prote	675	31	43.7	423	2	T38056	nicotinic acetylch
603	31	43.7	261	2	T16650	hypothetical prote	676	31	43.7	423	2	T23223	hypothetical prote
604	31	43.7	272	2	T40707	hypothetical prote	677	31	43.7	424	2	A55089	vasopressin V3 rec
605	31	43.7	273	2	AD1804	rhamnulose-1-phosp	678	31	43.7	425	2	T03605	probable DNA bindi
606	31	43.7	273	2	AF1430	rhamnulose-1-phosp	679	31	43.7	428	2	H87214	probable glycosyl
607	31	43.7	274	2	H81187	conserved hypothet	680	31	43.7	428	2	JQ1864	hypothetical 47.0K
608	31	43.7	274	2	G81914	hypothetical prote	681	31	43.7	430	2	B86854	transport protein
609	31	43.7	277	2	AE2012	transcription regu	682	31	43.7	430	2	F82625	TolB protein precu
610	31	43.7	280	2	A39415	fimbrial adhesin s	683	31	43.7	431	2	H84392	O-acetyl homoserin
611	31	43.7	280	2	T13191	zinc finger protei	684	31	43.7	431	2	T09048	probable mannan en
612	31	43.7	285	1	S73465	MG011 homolog D12	685	31	43.7	434	2	G69975	hemolysin-like hom
613	31	43.7	287	2	AF2333	hypothetical prote	686	31	43.7	434	2	AH1353	hypothetical prote

687	31	43.7	434	2	A11723	hypothetical prote	760	31	43.7	654	2	AG3522	iron-regulated out
688	31	43.7	436	2	S29891	preprotein tranalo	761	31	43.7	668	2	T05803	hypothetical prote
689	31	43.7	436	2	A31744	conserved hypothet	762	31	43.7	673	2	B86437	F28K20.8 protein -
690	31	43.7	436	2	AG1374	conserved hypothet	763	31	43.7	686	2	T39850	probable multifunc
691	31	43.7	439	2	S16572	S-locus-specific g	764	31	43.7	686	2	A75126	hypothetical prote
692	31	43.7	439	2	AC0462	hypocetol-3-phospha	765	31	43.7	689	2	T34025	hypothetical prote
693	31	43.7	440	2	T24323	hypothetical prote	766	31	43.7	694	2	A83126	probable TonB-depe
694	31	43.7	442	2	E69958	conserved hypothet	767	31	43.7	702	2	A96959	oxygen-sensitive r
695	31	43.7	443	2	F71929	heat shock protein	768	31	43.7	705	2	H89900	translation initia
696	31	43.7	445	2	I49458	acetylcholine rece	769	31	43.7	737	2	T20069	hypothetical prote
697	31	43.7	445	2	T02030	GDP dissociation i	770	31	43.7	740	1	S28666	multifunctional fo
698	31	43.7	445	2	T02032	GDP dissociation i	771	31	43.7	761	1	B64506	DNA topoisomerase
699	31	43.7	447	2	AB2135	hypothetical prote	772	31	43.7	764	2	H71607	hypothetical prote
700	31	43.7	450	2	T31256	terminal oxygenase	773	31	43.7	774	2	A28392	penicillin amidase
701	31	43.7	451	2	S75588	phosphomevalonate	774	31	43.7	781	2	A26641	Na+/K+-exchanging
702	31	43.7	451	2	F96546	hypothetical prote	775	31	43.7	797	2	B28551	levanucrase (EC 2
703	31	43.7	452	1	WHUF	phenylalanine 4-mo	776	31	43.7	804	1	Y0MU	sucrose synthase (
704	31	43.7	452	2	A35721	nicotinic acetylch	777	31	43.7	806	2	AD0351	probable exported
705	31	43.7	452	2	G95306	putrescine/ornithi	778	31	43.7	820	2	D81382	probable transmemb
706	31	43.7	452	2	B69229	conserved hypothet	779	31	43.7	842	2	AB2101	mannose-1-phosphat
707	31	43.7	453	1	WRTF	phenylalanine 4-mo	780	31	43.7	891	2	H83218	heme acquisition p
708	31	43.7	453	1	S15758	phenylalanine 4-mo	781	31	43.7	903	2	G87372	TonB-dependent rec
709	31	43.7	456	1	ACCHAN	nicotinic acetylch	782	31	43.7	905	1	IUXLC1	N-cadherin 1 precu
710	31	43.7	456	2	H84278	hypothetical prote	783	31	43.7	906	1	IUXLC2	N-cadherin 2 precu
711	31	43.7	457	1	ACBOA1	nicotinic acetylch	784	31	43.7	915	2	H96709	hypothetical prote
712	31	43.7	457	1	ACHUA1	nicotinic acetylch	785	31	43.7	919	2	T16693	hypothetical prote
713	31	43.7	457	2	A24383	nicotinic acetylch	786	31	43.7	933	2	A59250	myosin - Acetabula
714	31	43.7	457	2	S13872	nicotinic acetylch	787	31	43.7	941	2	T32449	hypothetical prote
715	31	43.7	459	1	S04904	glutamate dehydrog	788	31	43.7	946	2	G71617	SEK1 antigen/papai
716	31	43.7	461	2	B69827	hemolysin homolog	789	31	43.7	957	2	G84528	hypothetical prote
717	31	43.7	464	2	JH0824	gamma-aminobutyric	790	31	43.7	967	1	HXAD2	hexon protein - hu
718	31	43.7	466	2	G98825	hypothetical prote	791	31	43.7	987	2	A64474	hypothetical prote
719	31	43.7	468	2	A38223	nicotinic acetylch	792	31	43.7	1004	2	T00046	surface layer prot
720	31	43.7	471	2	G75627	hypothetical prote	793	31	43.7	1010	2	B37227	Na+/K+-exchanging
721	31	43.7	476	2	C64119	starch synthase (E	794	31	43.7	1013	1	S00801	Na+/K+-exchanging
722	31	43.7	478	2	T03750	violaxanthin de-ep	795	31	43.7	1013	2	C24639	Na+/K+-exchanging
723	31	43.7	478	4	T41193	probable capsid pr	796	31	43.7	1021	1	PWSHNA	Na+/K+-exchanging
724	31	43.7	483	2	JH0532	catalase (EC 1.11.	797	31	43.7	1021	1	S04630	Na+/K+-exchanging
725	31	43.7	487	2	F72126	CI339 hypothetical	798	31	43.7	1021	2	B24862	Na+/K+-exchanging
726	31	43.7	487	2	E86495	conserved hypothet	799	31	43.7	1022	1	S00503	Na+/K+-exchanging
727	31	43.7	487	2	A81545	NADH2 dehydrogenas	800	31	43.7	1022	2	S49127	Na+/K+-exchanging
728	31	43.7	491	2	B70414	hypothetical prote	801	31	43.7	1023	1	A24639	Na+/K+-exchanging
729	31	43.7	492	2	A86940	hypothetical prote	802	31	43.7	1023	1	S24650	Na+/K+-exchanging
730	31	43.7	493	2	T21445	hypothetical prote	803	31	43.7	1023	2	A24414	Na+/K+-exchanging
731	31	43.7	501	2	H95859	probable ABC trans	804	31	43.7	1025	2	A60444	Na+/K+-exchanging
732	31	43.7	519	2	JC4762	RNA-directed RNA p	805	31	43.7	1027	1	PWCCNM	Na+/K+-exchanging
733	31	43.7	527	2	A48076	glucose transporte	806	31	43.7	1030	2	S11034	gene P1 protein -
734	31	43.7	527	2	A45611	probable hexose tr	807	31	43.7	1055	2	T05663	hypothetical prote
735	31	43.7	529	2	T33738	hypothetical prote	808	31	43.7	1055	2	T05663	acidic nuclear pro
736	31	43.7	534	2	E96661	GMP synthase, 6170	809	31	43.7	1063	2	A40253	hypothetical prote
737	31	43.7	538	2	C96976	PPE-family protein	810	31	43.7	1063	2	D83789	alkaline amylopull
738	31	43.7	539	2	A70899	probable PPE prote	811	31	43.7	1072	2	A84112	membrane protein p
739	31	43.7	548	2	D75103	hypothetical prote	812	31	43.7	1112	2	H95964	probable outer mem
740	31	43.7	548	2	T22137	hypothetical prote	813	31	43.7	1123	2	D36790	hypothetical prote
741	31	43.7	550	2	T26562	hypothetical prote	814	31	43.7	1132	1	OSBPL	host specificity p
742	31	43.7	556	2	E84102	flagellar hook-ass	815	31	43.7	1144	2	A81983	probable DNA-direc
743	31	43.7	563	2	T32479	hypothetical prote	816	31	43.7	1144	2	H81037	DNA polymerase III
744	31	43.7	565	2	T29813	hypothetical prote	817	31	43.7	1155	2	G87477	transcription-repa
745	31	43.7	567	2	AB3023	potassium-transpor	818	31	43.7	1170	2	AG3595	transcription-repa
746	31	43.7	567	2	H98261	hypothetical prote	819	31	43.7	1234	2	S72640	endo-1,4-beta-xyla
747	31	43.7	567	2	G90537	lipoprotein (impor	820	31	43.7	1257	2	AC2841	methionine synthas
748	31	43.7	567	2	T40057	probable single-st	821	31	43.7	1259	2	E97618	methionine synthas
749	31	43.7	580	2	T30583	probable peptide a	822	31	43.7	1275	2	T41523	hypothetical rho1
750	31	43.7	583	2	S36781	esterase D - Pseud	823	31	43.7	1286	2	T33476	hypothetical prote
751	31	43.7	592	2	H83580	probable acyl-coA	824	31	43.7	1345	2	B71608	DNA-directed RNA p
752	31	43.7	598	2	T33240	hypothetical prote	825	31	43.7	1379	2	S64603	YTA7 protein - yea
753	31	43.7	617	2	T49535	probable multifunc	826	31	43.7	1528	2	T14279	myosin-like protei
754	31	43.7	638	2	T47569	hypothetical prote	827	31	43.7	1588	2	A86036	probable adhesin z
755	31	43.7	640	2	B84478	probable replicati	828	31	43.7	1588	2	H91188	probable adhesin E
756	31	43.7	642	2	T45298	dnak-type molecula	829	31	43.7	1661	2	H71439	hypothetical prote
757	31	43.7	651	2	AD3064	acetoacetyl-CoA sy	830	31	43.7	2150	1	GNNYH2	genome polyprotein
758	31	43.7	651	2	D98222	acetoacetyl-CoA sy	831	31	43.7	2164	1	GNNYH9	genome polyprotein
759	31	43.7	653	1	S44749	C06G4.2 protein -	832	31	43.7	2352	2	C83229	probable non-ribos

833	31	43.7	2422	2	T12687	ALR protein homolo	906	30	42.3	117	2	S31109	Ig heavy chain - h
834	31	43.7	2657	2	T18497	hypothetical prote	907	30	42.3	117	2	B33989	Ig heavy chain v-2
835	31	43.7	3110	2	AC0116	probable virulence	908	30	42.3	117	2	S78486	Ig heavy chain v r
836	31	43.7	4152	2	T31102	filamentous hemagg	909	30	42.3	118	2	S38491	Ig heavy chain - h
837	31	43.7	4910	2	S64942	probable membrane	910	30	42.3	118	2	S36265	Ig heavy chain v r
838	31	43.7	4919	2	T31105	hypothetical prote	911	30	42.3	119	2	S24665	Ig heavy chain v r
839	30.5	43.0	228	2	C36794	hypothetical prote	912	30	42.3	119	2	S24657	Ig heavy chain v r
840	30.5	43.0	253	2	AB0327	conserved hypothet	913	30	42.3	119	2	S24662	Ig heavy chain v r
841	30.5	43.0	289	1	SYRCSA	succinate-CoA liga	914	30	42.3	119	2	S24659	Ig heavy chain v r
842	30.5	43.0	289	2	AG0591	succinyl-CoA synth	915	30	42.3	119	2	S31107	Ig heavy chain - h
843	30.5	43.0	289	2	B90723	succinyl-CoA synth	916	30	42.3	119	2	C36005	Ig heavy chain v r
844	30.5	43.0	289	2	A85574	succinyl-CoA synth	917	30	42.3	119	2	S31108	Ig heavy chain - h
845	30.5	43.0	315	1	A28626	Shigella toxin cha	918	30	42.3	119	2	S09955	Ig heavy chain v-D
846	30.5	43.0	315	1	UN07P9	Shiga-like toxin c	919	30	42.3	119	2	P80091	Ig heavy chain v r
847	30.5	43.0	315	2	JX0582	Shiga-like toxin I	920	30	42.3	120	2	S24654	Ig heavy chain v r
848	30.5	43.0	315	2	F91000	Shiga toxin I subu	921	30	42.3	120	2	S24664	Ig heavy chain v r
849	30.5	43.0	315	2	H85845	Shiga toxin I subu	922	30	42.3	120	2	S44111	Ig heavy chain v-D
850	30.5	43.0	315	2	A53887	Shiga-like toxin I	923	30	42.3	120	2	S31112	Ig heavy chain - h
851	30.5	43.0	367	2	AB0942	hypothetical prote	924	30	42.3	120	2	S24697	Ig heavy chain v6
852	30.5	43.0	367	2	T09376	hypothetical prote	925	30	42.3	120	2	S48798	Ig heavy chain v r
853	30.5	43.0	407	2	T40582	hypothetical prote	926	30	42.3	120	2	PH0962	Ig heavy chain v r
854	30.5	43.0	435	2	AF3013	tolB protein limpo	927	30	42.3	120	2	S36273	Ig heavy chain v r
855	30.5	43.0	437	1	VCEVCV	major capsid prote	928	30	42.3	120	2	S36278	Ig heavy chain v r
856	30.5	43.0	443	2	A98271	colB protein precu	929	30	42.3	120	2	S31999	Ig heavy chain v r
857	30.5	43.0	590	2	I39685	polyhydroxyalkanoi	930	30	42.3	120	2	B42848	L6 mAb heavy chain
858	30.5	43.0	631	1	E32227	mercury(II) reduct	931	30	42.3	121	2	P80089	Ig heavy chain v r
859	30.5	43.0	664	2	D84374	hypothetical prote	932	30	42.3	121	2	S24660	Ig heavy chain v r
860	30.5	43.0	675	2	T47378	probable transposa	933	30	42.3	121	2	H36005	Ig heavy chain v r
861	30.5	43.0	794	2	T36972	probable membrane	934	30	42.3	121	2	I56673	Ig heavy chain - h
862	30.5	43.0	806	2	T01164	hypothetical prote	935	30	42.3	121	2	S19686	Ig heavy chain v r
863	30.5	43.0	819	2	AB4504	Mutator-like trans	936	30	42.3	121	2	S20783	Ig heavy chain v r
864	30.5	43.0	996	2	D86872	beta-galactosidase	937	30	42.3	121	2	S26798	Ig heavy chain v r
865	30.5	43.0	1362	2	A75207	amylopullulanase P	938	30	42.3	121	2	H27888	Ig heavy chain v r
866	30	42.3	16	2	S03532	Ig heavy chain J r	939	30	42.3	121	2	G36005	Ig heavy chain v r
867	30	42.3	16	2	D49021	Ig heavy chain J7	940	30	42.3	122	2	S31117	Ig heavy chain - h
868	30	42.3	27	2	S31605	Ig heavy chain v r	941	30	42.3	122	2	S36271	Ig heavy chain v r
869	30	42.3	53	2	B36005	Ig heavy chain v r	942	30	42.3	122	2	S31675	Ig heavy chain v r
870	30	42.3	76	2	S31592	Ig heavy chain v r	943	30	42.3	122	2	S69910	Ig V-D-J region (K
871	30	42.3	80	2	A84528	hypothetical prote	944	30	42.3	122	2	PC4279	anti-SS-A/RO 60K p
872	30	42.3	83	2	S34151	Ig mu chain - axol	945	30	42.3	122	2	PC4280	anti-SS-A/RO 60K p
873	30	42.3	83	2	S21593	Ig heavy chain v r	946	30	42.3	123	2	A36006	Ig heavy chain v r
874	30	42.3	84	2	S62867	toxin gamma precu	947	30	42.3	123	2	S24701	Ig heavy chain v6
875	30	42.3	85	2	AC1066	hypothetical prote	948	30	42.3	123	2	S31114	Ig heavy chain - h
876	30	42.3	86	2	S39579	DNA-directed RNA p	949	30	42.3	123	2	S24693	Ig heavy chain v6
877	30	42.3	86	2	S26788	Ig heavy chain v r	950	30	42.3	123	2	S24684	Ig heavy chain v6
878	30	42.3	86	2	D33989	Ig heavy chain v-4	951	30	42.3	123	2	S24685	Ig heavy chain v6
879	30	42.3	90	2	A03625	cell division inhi	952	30	42.3	123	2	PH1413	Ig heavy chain v r
880	30	42.3	90	2	AB1459	B. subtilis Yaza p	953	30	42.3	123	2	S33548	Ig heavy chain v-1
881	30	42.3	107	1	MNNZLG	gene 1 protein - p	954	30	42.3	124	2	D34653	Ig heavy chain v r
882	30	42.3	108	2	PH1664	Ig heavy chain v r	955	30	42.3	124	2	S24653	Ig heavy chain v r
883	30	42.3	108	2	PH0248	Ig heavy chain v r	956	30	42.3	124	2	A49002	Ig heavy chain v r
884	30	42.3	109	2	PH1653	Ig heavy chain v r	957	30	42.3	124	2	S20782	Ig heavy chain v r
885	30	42.3	109	2	PH1023	Ig heavy chain v r	958	30	42.3	125	2	S24688	Ig heavy chain v6
886	30	42.3	109	2	S23942	Ig heavy chain v r	959	30	42.3	125	2	S20785	Ig heavy chain v r
887	30	42.3	109	2	PH1671	spermadhesin PSP-I	960	30	42.3	125	2	S24700	Ig heavy chain v6
888	30	42.3	109	2	PH1646	Ig heavy chain v r	961	30	42.3	125	2	S30531	Ig heavy chain v r
889	30	42.3	109	2	PH1644	Ig heavy chain v r	962	30	42.3	126	2	PH1412	Ig heavy chain v r
890	30	42.3	111	2	PH1007	Ig heavy chain v r	963	30	42.3	126	2	C33989	Ig heavy chain v-3
891	30	42.3	111	2	PH1643	Ig heavy chain v r	964	30	42.3	127	2	PH1409	Ig heavy chain - h
892	30	42.3	112	2	PH1654	Ig heavy chain v r	965	30	42.3	127	2	S38489	Ig heavy chain v r
893	30	42.3	112	2	PH1654	Ig heavy chain v r	966	30	42.3	127	2	PH1411	Ig heavy chain v r
894	30	42.3	114	2	S46390	Ig heavy chain v r	967	30	42.3	129	2	A33548	Ig heavy chain v-1
895	30	42.3	114	2	S46391	Ig heavy chain v r	968	30	42.3	129	2	S03534	Ig heavy chain pre
896	30	42.3	114	2	S31120	Ig heavy chain - h	969	30	42.3	129	2	A95172	Ig heavy chain v r
897	30	42.3	115	2	S24663	Ig heavy chain v r	970	30	42.3	129	2	A98038	hypothetical prote
898	30	42.3	115	2	S44112	Ig heavy chain v r	971	30	42.3	130	2	S31690	Ig heavy chain v r
899	30	42.3	115	2	A25803	Ig heavy chain v r	972	30	42.3	130	2	S31601	Ig heavy chain v r
900	30	42.3	115	2	S19968	Ig heavy chain v r	973	30	42.3	130	2	S65682	elkP protein - Sta
901	30	42.3	116	1	M3HUGL	Ig heavy chain v-1	974	30	42.3	130	2	PL0098	Ig heavy chain pre
902	30	42.3	116	2	T08098	probable DNA misma	975	30	42.3	132	2	S31603	Ig heavy chain v r
903	30	42.3	117	2	S24658	Ig heavy chain v r	976	30	42.3	132	2	PH1427	Ig heavy chain v r
904	30	42.3	117	2	S24656	Ig heavy chain v r	977	30	42.3	134	2	S31699	Ig heavy chain v r
905	30	42.3	117	2	S24661	Ig heavy chain v r	978	30	42.3	134	2	S31679	Ig heavy chain v r

979 30 42.3 135 2 S31598 Ig heavy chain V r
980 30 42.3 135 2 B31933 Ig heavy chain pre
981 30 42.3 136 2 PH1539 Ig heavy chain V r
982 30 42.3 136 2 JQ1359 C2 protein - Misc
983 30 42.3 137 2 I51292 aldolase A - chick
984 30 42.3 137 2 PH1562 Ig heavy chain V r
985 30 42.3 137 2 C45893 T-cell receptor al
986 30 42.3 137 2 T12880 hypothetical prote
987 30 42.3 138 2 A35676 Ig heavy chain pre
988 30 42.3 138 2 C28035 Ig heavy chain V-I
989 30 42.3 138 2 A28035 Ig heavy chain V-I
990 30 42.3 138 2 S31513 Ig heavy chain - h
991 30 42.3 138 2 D28035 Ig heavy chain V-I
992 30 42.3 138 2 B28035 Ig heavy chain V-I
993 30 42.3 138 2 S03526 Ig heavy chain pre
994 30 42.3 139 2 PH1558 Ig heavy chain pre
995 30 42.3 139 2 S01158 Ig variable region
996 30 42.3 140 2 I37782 Ig heavy chain pre
997 30 42.3 140 2 S78052 Ig heavy chain V r
998 30 42.3 140 2 S31686 Ig heavy chain pre
999 30 42.3 140 2 S22657 Ig heavy chain V r
1000 30 42.3 140 2 A49045 Ig heavy chain V r

ALIGNMENTS

RESULT 1
F71351
probable preprotein translocase subunit (secY) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: F71351
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: F71351
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-450 <COL>
A:Cross-references: UNIPROT:O83238; UNIPARC:UPI00000D3218; GB:AE001203; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0208
C:Superfamily: preprotein translocase secY

Query Match 60.6%; Score 43; DB 2; Length 450;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YGGQSTTV 10
|||
Db 253 YGGQSTVI 260
|||
RESULT 2
AH0366
probable sugar transporter YPO3016 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C:Accession: AH0366
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0366
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-510 <KUR>
A:Cross-references: UNIPARC:UPI00000DCA01; GB:AL590842; PIDN:CAC922259.1; PID:G15980970;
C:Genetics:
A:Gene: YPO3016

Query Match 60.6%; Score 43; DB 2; Length 510;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMDA 13
:|||
Db 138 EYGSSTYVMES 149
:|||

RESULT 3
T33749
hypothetical protein R11E3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33749
R:Langston, Z.; Wohldmann, P.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid R11E3.
A:Reference number: Z21397
A:Accession: T33749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-909 <LAN>
A:Cross-references: UNIPROT:Q9TYX3; UNIPARC:UPI000007F9EE; EMBL:AF100669; PIDN:AAC68991.
A:Experimental source: strain Bristol N2; clone R11E3
C:Genetics:
A:Gene: CESP:R11E3.6
A:Map position: 4
A:Introns: 28/1; 121/3; 159/3; 207/2; 265/2; 351/2; 376/1; 437/3; 504/1; 565/2; 599/1; 6
F:28-129/Domain: POZ domain homology <POZ>

Query Match 57.7%; Score 41; DB 2; Length 909;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
:|||
Db 736 NDYGGPSTY 744
:|||

RESULT 4
A95017
ABC transporter, substrate-binding protein SP0148 [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95017
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, .
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <KUR>
A:Cross-references: UNIPROT:Q97T12; UNIPARC:UPI0000051305; GB:AE005672; PIDN:AAK74330.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0148

Query Match 56.3%; Score 40; DB 2; Length 276;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
:|||


```

Db      141 DDIGKSTEVVQA 153

RESULT 5
B97890
hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B97890
R:Hoskins, J.A.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A37872; MUID:21429245; PMID:11544234
A:Accession: B97890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <KUR>
A:Cross-references: UNIPROT:Q8DRG2; UNIPARC:UPI00000E33C4; GB:AE007317; PIDN:AAK98950.1;
C:Genetics:
A:Gene: ABC-SBP

Query Match      56.3%; Score 40; DB 2; Length 276;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGQSTYVMDA 13
      |||||:|
Db      141 DDIGKSTEVVQA 153

RESULT 6
D81032
hypothetical protein NMB1870 [imported] - Neisseria meningitidis (strain MC58 serogroup
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81032
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81032
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <TET>
A:Cross-references: UNIPROT:Q9JXV4; UNIPARC:UPI00000C47F4; GB:AE002537; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1870
C:Superfamily: Neisseria meningitidis probable lipoprotein NMA0586

Query Match      56.3%; Score 40; DB 2; Length 320;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DDYGQSTYVMD 12
      |||||:|
Db      225 DDAGGKLYTID 236

RESULT 7
T18396
erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fragm
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18396
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.
Cell 82, 77-87, 1995

Query Match      54.9%; Score 39; DB 2; Length 2924;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9
      |||||:
Db      90 DEYGGQCTF 98

Query Match      54.9%; Score 39; DB 2; Length 1729;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9
      |||||:
Db      90 DEYGGQCTF 98

RESULT 8
T16199
hypothetical protein F28B4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16199
R:Leimbach, D.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F28B4.
A:Reference number: Z18475
A:Accession: T16199
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2229 <LEI>
A:Cross-references: UNIPROT:Q19853; UNIPARC:UPI000007A3FF; EMBL:U42834; NID:g1125756; P1
C:Genetics:
A:Gene: CESP:F28B4.3
A:Introns: 60/3; 98/1; 305/3; 326/1; 383/1; 407/1; 471/1; 510/2; 550/3; 598/3; 1535/1; 1

Query Match      54.9%; Score 39; DB 2; Length 2229;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9
      |||||:
Db      1167 DDTGQSVY 1175

RESULT 9
T18378
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18378
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T
Cell 82, 77-87, 1995
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and
A:Reference number: Z18925; MUID:95330812; PMID:7541722
A:Accession: T18378
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2924 <BAR>
A:Cross-references: UNIPROT:Q25733; UNIPARC:UPI0000079077; EMBL:U27338; NID:g914918; PID
C:Genetics:
A:Gene: EMP1
A:Introns: 2476/3

Query Match      54.9%; Score 39; DB 2; Length 2924;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9

```

```

A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and
A:Reference number: Z18925; MUID:95330812; PMID:7541722
A:Accession: T18396
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1729 <BAR>
A:Cross-references: UNIPROT:Q25734; UNIPARC:UPI0000082845; EMBL:U27339; NID:g914920; PID
C:Genetics:
A:Gene: EMP1
A:Note: var-2

Query Match      54.9%; Score 39; DB 2; Length 1729;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9
      |||||:
Db      90 DEYGGQCTF 98

RESULT 8
T16199
hypothetical protein F28B4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16199
R:Leimbach, D.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F28B4.
A:Reference number: Z18475
A:Accession: T16199
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2229 <LEI>
A:Cross-references: UNIPROT:Q19853; UNIPARC:UPI000007A3FF; EMBL:U42834; NID:g1125756; P1
C:Genetics:
A:Gene: CESP:F28B4.3
A:Introns: 60/3; 98/1; 305/3; 326/1; 383/1; 407/1; 471/1; 510/2; 550/3; 598/3; 1535/1; 1

Query Match      54.9%; Score 39; DB 2; Length 2229;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9
      |||||:
Db      1167 DDTGQSVY 1175

RESULT 9
T18378
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18378
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T
Cell 82, 77-87, 1995
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and
A:Reference number: Z18925; MUID:95330812; PMID:7541722
A:Accession: T18378
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2924 <BAR>
A:Cross-references: UNIPROT:Q25733; UNIPARC:UPI0000079077; EMBL:U27338; NID:g914918; PID
C:Genetics:
A:Gene: EMP1
A:Introns: 2476/3

Query Match      54.9%; Score 39; DB 2; Length 2924;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DDYGQSTY 9

```


Db 90 DYGGQCTF 98
|:|||||:

RESULT 10

S34152
Ig mu chain - axolotl (fragment)
C:Species: Ambystoma mexicanum (axolotl)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S34152
R:Fellah, J.S.; Jacques, C.; Charlemagne, J.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34149
A:Accession: S34152
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <FEL>
A:Cross-references: UNIPARC:UPI0000116C7D; EMBL:X73557; NID:G313184; PID:G313185
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-116/Domain: immunoglobulin homology <IMM>

Query Match 53.5%; Score 38; DB 2; Length 137;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DYGGQSTYV 10
||| |||

Db 124 DYWGQGTIV 132
||| |||

RESULT 11

AE2876
conserved hypothetical protein Atu2439 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Dec-2002
C:Accession: AE2876
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2876
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <KUR>
A:Cross-references: UNIPARC:UPI0000164716; GB:AE008688; PIDN:AAL43427.1; PID:g17740928;
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: Atu2439
A:Map position: circular chromosome
C:Superfamily: uncharacterized conserved protein

Query Match 53.5%; Score 38; DB 2; Length 196;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYV 11
|||||

Db 117 DYGGQGTIV 126
|||||

RESULT 12

G97652
hypothetical protein AGR_C_4424 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Dec-2002
C:Accession: G97652
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97652
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <KUR>
A:Cross-references: UNIPARC:UPI00000D1EDC; GB:AE007869; PIDN:AAK88176.1; PID:g15157620;
C:Genetics:
A:Gene: AGR_C_4424
A:Map position: circular chromosome
C:Superfamily: uncharacterized conserved protein

Query Match 53.5%; Score 38; DB 2; Length 198;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYV 11
|||||

Db 119 DYGGQGTIV 128
|||||

RESULT 13

T17207
hypothetical protein DKFZps86F0222.1 - human
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17207
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: T17207
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-215 <KOE>
A:Cross-references: UNIPROT:P31942; UNIPARC:UPI000002B2A1; EMBL:AL117395
A:Experimental source: adult uterus; clone DKFZps86F0222
C:Genetics:

A:Note: DKFZps86F0222.1
C:Superfamily: glycine-rich cell wall structural protein 1

Query Match 53.5%; Score 38; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
|||||

Db 20 DDYGGYNNY 28
|||||

RESULT 14

E64411
flagellin B3 precursor - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: E64411
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: E64411
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <BUL>

A:Cross-references: UNIPARC:UPI0000165FD5; GB:U67533; GB:I77117; NID:G2826346; PIDN:AAB9
C:Comment: Homology to other archaeal flagellins suggests that translation should begin
C:Genetics:
A:Gene: flaB3
A:Map position: FOR823179-823850
A:Start codon: TTG

C:Superfamily: archaeal flagellin

C:Keywords: flagellum

F:1-18/Domain: (or 8-18) signal sequence #status predicted <SIG>
F:19-223/Product: flagellin B3 #status predicted <MAT>

Query Match 53.5%; Score 38; DB 1; Length 223;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGGQSTTV 10
|||||
DB 118 YGGQITTV 125

RESULT 15

D96648

Hypothetical protein F19K23.12 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D96648

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: D96648

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-295 <STO>

A:Cross-references: UNIPROT:O04584; UNIPARC:UPI00000AB14C; GB:AE005173; NID:G2160143; PI

C:Genetics:

A:Gene: F19K23.12

A:Map position: 1

Query Match 53.5%; Score 38; DB 2; Length 295;
Best Local Similarity 53.8%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTTVMDA 13
|:|:|:|:|:|:|
DB 123 DNYGGASTPIVGA 135

RESULT 16

T44109

conserved hypothetical protein [imported] - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44109

R:Ito, T.; Katayama, Y.; Hiramatsu, K.

Antimicrob. Agents Chemother. 43, 1449-1458, 1999

A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth

A:Reference number: Z22733; MUID:99278010; PMID:10348769

A:Accession: T44109

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-354 <ITO>

A:Cross-references: UNIPROT:Q9XB85; UNIPARC:UPI0000006C7D; EMBL:D86934; PIDN:BAA82211.1

A:Experimental source: strain N315

Query Match 53.5%; Score 38; DB 2; Length 354;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DYGGQSTTV 10
|||||
DB 334 DYGGVGTVI 342

RESULT 17

D86153

Hypothetical protein T6A9.1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D86153

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: D86153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <STO>

A:Cross-references: UNIPROT:Q9FZ29; UNIPARC:UPI00000AC4D2; GB:AE005172; NID:G9857528; P

C:Genetics:

A:Map position: 1

Query Match 53.5%; Score 38; DB 2; Length 411;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTTV 10
|:|:|:|:|:|:|
DB 135 EDYGGKKYV 144

RESULT 18

H87370

major facilitator family transporter CC0980 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: H87370

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: H87370

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-567 <STO>

A:Cross-references: UNIPROT:Q9A9K0; UNIPARC:UPI000000C7228; GB:AE005673; NID:G13422262; F

C:Genetics:

A:Gene: CC0980

Query Match 53.5%; Score 38; DB 2; Length 567;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DYGGQSTTVMD 12
|:|:|:|:|:|:|
DB 152 EYGGAAITVAE 162

RESULT 19

A12882

MFS permease [sugar] [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: A12882

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AF2882
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-614 <KUR>
 A:Cross-references: UNIPROT:Q8UCJ2; UNIPARC:UPI0000164720; GB:AE008688; PIDN:AAL43479.1;
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: mtbA
 A:Map position: circular chromosome

 Query Match 53.5%; Score 38; DB 2; Length 614;
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 DYGGQSTYVMD 12
 :|||:||||:
 Db 126 EYGAATYVAE 136

 RESULT 20
 A70525
 hypothetical protein Rv0312 - *Mycobacterium tuberculosis* (strain H37RV)
 C:Species: *Mycobacterium tuberculosis*
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: A70525
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: A70525
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-620 <COL>
 A:Cross-references: UNIPROT:Q07239; UNIPARC:UPI00000D10D7; GB:Z96800; GB:AL123456; NID:9
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv0312

 Query Match 53.5%; Score 38; DB 2; Length 620;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 DYGGQSTYV 10
 :|||:||||:
 Db 165 DFGGSATYV 173

 RESULT 21
 AE3560
 proline/betaine transporter BMEI10406 [imported] - *Brucella melitensis* (strain 16M)
 C:Species: *Brucella melitensis*
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AE3560
 R:DeLVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Levese
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AE3560
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-632 <KUR>
 A:Cross-references: UNIPROT:Q8YCX2; UNIPARC:UPI0000058485; GB:AE008918; PIDN:AAL53648.1;
 A:Experimental source: strain 16M

C:Genetics:
 A:Gene: BMEI10406
 A:Map position: II

 Query Match 53.5%; Score 38; DB 2; Length 632;
 Best Local Similarity 54.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 DYGGQSTYVMD 12
 :|||:||||:
 Db 139 EYGAATYVAE 149

 RESULT 22
 G97658
 hypothetical protein AGR_C_4527 [imported] - *Agrobacterium tumefaciens* (strain C58, Cere
 C:Species: *Agrobacterium tumefaciens*
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: G97658
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G97658
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-657 <KUR>
 A:Cross-references: UNIPROT:Q8UCJ2; UNIPARC:UPI00000D1F0E; GB:AE007869; PIDN:AAK88224.1;
 C:Genetics:
 A:Gene: AGR_C_4527
 A:Map position: circular chromosome

Query Match 53.5%; Score 38; DB 2; Length 657;
 Best Local Similarity 54.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 DYGGQSTYVMD 12
 :|||:||||:
 Db 169 EYGAATYVAE 179

RESULT 23
 D72278
 endo-1,4-beta-mannosidase - *Thermotoga maritima* (strain MSB8)
 C:Species: *Thermotoga maritima*
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: D72278
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.

Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: D72278
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-669 <ARN>
 A:Cross-references: UNIPROT:Q9XOV4; UNIPARC:UPI00000D38F2; GB:AE001779; GB:AE000512; NID
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1227

Query Match 53.5%; Score 38; DB 2; Length 669;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 DDYGGQSTYV 10
 :|||:||||:
 Db 136 DDFGGMQYV 145

RESULT 24

AI2428
sucrose synthase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AI2428
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurtz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2428
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-806 <KUR>
A:Cross-references: UNIPROT:Q8YME9; UNIPARC:UIP00000CED07; GB:BAO00019; PIDN:EAB76684.1.
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: susA
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match 53.5%; Score 38; DB 2; Length 806;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGGQSTYVMD 12
| | | | |
Db 292 DTGGGVVVLD 302

RESULT 25
B86194
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86194
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86194
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1251 <STO>
A:Cross-references: UNIPROT:Q9MA34; UNIPARC:UIP00000AA4622; GB:AE005172; NID:g6850321; PI
C:Genetics:
A:Map position: 1

Query Match 53.5%; Score 38; DB 2; Length 1251;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGGQSTYVMD 12
| | | | |
Db 422 DDIGGLSEYIND 433

RESULT 26
T32452
hypothetical protein F48A11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32452
R;Bradshaw, H.
submitted to the EMBL Data Library, September 1997
A>Description: The sequence of C. elegans cosmid F48A11.

A:Reference number: Z21171
A:Accession: T32452
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1635 <BRA>
A:Cross-references: UNIPROT:O17368; UNIPARC:UPI000007ACA2; EMBL:AF026210; PIDN:AAB71283
A:Experimental source: strain Bristol N2; clone F48A11
C:Genetics:
A:Gene: CESP:F48A11.1
A:Map position: 2
A:Introns: 84/2, 108/1, 198/2, 293/3, 336/2, 477/3, 560/3, 612/2, 719/2, 952/2, 1371/1, 1371/1;
Query Match 53.5%; Score 38; DB 2; Length 1635;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YGGQSTYVM 11
Db 799 YGGKTYIM 807
|||||:|:|

RESULT 27
T28432
Variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28432
R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, P.; Herrfeldt, J.A.; Peterson, D.; Cell 82, 89-100, 1995
A:Title: The large diverse gene family var encodes proteins involved in cytoadherence at A:Reference number: Z20487; MUID:95330813; PMID:7606788
A:Accession: T28432
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3078 <SUX>
A:Cross-references: UNIPROT:Q26031; UNIPARC:UPI00000820C2; EMBL:L40608; NID:9886374; PFI C:Genetics:
A:Gene: var-1
A:Introns: 2611/3

Query Match 53.5%; Score 38; DB 2; Length 3078;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
Db 100 DEYGGQCTH 108
|:|||||:

RESULT 28
VF1HB1
F1 protein - avian infectious bronchitis virus (strain Beaudette)
C:Species: avian infectious bronchitis virus, IBV
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A33094
R:Bourgnell, M.E.G.; Brown, T.D.K.; Foulds, I.J.; Green, P.F.; Tomley, F.M.; Binns, M.M. J. Gen. Virol. 68, 57-77, 1987
A:Title: Completion of the sequence of the genome of the coronavirus avian infectious br A:Reference number: A33094; MUID:87111468; PMID:3027249
A:Accession: A33094
A:Molecule type: genomic RNA
A:Residues: 1-3951 <BOU>
A:Cross-references: UNIPROT:P27920; UNIPARC:UPI000001015; GB:M94356; GB:M29496; NID:933 C:Superfamily: avian infectious bronchitis virus F1 protein

Query Match 53.5%; Score 38; DB 1; Length 3951;
Best Local Similarity 60.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
Db 1972 DDYGHQNTFM 1981
|||||:|:|

RESULT 29
168600
dipeptidyl aminopeptidase like protein - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I68600
R:Yokotani, N.; Doi, K.; Wenthhold, R.J.; Wada, K.
Hum. Mol. Genet. 2, 1037-1039, 1993
A:Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related
A:Reference number: 154331; MUID:93372805; PMID:8103397
A:Accession: I68600
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-803 <RES>
A:Cross-references: UNIPARC:UPI000016A7F9; GB:M96860; NID:g306707; PIDN:AAA35761.1; PID:
C:Superfamily: dipeptidyl-peptidase IV

Query Match 52.8%; Score 37.5; DB 2; Length 803;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 2 DYGGQ-STYVMDA 13
||| |||:
Db 650 DYGYLSTYILPA 662

RESULT 30
154331
dipeptidyl aminopeptidase like protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I54331
R:Yokotani, N.; Doi, K.; Wenthhold, R.J.; Wada, K.
Hum. Mol. Genet. 2, 1037-1039, 1993
A:Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related
A:Reference number: 154331; MUID:93372805; PMID:8103397
A:Accession: I54331
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-865 <RES>
A:Cross-references: UNIPROT:P42658; UNIPARC:UPI0000047378; GB:M96859; NID:g306705; PIDN:
C:Superfamily: dipeptidyl-peptidase IV

Query Match 52.8%; Score 37.5; DB 2; Length 865;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 2 DYGGQ-STYVMDA 13
||| |||:
Db 712 DYGYLSTYILPA 724

RESULT 31
A49026
Ig heavy chain V region, anti-idiotypic monoclonal antibody - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: A49026
R:Kozumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
Eur. J. Immunol. 21, 2185-2193, 1991
A:Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MUR-lpr/lpr mice.
A:Reference number: A49026; MUID:91364791; PMID:1909645
A:Accession: A49026
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-118 <KOI>
A:Cross-references: UNIPARC:UPI0000176BFC
A:Experimental source: MUR-lpr/lpr
A>Note: sequence extracted from NCBI backbone (NCBIP:60853)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 52.1%; Score 37; DB 2; Length 118;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMDA 13
:| ||| |:
Db 52 NYDGSSTYILDS 63

RESULT 32
S18459
gamma-crystallin m1 - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: S18459
R;Chang, T.; Lin, C.L.; Chen, P.H.; Chang, W.C.
Biochim. Biophys. Acta 1090, 261-264, 1991
A:Title: Gamma-crystallin genes in carp: cloning and characterization.
A:Reference number: S18459; MUID:92031705; PMID:1840497
A:Accession: S18459
A:Molecule type: DNA
A:Residues: 1-178 <CHA>
A:Cross-references: UNIPROT:P10043; UNIPARC:UPI00001711CD; EMBL:X55945; NID:G62605; PIDN:
A>Note: the authors translated the codon GAC for residue 8 as Glu and AGA for residue 9
C:Genetics:
A:Introns: 3/3; 87/3
C:Superfamily: beta-crystallin
C:Keywords: duplication; eye lens

Query Match 52.1%; Score 37; DB 2; Length 178;
Best Local Similarity 58.3%; Pred. No. 48;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|: ||| |:
Db 100 DNFGGQMHEVMD 111

RESULT 33
S50006
preprotein translocase secY - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 13-Jan-1995 #sequence_revision 12-Dec-1997 #text_change 24-Apr-1998
C:Accession: S50006
R:Loriaux, A.; Brans, A.; Dusat, J.
submitted to the EMBL Data Library, November 1994
A:Description: Cloning and sequencing of the secY locus from Streptomyces coelicolor A3(1)
A:Reference number: S50000
A:Accession: S50006
A:Molecule type: DNA
A:Residues: 1-437 <LOR>
A:Cross-references: UNIPARC:UPI00001787AB; EMBL:X83011; NID:G600030; PID:G600037
C:Genetics:
A:Gene: secY
A:Start codon: GTG
C:Superfamily: preprotein translocase secY
C:Keywords: protein transport; transmembrane protein

Query Match 52.1%; Score 37; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YGGQSTYV 10
||| |:
Db 260 YGGTSTYI 267

RESULT 34
JC5115
preprotein translocase secY - Streptomyces lividans
N;Alternate names: SecY protein

```
C:Species: Streptomyces lividans
C:Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: JCS115; PC4232
R:Ostiguy, S.; Gilbert, M.; Shareck, F.; Kluepfel, D.; Morosoli, R.
Gene 176, 265-267, 1996
A:Title: Cloning and sequencing of the secY homolog from Streptomyces lividans 1326.
A:Reference number: JCS115; MUID:97075942; PMID:8918465
A:Accession: JCS115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <OST>
A:Cross-references: UNIPROT:P49977; UNIPARC:UPI00001357F9; GB:U27324; NID:g862995; PIDN:
A:Accession: PC4232
A:Status: preliminary
A:Molecule type: protein
A:Residues: 78-85; 276-282 <OS2>
A:Cross-references: UNIPARC:UPI00001787AC; UNIPARC:UPI00001787AD
C:Genetics:
A:Gene: secY
A:Start codon: GTG
C:Superfamily: preprotein translocase secY
C:Keywords: protein transport; transmembrane protein

Query Match 52.1%; Score 37; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGGQSTYV 10
||| |||
Db 260 YGGTSTYI 267

RESULT 35
JC4288
preprotein translocase secY - Streptomyces scabies
C:Species: Streptomyces scabies
C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4288
R:Hale, V.A.; O'Brien, I.; Schottel, J.L.
Gene 163, 87-92, 1995
A:Title: Cloning and sequencing of a secY homolog from Streptomyces scabies.
A:Reference number: JC4288; MUID:96001249; PMID:7557484
A:Accession: JC4288
A:Molecule type: DNA
A:Residues: 1-437 <HAL>
A:Cross-references: UNIPROT:P43416; UNIPARC:UPI00001357FA; GB:U19606; NID:g639485; PIDN:
C:Comment: This protein is an integral transmembrane component of prokaryotic protein tr
translocase complex.
C:Genetics:
A:Gene: secY
A:Start codon: GTG
C:Superfamily: preprotein translocase secY
C:Keywords: protein transport; transmembrane protein
F:22-35/Domain: transmembrane #status predicted <TM1>
F:76-92/Domain: transmembrane #status predicted <TM2>
F:123-132/Domain: transmembrane #status predicted <TM3>
F:161-173/Domain: transmembrane #status predicted <TM4>
F:189-205/Domain: transmembrane #status predicted <TM5>
F:226-235/Domain: transmembrane #status predicted <TM6>
F:278-289/Domain: transmembrane #status predicted <TM7>
F:323-332/Domain: transmembrane #status predicted <TM8>
F:378-393/Domain: transmembrane #status predicted <TM9>
F:408-416/Domain: transmembrane #status predicted <TM10>

Query Match 52.1%; Score 37; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGGQSTYV 10
||| |||
Db 260 YGGTSTYI 267
```

```
RESULT 36
S24966
sucrose synthase (EC 2.4.1.13) - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: S24966
R:Brandt, J.; Thordal-Christensen, H.; Collinge, D.B.
submitted to the EMBL Data Library, June 1992
A:Reference number: S24966
A:Accession: S24966
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-586 <BRA>
A:Cross-references: UNIPARC:UPI000016DDE5; EMBL:X66728; NID:g19107; PIDN:CAA47264.1; PI
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:54-528/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 52.1%; Score 37; DB 2; Length 586;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DYGGQSTYVMD 12
||| ||| |||
Db 73 DTGGQVVYILD 83

RESULT 37
T02951
probable mitogen activated protein kinase - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02951
R:Kim, C.Y.; Cheon, S.Y.; Cho, M.J.
submitted to the EMBL Data Library, July 1998
A:Description: Identification and characterization of fungal elicitor responsive rice gr
A:Reference number: Z14788
A:Accession: T02951
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-677 <KIM>
A:Cross-references: UNIPROT:O81637; UNIPARC:UPI00000A443B; EMBL:AF080436; NID:g3450841;
A:Experimental source: cultivar Millyang 117
C:Genetics:
A:Gene: MEK1

Query Match 52.1%; Score 37; DB 2; Length 677;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
||| ||| |||
Db 509 DDGGQQTQHVXD 520

RESULT 38
T14338
sucrose synthase (EC 2.4.1.13) isoform II - carrot
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14338
R:Sturm, A.; Leinhard, S.; Schatt, S.; Hardeggar, M.
Plant Mol. Biol. 39, 349-360, 1999
A:Title: Tissue-specific expression of two genes for sucrose synthase in carrot (Daucus
A:Reference number: Z17990; MUID:99178785; PMID:10080700
A:Accession: T14338
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-801 <STU>
A:Cross-references: UNIPROT:O49845; UNIPARC:UPI0000136273; EMBL:Y16091; NID:g2760540; PI
A:Experimental source: cultivar Namtaise; mature leaves
C:Genetics:
A:Gene: Susy*Dc2
```


A:Description: Nucleotide sequence of a cDNA clone coding for sucrose synthase from carrot
A:Reference number: S37560
A:Accession: S37560
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-808 <STU>
A:Cross-references: UNIPROT:P49035; UNIPARC:UPI000013626D; EMBL:X75332; NID:g406316; PID:P49035
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:281-755/Domain: sucrose-phosphate synthase homology <SSPS>

Query Match 52.1%; Score 37; DB 2; Length 808;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMD 12
| ||| | : |
Db 300 DTGGQVVYILD 310

RESULT 44
S23543
sucrose synthase (EC 2.4.1.13) 1 - rice
N:Alternate names: sucrose-UDP glucosyltransferase 1
C:Species: Oryza sativa (rice)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S23543; S25526
R:Wang, M.B.; Boulter, D.; Gatehouse, J.A.
Plant Mol. Biol. 19, 881-885, 1992
A:Title: A complete sequence of the rice sucrose synthase-1 (RSs1) gene.
A:Reference number: S23543; MUID:92353399; PMID:1386537
A:Accession: S23543
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <WAN>
A:Cross-references: UNIPROT:P30298; UNIPARC:UPI000000008D; EMBL:X64770; NID:g20365; PID:P30298
R:Odegaard, W.; de Lumen, B.O.
submitted to the EMBL Data Library, August 1992
A:Description: Isolation and sequence of a sucrose synthase cDNA from developing rice seed
A:Reference number: S25526
A:Accession: S25526
A:Molecule type: mRNA
A:Residues: 1-190, 'P', 192-808 <ODE>
A:Cross-references: UNIPARC:UPI0000136270; EMBL:Z15028; NID:g20373; PID:CAA78747.1; PID:Z15028
C:Genetics:
A:Introns: 32/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 666/2
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:276-750/Domain: sucrose-phosphate synthase homology <SSPS>

Query Match 52.1%; Score 37; DB 2; Length 808;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMD 12
| ||| | : |
Db 295 DTGGQVVYILD 305

RESULT 45
T49233
sucrose synthase-like protein - Arabidopsis thaliana
N:Alternate names: protein F7K15.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Accession: T49233
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25019
A:Accession: T49233
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <OBE>

A;Cross-references: UNIPROT:Q9LXL5; UNIPARC:UPI00000487BD; EMBL:AL353871; GSPDB:GN00061
A;Experimental source: cultivar Columbia; BAC clone F7K15
C;Genetics:
A;Gene: ATSP:F7K15.40
A;Map position: 3
A;introns: 35/2; 128/2; 192/3; 304/3; 336/3; 394/3; 433/3; 489/2; 564/2; 752/2; 798/3
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match 52.1%; Score 37; DB 2; Length 808;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMD 12
| | | | | : : |
Db 300 DTGGQVWYILD 310

RESULT 46
T01420
sucrose synthase (EC 2.4.1.13) T2H3.8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01420
F;Kalicki, J.; Gibson, A.
submitted to the EMBL Data Library, August 1998
A;Description: The sequence of A. thaliana T2H3.
A;Reference number: Z14324
A;Accession: T01420
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-808 <KAL>
A;Cross-references: UNIPROT:Q9SBD5; UNIPARC:UPI00000A5966; EMBL:AF075597; NID:G3298610;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;introns: 33/2; 77/3; 192/3; 304/3; 327/2; 421/3; 477/2; 552/2; 659/3; 741/2
A;Note: T2H3.8
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
F;281-744/domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 52.1%; Score 37; DB 2; Length 808;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMD 12
| | | | | : : |
Db 300 DTGGQVWYILD 310

RESULT 47
B85029
probable sucrose synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85029
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85029
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-809 <STO>
A;Cross-references: UNIPROT:Q9M111; UNIPARC:UPI00000488E3; GB:NC_001268; NID:g7269888; P
C;Genetics:
A;Gene: AT4g02280
A;Map position: 4
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology

Query Match 52.1%; Score 37; DB 2; Length 809;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;


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Qy      2 DYGGQSTYVMD 12
      |||||  |::|
Db      300 DTGGQVVYILD 310

RESULT 48
T06497
Probable sucrose synthase (EC 2.4.1.13) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06497
R: Buchner, P.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z15720
A:Accession: T06497
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-809 <BUC>
A:Cross-references: UNIPROT:O24301; UNIPARC:UPI0000136276; EMBL:AJ001071; PIDN:CAA04512.
A:Experimental source: cultivar Frisson
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:282-757/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match      52.1%; Score 37; DB 2; Length 809;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DYGGQSTYVMD 12
      |||||  |::|
Db      301 DTGGQVVYILD 311

RESULT 49
S32451
sucrose synthase (EC 2.4.1.13) Ss2 - barley
C:Species: Hordeum vulgare (barley)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S31501
R: Martinez de Ilarduya, O.; Vicente-Carabajosa, J.; Sanchez de la Hoz, P.; Carbonero, P.
FEBS Lett. 320, 177-181, 1993
A:Title: Sucrose synthase genes in barley. cDNA cloning of the Ss2 type and tissue-specific
A:Reference number: S32451; MUID:93209382; PMID:8458435
A:Accession: S32451
A:Molecule type: mRNA
A:Residues: 1-816 <MAR>
A:Cross-references: UNIPROT:P31923; UNIPARC:UPI0000136274; EMBL:X69931; NID:g19099; PIDN
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:284-758/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
F:106,129,146,417,589,640/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      52.1%; Score 37; DB 2; Length 816;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DYGGQSTYVMD 12
      |||||  |::|
Db      303 DTGGQVVYILD 313

RESULT 50
S19139
sucrose synthase (EC 2.4.1.13) 2 - rice
N:Alternate names: sucrose-UDP glucosyltransferase 2
C:Species: Oryza sativa (rice)
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S19139; S77947; S22536
R: Yu, W.P.; Wang, A.Y.; Juang, R.H.; Sung, H.Y.; Su, J.C.
Plant Mol. Biol. 18, 139-142, 1992
A:Title: Isolation and sequences of rice sucrose synthase cDNA and genomic DNA.
A:Reference number: S19139; MUID:92119223; PMID:1531032

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A:Accession: S19139
A:Molecule type: DNA
A:Residues: 1-816 <YUW>
A:Cross-references: UNIPROT:P31924; UNIPARC:UPI00001753C6; EMBL:X59046
A:Accession: S77947
A:Molecule type: mRNA
A:Residues: 1-816 <YUL>
A:Cross-references: UNIPARC:UPI00001753C6; EMBL:X59046
R: Su, J.C.
submitted to the EMBL Data Library, April 1991
A:Reference number: S77943
A:Accession: S77943
A:Molecule type: DNA
A:Residues: 1-447, 'Y', 449-816 <SUJ>
A:Cross-references: UNIPARC:UPI0000000B31; EMBL:X59046; NID:q20094; PIDN:CAA41774.1; PID
R: Wang, A.Y.; Yu, W.P.; Juang, R.H.; Huang, J.W.; Sung, H.Y.; Su, J.C.
Plant Mol. Biol. 18, 1191-1194, 1992
A:Title: Presence of three rice sucrose synthase genes as revealed by cloning and sequen
A:Reference number: S22535; MUID:92288314; PMID:1534703
A:Accession: S22536
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 605-816 <WAN>
A:Cross-references: UNIPARC:UPI00001753C7
A:Experimental source: cv. Tainong 67
C:Genetics:
A:Introns: 37/2; 80/3; 131/2; 195/3; 235/2; 307/3; 339/3; 397/3; 436/3; 492/2; 567/2; 67
C:Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase
F:284-758/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match      52.1%; Score 37; DB 2; Length 816;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DYGGQSTYVMD 12
      |||||  |::|
Db      303 DTGGQVVYILD 313

Search completed: May 11, 2006, 16:37:53
Job time : 33.1803 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 120.197 Seconds
(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-3
Perfect score: 71
Sequence: 1 DDYGGQSYVMDA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	77.5	745	2 Q6LZ19 METMP	Q6LZ19 methanococc
2	43	60.6	313	2 Q5B9S1 EMENI	Q5B9S1 aspergillus
3	43	60.6	381	2 Q5AR04 EMENI	Q5AR04 aspergillus
4	43	60.6	411	2 Q5V2G0 HALMA	Q5V2G0 haloarcula
5	43	60.6	450	2 Q83238 TREPA	Q83238 treponema p
6	43	60.6	466	2 Q4WBS1 ASPFU	Q4WBS1 aspergillus
7	43	60.6	477	2 Q4WAF0 ASPFU	Q4WAF0 aspergillus
8	43	60.6	510	1 NANT YERPE	Q8ZCH3 yersinia ps
9	43	60.6	520	1 NANT YERPE	Q668K2 yersinia ps
10	43	60.6	520	2 Q5W6G0 ORYSA	Q5W6G0 oryza sativ
11	42	59.2	230	2 Q53NM5 ORYSA	Q53NM5 oryza sativ
12	42	59.2	311	2 Q5LM44 ARATH	Q5LM44 arabidopsis
13	42	59.2	408	2 Q5SG95 ARATH	Q5SG95 arabidopsis
14	41	57.7	82	2 Q5YVQ1 NOCPA	Q5YVQ1 nocardia fa
15	41	57.7	551	2 Q6FR37 CANGA	Q6FR37 candida gla
16	41	57.7	631	2 Q8ALH8 BACTN	Q8ALH8 bacteroides
17	41	57.7	666	2 Q5FUB1 CANGA	Q5FUB1 candida gla
18	41	57.7	778	2 Q73HF1 WOLPM	Q73HF1 wolbachia p
19	41	57.7	909	2 Q5TYX3 CABEL	Q5TYX3 caenorhabdi
20	41	57.7	2247	2 Q39818 9PICO	Q39818 equine rhin
21	40.5	57.0	410	2 Q4M003 9BURK	Q4M003 burkholderi
22	40	56.3	130	2 Q6VRX5 NEILA	Q6VRX5 neisseria l
23	40	56.3	238	2 Q7N8EO PHOLL	Q7N8EO photorhabdi
24	40	56.3	249	2 Q63UI8 BURPS	Q63UI8 burkholderi
25	40	56.3	254	2 Q6VS10 NEIME	Q6VS10 neisseria m
26	40	56.3	254	2 Q6VS11 NEIME	Q6VS11 neisseria m
27	40	56.3	254	2 Q6VS12 NEIME	Q6VS12 neisseria m
28	40	56.3	254	2 Q6VS14 NEIME	Q6VS14 neisseria m
29	40	56.3	254	2 Q6VS19 NEIME	Q6VS19 neisseria m
30	40	56.3	254	2 Q6VS24 NEIME	Q6VS24 neisseria m
31	40	56.3	254	2 Q6VS26 NEIME	Q6VS26 neisseria m

32	40	56.3	255	2 Q6VRX9 NEIME	Q6VRX9 neisseria m
33	40	56.3	255	2 Q6VRX1 NEIME	Q6VRX1 neisseria m
34	40	56.3	255	2 Q6VRX3 NEIME	Q6VRX3 neisseria m
35	40	56.3	255	2 Q6VRX8 NEIME	Q6VRX8 neisseria m
36	40	56.3	255	2 Q6VR20 NEIME	Q6VR20 neisseria m
37	40	56.3	255	2 Q6VR26 NEIME	Q6VR26 neisseria m
38	40	56.3	257	2 Q6VS27 NEIME	Q6VS27 neisseria m
39	40	56.3	260	2 Q6VRX4 NEIME	Q6VRX4 neisseria m
40	40	56.3	261	2 Q6VS29 NEIME	Q6VS29 neisseria m
41	40	56.3	274	2 Q6QCB7 NEIME	Q6QCB7 neisseria m
42	40	56.3	274	2 Q6QCB9 NEIME	Q6QCB9 neisseria m
43	40	56.3	274	2 Q6QCC0 NEIME	Q6QCC0 neisseria m
44	40	56.3	274	2 Q6QCC2 NEIME	Q6QCC2 neisseria m
45	40	56.3	276	2 Q8DRG2 STRR6	Q8DRG2 streptococc
46	40	56.3	276	2 Q97T12 STRR6	Q97T12 streptococc
47	40	56.3	320	2 Q9JXV4 NEIMB	Q9JXV4 neisseria m
48	40	56.3	335	2 Q6BJM7 DRBHA	Q6BJM7 debaryomyce
49	40	56.3	383	2 Q5B7X2 EMENI	Q5B7X2 aspergillus
50	40	56.3	435	2 Q5LKK1 SILPO	Q5LKK1 silicibacte
51	40	56.3	438	2 Q8KZF3 THETH	Q8KZF3 thermus the
52	40	56.3	438	2 Q5SHQ8 THETH	Q5SHQ8 thermus the
53	40	56.3	438	2 Q72124 THETH	Q72124 thermus the
54	40	56.3	438	2 Q73PL2 TREDE	Q73PL2 treponema d
55	40	56.3	492	2 Q9N566 CABEL	Q9N566 caenorhabdi
56	40	56.3	710	2 Q936A7 SYNXP	Q936A7 synecococc
57	39.5	55.6	208	2 Q9UN87 HUMAN	Q9UN87 homo sapien
58	39	54.9	29	2 Q9UN87 HUMAN	Q9UN87 homo sapien
59	39	54.9	53	2 Q4HLW9 CAMLA	Q4HLW9 campylobact
60	39	54.9	150	2 Q8XTL1 RALSO	Q8XTL1 ralstonia s
61	39	54.9	201	2 Q979A4 THEVO	Q979A4 thermoplasma
62	39	54.9	288	2 P92136 ENTDI	P92136 entamoeba d
63	39	54.9	298	2 Q5QN41 ORYSA	Q5QN41 oryza sativ
64	39	54.9	304	2 Q9NJY0 GIALA	Q9NJY0 giardia lam
65	39	54.9	339	2 Q5V481 HALMA	Q5V481 haloarcula
66	39	54.9	342	2 Q7QV94 GIALA	Q7QV94 giardia lam
67	39	54.9	357	1 CCR9 HUMAN	P51686 homo sapien
68	39	54.9	357	2 Q549E0 HUMAN	Q549E0 homo sapien
69	39	54.9	365	2 Q4VBM3 HUMAN	Q4VBM3 homo sapien
70	39	54.9	369	2 Q9UQ06 HUMAN	Q9UQ06 homo sapien
71	39	54.9	644	2 Q5V3E3 HALMA	Q5V3E3 haloarcula
72	39	54.9	810	2 Q5CQ27 CHYPV	Q5CQ27 cryptospori
73	39	54.9	810	2 Q5CJ69 CRYHO	Q5CJ69 cryptospori
74	39	54.9	883	2 Q6QXH8 GVAS	Q6QXH8 agrotis seg
75	39	54.9	885	2 Q4HZL6 GIBZE	Q4HZL6 gibberella
76	39	54.9	1502	2 Q412P4 GIBZE	Q412P4 gibberella
77	39	54.9	1637	2 Q8AGY0 GRETR	Q8AGY0 python molu
78	39	54.9	1678	2 Q9BMP2 STVMT	Q9BMP2 stylonychia
79	39	54.9	1729	2 Q25734 PLAF7	Q25734 plasmodium
80	39	54.9	2229	2 Q19853 CABEL	Q19853 caenorhabdi
81	39	54.9	2879	2 Q6LFO9 PLAF7	Q6LFO9 plasmodium
82	39	54.9	2924	2 Q25733 PLAF7	Q25733 plasmodium
83	38	53.5	180	2 Q6S909 PLAF7	Q6S909 plasmodium
84	38	53.5	196	2 Q8UCP4 AGRTS	Q8UCP4 agrobacteri
85	38	53.5	198	2 Q7CX21 AGRTS	Q7CX21 agrobacteri
86	38	53.5	216	1 FLAB3 METJA	Q59303 methanococc
87	38	53.5	218	2 Q5GQV7 9CAUD	Q5GQV7 bacterioph
88	38	53.5	255	1 PRIO CANPA	Q46501 canis famil
89	38	53.5	260	2 Q9GU53 9TRYP	Q9GU53 trypanosoma
90	38	53.5	267	2 Q61076 PLAF7	Q61076 plasmodium
91	38	53.5	294	2 Q5K2L9 BACLI	Q5K2L9 bacillus li
92	38	53.5	295	2 Q04584 ARATH	Q04584 arabidopsis
93	38	53.5	329	1 HLDD BORBR	Q7WGU9 bordetella
94	38	53.5	329	1 HLDD BORPE	Q7WZf5 bordetella
95	38	53.5	342	1 Q5F3D2 CHICK	Q5F3D2 gallus gall
96	38	53.5	342	2 Q9KWS0 PSESP	Q9KWS0 pseudomonas
97	38	53.5	343	2 Q54A02 FSEPU	Q54A02 pseudomonas
98	38	53.5	346	1 HNRH3 HUMAN	P31942 homo sapien
99	38	53.5	346	2 Q53F48 HUMAN	Q53F48 homo sapien
100	38	53.5	349	2 Q4J2F6 AZOVI	Q4J2F6 azotobacter
101	38	53.5	354	2 Q4JF96 STAAU	Q4JF96 staphylococ
102	38	53.5	354	2 Q9XB85 STAAU	Q9XB85 staphylococ
103	38	53.5	354	2 Q6GKQ3 STAAU	Q6GKQ3 staphylococ
104	38	53.5	354	2	

105	38	53.5	354	2	Q5HK36	staphylococ	Q5hk36	staphylococ	178	38	53.5	1865	2	Q5AOT8	EMENI	Q5aqt8	aspergillus
106	38	53.5	354	2	Q7A303	STAAM	Q7a303	staphylococ	179	38	53.5	1972	2	Q4U971	THEAN	Q4u971	theileria a
107	38	53.5	354	2	Q7A8C3	STAAM	Q7a8c3	staphylococ	180	38	53.5	2251	2	Q7RNK7	PLAYO	Q7rnk7	plasmodium
108	38	53.5	371	2	Q6J692	9BURK	Q6j692	collimonas	181	38	53.5	3003	2	Q4KCE4	PSEF5	Q4kce4	pseudomonas
109	38	53.5	381	2	Q5AVP1	EMENI	Q5avp1	aspergillus	182	38	53.5	3078	2	Q26031	PLAFA	Q26031	plasmodium
110	38	53.5	395	2	Q65J76	BACLD	Q65j76	bacillus li	183	38	53.5	3950	2	Q4ZJT2	9CORO	Q4zjt2	avian infec
111	38	53.5	410	2	Q93X40	LACSA	Q93x40	lactuca sat	184	38	53.5	3951	2	Q5MNZ4	9CORO	Q5mnz4	avian infec
112	38	53.5	411	2	Q9FZ29	ARATH	Q9fz29	arabidopsis	185	38	53.5	3951	2	Q4ZJT4	9CORO	Q4zjt4	avian infec
113	38	53.5	418	2	Q8R7X3	THETN	Q8r7x3	thermoanaer	186	38	53.5	3953	2	Q515Y1	9CORO	Q5i5y1	avian infec
114	38	53.5	422	2	Q8ZU15	PYRAE	Q8zu15	pyrobaculum	187	38	53.5	6610	2	Q6DV55	9CORO	Q6dv55	avian infec
115	38	53.5	447	2	Q7URR5	RHOBA	Q7urr5	rhodopirell	188	38	53.5	6629	2	RIAB	IBVBC	P27920	a replicase
116	38	53.5	454	2	Q6MK94	BDEBA	Q6mk94	bdellovibri	189	38	53.5	6629	1	RIAB	IBVBC	Q62th2	homo sapien
117	38	53.5	474	2	Q5N3X6	SYNPG	Q5n3x6	synechococc	190	37.5	52.8	180	2	Q6ZTH2	HUMAN	Q6zth2	homo sapien
118	38	53.5	489	2	Q4UCR8	THEAN	Q4ucr8	theileria a	191	37.5	52.8	183	2	Q6ZMS9	HUMAN	Q6zms9	homo sapien
119	38	53.5	490	2	Q5TEQ1	BRARE	Q5teq1	brachydanio	192	37.5	52.8	481	2	Q4R3B2	MACFA	Q4r3b2	macaca fasc
120	38	53.5	490	2	Q7SXR5	BRARE	Q7sxr5	brachydanio	193	37.5	52.8	525	2	Q65388	ORYSA	Q65388	oryza sativ
121	38	53.5	510	2	Q4HUW6	GIBZE	Q4huw6	gibberella	194	37.5	52.8	570	2	Q75MF0	HUMAN	Q75mf0	homo sapien
122	38	53.5	537	2	Q72WA0	LEPIC	Q72wa0	leptospiro	195	37.5	52.8	724	2	Q51895	9PRIM	Q5i895	saimiri bol
123	38	53.5	537	2	Q8F925	LEPIN	Q8f925	leptospira	196	37.5	52.8	801	2	Q5U4C2	MOUSE	Q5u4c2	mus musculus
124	38	53.5	539	2	Q88RS2	PSEPK	Q88rs2	pseudomonas	197	37.5	52.8	803	1	DPP6	PANTR	Q5i850	pan troglod
125	38	53.5	540	2	Q4KDU0	PSEF5	Q4kdu0	pseudomonas	198	37.5	52.8	803	2	Q9QVT8	9MURI	Q9qvt8	rattus sp.
126	38	53.5	552	2	Q7X4L6	BURCE	Q7x4l6	burkholderi	199	37.5	52.8	803	2	Q8QVM5	MOUSE	Q8qvm5	mus musculus
127	38	53.5	552	2	Q4LU80	9BURK	Q4lu80	burkholderi	200	37.5	52.8	804	1	DPP6	MOUSE	Q9z218	mus musculus
128	38	53.5	552	2	Q6ZMH3	BURMA	Q6zmh3	burkholderi	201	37.5	52.8	859	1	DPP6	RAT	P46101	rattus norv
129	38	53.5	554	2	Q6NBH7	RHOPE	Q6nbh7	rhodopseudo	202	37.5	52.8	865	1	DPP6	HUMAN	P42658	homo sapien
130	38	53.5	555	2	Q5JMW8	BRAJA	Q5jmw8	bradyrhizob	203	37.5	52.8	2401	2	Q7RF52	PLAYO	Q7rf52	plasmodium
131	38	53.5	556	2	Q5JW88	BURPS	Q5jw88	burkholderi	204	37	52.1	151	2	Q89885	BRAJA	Q89885	bradyrhizob
132	38	53.5	558	2	Q88J58	PSEPK	Q88j58	pseudomonas	205	37	52.1	155	2	Q63KA3	BURFS	Q63ka3	burkholderi
133	38	53.5	558	2	Q7WKN2	BORBR	Q7wkn2	borderella	206	37	52.1	155	2	Q62CS9	BURMA	Q62cs9	burkholderi
134	38	53.5	558	2	Q7W796	BORPA	Q7w796	borderella	207	37	52.1	161	2	Q895Y7	CLOTE	Q895y7	clostridium
135	38	53.5	558	2	Q7VVT8	BORPE	Q7vvt8	borderella	208	37	52.1	164	2	Q811Y0	MOUSE	Q811y0	mus musculus
136	38	53.5	563	2	Q4NTD4	9DELT	Q4ntd4	anaeromyxob	209	37	52.1	177	1	CRGM1	CYPCA	P10043	cyprinus ca
137	38	53.5	567	2	Q8Y120	RALSO	Q8y120	ralstonia s	210	37	52.1	200	2	Q4TWK1	9SPHN	Q4tmk1	erythrobact
138	38	53.5	567	2	Q9A9K0	CAUCR	Q9a9k0	caulobacter	211	37	52.1	205	2	Q946X3	PRUPE	Q946x3	prunus pers
139	38	53.5	596	2	Q4Z0N8	FLABE	Q4z0n8	plasmodium	212	37	52.1	211	1	UPP	STRAW	Q82f84	streptomyce
140	38	53.5	614	2	Q8UCJ2	AGRT5	Q8ucj2	agrobacteri	213	37	52.1	211	1	UPP	STRCO	Q82f84	streptomyce
141	38	53.5	620	2	Q7U2A5	MYCBO	Q7u2a5	mycobacteri	214	37	52.1	226	2	Q828F2	STRAW	Q828f2	streptomyce
142	38	53.5	620	2	Q07239	MYCTU	Q07239	mycobacteri	215	37	52.1	239	2	Q688M8	ORYSA	Q688m8	oryza sativ
143	38	53.5	629	2	Q92K36	RHIME	Q92k36	rhizobium m	216	37	52.1	239	2	Q944U6	CARPA	Q944u6	carica papa
144	38	53.5	629	2	Q98N22	RHILO	Q98n22	rhizobium l	217	37	52.1	249	2	Q70KR0	COFAR	Q70kr0	coffea arab
145	38	53.5	630	2	Q4H972	9DEIO	Q4h972	deinococcus	218	37	52.1	260	2	Q58Y23	MACPU	Q58y23	macropus eu
146	38	53.5	632	2	Q579A9	BRUAB	Q579a9	brucella ab	219	37	52.1	265	2	Q6E6L6	PLALA	Q6e6l6	plantaio la
147	38	53.5	632	2	Q89V63	BRAJA	Q89v63	bradyrhizob	220	37	52.1	267	2	Q5PGF8	SALPA	Q5pgf8	salmonella
148	38	53.5	632	2	Q8FVP5	BRUSU	Q8fvp5	brucella su	221	37	52.1	271	2	Q59IU7	PYRCO	Q59iu7	pyrus commu
149	38	53.5	632	2	Q8YCX2	BRUME	Q8ycx2	brucella me	222	37	52.1	288	2	Q24846	ENTHI	Q24846	entamoeba h
150	38	53.5	657	2	Q54YD9	DICDI	Q54yd9	dictyosteli	223	37	52.1	288	2	Q8AYU9	9CIRC	Q8ayu9	goose circo
151	38	53.5	657	2	Q7CWX7	AGROBACT	Q7cw7	agrobacteri	224	37	52.1	293	2	Q8AYV0	9CIRC	Q8ayv0	goose circo
152	38	53.5	666	2	Q9R1X7	THEME	Q9rik7	thermotoga	225	37	52.1	293	2	Q8AYY2	9CIRC	Q8ayy2	goose circo
153	38	53.5	669	2	Q9X0V4	THEMA	Q9x0v4	thermotoga	226	37	52.1	293	2	Q8BCC3	9CIRC	Q8bcc3	goose circo
154	38	53.5	677	2	Q7AY41	ANASP	Q7ay41	anabaena sp	227	37	52.1	293	2	Q6GV19	9CIRC	Q6gv19	goose circo
155	38	53.5	677	2	Q934C0	9NOST	Q934c0	anabaena sp	228	37	52.1	293	2	Q81605	MUSAC	Q81605	musa acumin
156	38	53.5	680	2	Q9R1K9	THEMA	Q9rik9	thermotoga	229	37	52.1	312	2	Q8AVV4	ORYSA	Q8avv4	oryza sativ
157	38	53.5	713	2	Q82V85	NITEU	Q82v85	nitrosomona	230	37	52.1	331	2	Q6VVA4	ORYSA	Q6vv44	oryza sativ
158	38	53.5	804	2	Q6E7L3	9CYAN	Q6e7l3	lyngbya maj	231	37	52.1	345	2	Q92R60	RHIME	Q92r60	rhizobium m
159	38	53.5	806	2	Q937E3	NOSPU	Q937e3	nostoc punc	232	37	52.1	347	2	Q9AT37	LOLRI	Q9at37	lolium rigi
160	38	53.5	806	2	Q9K5L4	ANAVA	Q9k5l4	anabaena va	233	37	52.1	350	1	CMTG	PSEPU	Q51983	pseudomonas
161	38	53.5	806	2	Q3ZEY2	9NOST	Q3zev2	anabaena sp	234	37	52.1	350	2	Q7D1G3	PSEPU	Q7d1g3	pseudomonas
162	38	53.5	806	2	Q9YME9	ANASP	Q9yme9	anabaena sp	235	37	52.1	360	2	Q4PCA2	USTWA	Q4pc2	ustilago ma
163	38	53.5	808	2	Q7NFB9	GLOVI	Q7nfb9	gloeobacter	236	37	52.1	365	2	Q4NOV4	THEPA	Q4nov4	theileria p
164	38	53.5	809	2	Q9ZPC6	CRAPL	Q9zpc6	craterostig	237	37	52.1	376	2	Q6YPQ8	ONYPE	Q6ypq8	onion yello
165	38	53.5	848	2	Q4P2C4	USTMA	Q4p2c4	ustilago ma	238	37	52.1	381	2	Q829D5	STRAW	Q829d5	streptomyce
166	38	53.5	1059	2	Q64J54	9CORY	Q64j54	corynebacte	239	37	52.1	390	2	Q7UVR5	RHOBA	Q7uvr5	rhodopirell
167	38	53.5	1060	2	Q64UJ2	9CORY	Q64j42	corynebacte	240	37	52.1	391	2	Q80428	ORYSA	Q80428	oryza sativ
168	38	53.5	1104	2	Q64U70	9CORY	Q64j70	corynebacte	241	37	52.1	392	2	Q8CK17	STRCO	Q8ck17	streptomyce
169	38	53.5	1109	2	Q64J59	9CORY	Q64j59	corynebacte	242	37	52.1	420	2	Q7SYN1	BRARE	Q7syn1	brachydanio
170	38	53.5	1116	2	Q64J55	9CORY	Q64j55	corynebacte	243	37	52.1	422	2	Q8W402	TOBAC	Q8w402	nicotiana t
171	38	53.5	1137	2	Q4UGR0	THEAN	Q4ugr0	theileria a	244	37	52.1	423	2	Q5V489	HALARMA	Q5v489	haloarcula
172	38	53.5	1210	2	Q93ZM5	ARATH	Q93zm5	arabidopsis	245	37	52.1	437	1	SECY	STRCO	P46785	streptomyce
173	38	53.5	1251	2	Q9MA34	ARATH	Q9ma34	arabidopsis	246	37	52.1	437	1	SECY	STRGB	Q59912	streptomyce
174	38	53.5	1628	2	Q4Q5H3	LEIMA	Q4q5h3	leishmania	247	37	52.1	437	1	SECY	STRLR	Q59916	streptomyce
175	38	53.5	1635	2	Q17368	CAENORHABDI	Q17368	caenorhabdi	248	37	52.1	437	1	SECY	STRLI	Q59977	streptomyce
176	38	53.5	1639	2	Q61QW0	CAEBR	Q61qm0	caenorhabdi	249	37	52.1	437	1	SECY	STRSC	P43416	streptomyce
177	38	53.5	1668	2	Q4VK26	CAEEL	Q4vk26	caenorhabdi	250	37	52.1	438	2	Q82DM6	STRAW	Q82dm6	streptomyce

251	37	52.1	444	2	O24566_MAIZE	O24566	zea mays (m	344	37	52.1	808	2	Q8W1W2_BAMOL	Q8W1W2 bambusa old
252	37	52.1	445	2	Q95AK0_ELEIN	Q95AK0	eleusine in	325	37	52.1	808	2	Q8W1W3_BAMOL	Q8W1W3 bambusa old
253	37	52.1	445	2	Q95AK1_ELEIN	Q95AK1	eleusine in	326	37	52.1	808	2	Q91XL5_ARATH	Q91XL5 arabidopsis
254	37	52.1	448	2	Q6ZL25_ORYSA	Q6ZL25	oryza sativ	327	37	52.1	808	2	Q9SBD5_ARATH	Q9SBD5 arabidopsis
255	37	52.1	454	2	Q9ZRC4_GOSHI	Q9ZRC4	gossypium h	328	37	52.1	808	2	Q82073_WHEAT	Q82073 triticum ae
256	37	52.1	468	2	Q8SAV1_ORYSA	Q8SAV1	oryza sativ	329	37	52.1	808	2	Q69V32_ORYSA	Q69V32 oryza sativ
257	37	52.1	472	2	O31059_BUTPI	O31059	butyrivibri	330	37	52.1	808	2	Q8DK33_SYNEL	Q8DK33 synecococc
258	37	52.1	477	2	Q51PM1_NOCFA	Q51PM1	nocardia fa	331	37	52.1	809	1	SUS2_PEA	O24301 pium sativ
259	37	52.1	481	2	Q7V172_HELHP	Q7V172	helicobacte	332	37	52.1	809	2	Q8L5H0_MAIZE	Q8L5H0 zea mays (m
260	37	52.1	482	2	Q7XR23_ORYSA	Q7XR23	oryza sativ	333	37	52.1	809	2	Q9M111_ARATH	Q9M111 arabidopsis
261	37	52.1	483	2	Q878W3_STRP6	Q878W3	streptococc	334	37	52.1	811	2	Q84T18_SOLTU	Q84T18 solanum tub
262	37	52.1	483	2	Q5XBK7_STRP6	Q5XBK7	streptococc	335	37	52.1	811	2	Q9SLV8_CITUN	Q9SLV8 citrus unsh
263	37	52.1	483	2	Q8K721_STRP3	Q8K721	streptococc	336	37	52.1	811	2	Q9SLV2_CITUN	Q9SLV2 citrus unsh
264	37	52.1	483	2	Q95Z85_STRP8	Q95Z85	streptococc	337	37	52.1	812	2	Q9ZPCS_CRAPL	Q9ZPCS craterostig
265	37	52.1	483	2	Q8F0H3_STRP8	Q8F0H3	streptococc	338	37	52.1	812	2	Q9FRX3_PYRPP	Q9FRX3 pyrus pyrri
266	37	52.1	489	2	Q4N0H6_THEPA	Q4N0H6	theileria p	339	37	52.1	814	2	Q4LEV2_9LILI	Q4LEV2 potamogeton
267	37	52.1	507	2	Q8ISB3_9NEOP	Q8ISB3	antheraea m	340	37	52.1	815	2	Q43223_WHEAT	Q43223 triticum ae
268	37	52.1	511	2	Q93VK6_ORYSA	Q93VK6	oryza sativ	341	37	52.1	816	1	SUS2_HORVU	P31923 hordeum vul
269	37	52.1	515	2	Q5VNW0_ORYSA	Q5VNW0	oryza sativ	342	37	52.1	816	1	SUS2_MAIZE	P49036 zea mays (m
270	37	52.1	517	2	Q7PXQ2_ANOGA	Q7PXQ2	anopheles g	343	37	52.1	816	1	SUS2_ORYSA	P31924 oryza sativ
271	37	52.1	530	2	Q4P7A5_USTMA	Q4P7A5	ustilago ma	344	37	52.1	816	1	SUS3_ORYSA	Q81009 oryza sativ
272	37	52.1	532	2	Q94CC8_ARATH	Q94CC8	arabidopsis	345	37	52.1	816	2	Q8LJT4_9ASPA	Q8LJT4 x mokara cv
273	37	52.1	534	2	Q6CR77_KLULA	Q6CR77	kluyveromyc	346	37	52.1	816	2	Q8LJT5_9ASPA	Q8LJT5 oncidium cv
274	37	52.1	538	2	Q5CNJ2_CRYHO	Q5CNJ2	cryptospori	347	37	52.1	816	2	Q437N0_ORYSA	Q437N0 oryza sativ
275	37	52.1	626	2	Q5G8S8_9CAUD	Q5G8S8	salmonella	348	37	52.1	816	2	Q437O6_MAIZE	Q437O6 zea mays (m
276	37	52.1	642	2	Q57SR4_SALCH	Q57SR4	salmonella	349	37	52.1	816	2	Q8GS23_ORYSA	Q8GS23 oryza sativ
277	37	52.1	642	2	Q8HG56_9HYPO	Q8HG56	torubiella	350	37	52.1	816	2	Q8W1W4_BAMOL	Q8W1W4 bambusa old
278	37	52.1	677	2	Q81637_ORYSA	Q81637	oryza sativ	351	37	52.1	816	2	Q5TK93_BAMOL	Q5TK93 bambusa old
279	37	52.1	692	1	NUSM_TFIRE	Q8ABP7	trichoderma	352	37	52.1	820	1	SUS2_TULGE	Q41607 tulipa gean
280	37	52.1	703	2	Q8ZL26_ORYSA	Q8ZL26	oryza sativ	353	37	52.1	822	2	Q94G60_BETVU	Q94G60 beta vulgar
281	37	52.1	704	1	CILU2_MOUSE	Q8BY89	mus musculus	354	37	52.1	842	2	Q4LEV1_9LILI	Q4LEV1 potamogeton
282	37	52.1	766	1	SUSY_BETVU	Q42652	beta vulgar	355	37	52.1	846	2	Q8K973_ORYSA	Q8K973 oryza sativ
283	37	52.1	772	2	Q7R3W9_GIALA	Q7R3W9	giardia lam	356	37	52.1	850	2	Q5BF08_EMENI	Q5BF08 aspergillus
284	37	52.1	787	2	Q5LITB8_SILPO	Q5LITB8	silicibacte	357	37	52.1	855	2	Q7XNX6_ORYSA	Q7XNX6 oryza sativ
285	37	52.1	794	2	Q820M5_NITEU	Q820M5	nitrosomona	358	37	52.1	871	2	Q52FT7_MAGGR	Q52FT7 magnaporthe
286	37	52.1	796	2	Q93WS3_MAIZE	Q93WS3	zea mays (m	359	37	52.1	883	2	Q5K9Z7_CRYNE	Q5K9Z7 cryptococcu
287	37	52.1	798	2	Q7XNQ9_ORYSA	Q7XNQ9	oryza sativ	360	37	52.1	887	2	Q9FHU4_ARATH	Q9FHU4 arabidopsis
288	37	52.1	801	1	SUS2_DAUC	Q49845	daucus caro	361	37	52.1	907	2	Q55S45_CRYNE	Q55S45 cryptococcu
289	37	52.1	802	1	SUS1_MAIZE	P04712	zea mays (m	362	37	52.1	907	2	Q5KGJ7_CRYNE	Q5KGJ7 cryptococcu
290	37	52.1	802	2	Q6VLN4_SACOF	Q6VLN4	saccharum o	363	37	52.1	942	2	Q9FX32_ARATH	Q9FX32 arabidopsis
291	37	52.1	802	2	Q91KR0_SACOF	Q91KR0	saccharum o	364	37	52.1	972	2	Q9M2D4_ARATH	Q9M2D4 arabidopsis
292	37	52.1	803	1	SUSY_AINGL	P49034	alnus glutu	365	37	52.1	1053	2	Q5QWXS_IDILO	Q5QWXS idiomarina
293	37	52.1	804	2	Q9LWB7_CHERU	Q9LWB7	chenopodium	366	37	52.1	1126	2	Q8GV68_CERPU	Q8GV68 ceratodon p
294	37	52.1	804	2	Q9AVR8_PEA	Q9AVR8	pium sativ	367	37	52.1	1230	2	Q4N8Y9_THEPA	Q4N8Y9 theileria p
295	37	52.1	805	1	SUS1_SOLTU	P10691	solanum tub	368	37	52.1	1370	2	Q8D624_VIBVU	Q8D624 vibrio vuln
296	37	52.1	805	1	SUS1_TULGE	Q41608	tulipa gean	369	37	52.1	1381	2	Q7MDV3_VIBVU	Q7MDV3 vibrio vuln
297	37	52.1	805	1	SUS2_ARATH	Q00917	arabidopsis	370	37	52.1	1485	2	Q6A031_MOUSE	Q6A031 mus musculu
298	37	52.1	805	1	SUS2_SOLTU	P49039	solanum tub	371	37	52.1	2227	2	Q66775_9PICO	Q66775 equine rhin
299	37	52.1	805	1	SUSY_LYCES	P49037	lycopersico	372	37	52.1	2248	2	Q66774_9PICO	Q66774 equine rhin
300	37	52.1	805	1	SUSY_MEDSA	Q65026	medicago sa	373	37	52.1	4876	2	Q9VH01_DROME	Q9VH01 drosophila
301	37	52.1	805	1	SUSY_PHAAR	P13708	glycine max	374	36.5	51.4	145	2	Q96N78_HUMAN	Q96N78 homo sapien
302	37	52.1	805	1	SUSY_SOYBN	Q82691	lycopersico	375	36.5	51.4	414	1	PYRC_THEAC	Q9H1M0 thermoplasma
303	37	52.1	805	2	Q82691_LYCES	Q82691	lycopersico	376	36.5	51.4	428	2	Q69KK0_ORYSA	Q69KK0 oryza sativ
304	37	52.1	805	2	Q82693_LYCES	Q82693	lycopersico	377	36	50.7	100	2	Q8LUM7_PHOPR	Q8LUM7 photobacter
305	37	52.1	805	2	Q6SJP5_BETVU	Q6SJP5	beta vulgar	378	36	50.7	119	1	HV3L_HUMAN	P01773 homo sapien
306	37	52.1	805	2	Q7Y078_SOLTU	Q7Y078	solanum tub	379	36	50.7	144	2	Q6SZF0_RHOFA	Q6SZF0 rhodococcu
307	37	52.1	805	2	Q84UC3_SOLTU	Q84UC3	solanum tub	380	36	50.7	151	2	Q96Z04_SULTO	Q96Z04 sulfolobus
308	37	52.1	805	2	Q8GTA3_PHAUV	Q8GTA3	phaseolus v	381	36	50.7	177	2	Q6S934_PLAFA	Q6S934 plasmodium
309	37	52.1	805	2	Q69FD8_POPTM	Q69FD8	populus tre	382	36	50.7	183	2	Q6L1W0_CAEFR	Q6L1W0 caenorhabdi
310	37	52.1	805	2	Q9SLY1_CITUN	Q9SLY1	citrus unsh	383	36	50.7	183	2	Q8S933_PLAFA	Q8S933 plasmodium
311	37	52.1	805	2	Q9T0M6_MEDTR	Q9T0M6	medicago tr	384	36	50.7	186	2	Q6B4J6_BACCE	Q6B4J6 bacillus ce
312	37	52.1	805	2	Q9XG65_MEDTR	Q9XG65	medicago tr	385	36	50.7	189	2	Q8DF72_VIBVU	Q8DF72 vibrio vuln
313	37	52.1	806	1	SUS1_ARATH	P49040	arabidopsis	386	36	50.7	205	1	BLVRB_HUMAN	P30043 homo sapien
314	37	52.1	806	1	SUSY_VICFA	P31926	vicia faba	387	36	50.7	210	2	Q5WNG5_CAEBR	Q5WNG5 caenorhabdi
315	37	52.1	806	2	Q81610_PEA	Q81610	pium sativ	388	36	50.7	247	2	Q57K89_SALCH	Q57K89 salmonella
316	37	52.1	806	2	Q9TOM9_PEA	Q9TOM9	pium sativ	389	36	50.7	247	2	Q5PL26_SALPA	Q5PL26 salmonella
317	37	52.1	806	2	Q9SBL8_CITLA	Q9SBL8	citullus l	390	36	50.7	247	2	Q8Z322_SALTY	Q8Z322 salmonella
318	37	52.1	806	2	Q9XGB7_GOSHI	Q9XGB7	gossypium h	391	36	50.7	247	2	Q8ZM91_SALTY	Q8ZM91 salmonella
319	37	52.1	806	2	Q4QZT3_COFCA	Q4QZT3	coffea cane	392	36	50.7	253	2	Q6CP21_KIULA	Q6CP21 kluyveromyc
320	37	52.1	807	1	SUS1_HORVU	P31922	hordeum vul	393	36	50.7	261	2	Q9VJN4_DROME	Q9VJN4 drosophila
321	37	52.1	807	2	Q8ABU6_BACTN	Q8ABU6	bacteroides	394	36	50.7	263	2	Q4LR99_BURK	Q4LR99 burkholderi
322	37	52.1	808	1	SUS1_DAUC	P49035	daucus caro	395	36	50.7	265	2	Q6ML35_BDEBA	Q6ML35 bdellovibri
323	37	52.1	808	1	SUS1_ORYSA	P30298	oryza sativ	396	36	50.7	267	2	Q8T413_DROME	Q8T413 drosophila

397	36	50.7	270	2	Q51H31_ENTHI	Q51h31_entamoeba h	470	36	50.7	431	2	Q63KS0_BURPS	Q63ks0_burkholderi
398	36	50.7	272	2	Q9JNN8_STRPY	Q9jnn8_streptococc	471	36	50.7	439	2	Q92401_AGABI	Q92401_agaricus bi
399	36	50.7	284	2	Q9JNX0_STRPY	Q9jnx0_streptococc	472	36	50.7	439	2	Q9P893_AGABI	Q9P893_agaricus bi
400	36	50.7	291	2	Q6FQX1_CANGA	Q6fqx1_candida gla	473	36	50.7	440	1	SECY_CORGL	P38376_corynebacte
401	36	50.7	296	2	Q615Y7_CABBR	Q615y7_caenorhabdi	474	36	50.7	440	2	Q521Q2_NOCFA	Q521q2_nocardia fa
402	36	50.7	296	2	Q9JN77_STRPY	Q9jnt7_streptococc	475	36	50.7	440	2	Q6N1J72_CORDI	Q6n1j72_corynebacte
403	36	50.7	296	2	Q9JN79_STRPY	Q9jnv9_streptococc	476	36	50.7	440	2	Q8FS40_COREF	Q8fs40_corynebacte
404	36	50.7	297	2	Q9JN66_STRPY	Q9jnx6_streptococc	477	36	50.7	441	2	O5YRL6_NOCFA	O5yrl6_nocardia fa
405	36	50.7	297	2	Q9JN77_STRPY	Q9jny7_streptococc	478	36	50.7	441	2	Q94963_HUMAN	Q94963_homo sapien
406	36	50.7	299	2	Q9JN22_STRPY	Q9jnx2_streptococc	479	36	50.7	444	2	Q80W42_MOUSE	Q80w42_mus musculu
407	36	50.7	299	2	Q9JN26_STRPY	Q9jnx6_streptococc	480	36	50.7	445	2	Q96CS3_HUMAN	Q96cs3_homo sapien
408	36	50.7	301	2	Q45872_CAEEL	Q45872_caenorhabdi	481	36	50.7	445	2	Q6A7K5_PROAC	Q6a7k5_propionibac
409	36	50.7	301	2	Q9JN75_STRPY	Q9jnt5_streptococc	482	36	50.7	445	2	Q8G329_BIFLO	Q8g329_bifidobacte
410	36	50.7	305	2	Q7Q405_ANOGA	Q7q405_anopheles g	483	36	50.7	446	2	Q8UB44_AGR75	Q8ue44_agrobacteri
411	36	50.7	305	2	Q54958_STRPY	Q54958_streptococc	484	36	50.7	447	2	Q4NX64_9DEL1	Q4nx64_aeromonas
412	36	50.7	306	2	Q9JN78_STRPY	Q9jnt8_streptococc	485	36	50.7	449	2	Q9BRP2_HUMAN	Q9brp2_homo sapien
413	36	50.7	309	2	Q9JN21_STRPY	Q9jnx1_streptococc	486	36	50.7	450	2	Q5FLD3_LACAC	Q5fld3_lactobacill
414	36	50.7	310	2	Q9JN71_STRPY	Q9jny1_streptococc	487	36	50.7	453	2	Q97XP6_SULSO	Q97xp6_sulfolobus
415	36	50.7	310	2	Q82X43_NITEU	Q82x43_nitrosomona	488	36	50.7	455	2	Q9BVM7_HUMAN	Q9bvm7_homo sapien
416	36	50.7	311	2	Q8YQ98_ANASP	Q8yq98_anabena sp	489	36	50.7	455	2	Q88U56_LACPL	Q88u56_lactobacill
417	36	50.7	313	2	Q9JN88_STRPY	Q9jnx8_streptococc	490	36	50.7	455	2	Q5FW31_XENTR	Q5fw31_xenopus tro
418	36	50.7	313	2	Q9JN22_STRPY	Q9jny2_streptococc	491	36	50.7	460	2	P91467_CAEEL	P91467_caenorhabdi
419	36	50.7	313	2	Q9JN73_STRPY	Q9jny3_streptococc	492	36	50.7	460	2	Q9L4T5_9NOCA	Q9l4t5_rhodococcus
420	36	50.7	313	2	Q9JN74_STRPY	Q9jny4_streptococc	493	36	50.7	464	2	Q7V9F3_PROMA	Q7v9f3_prochloroco
421	36	50.7	313	2	Q9JN78_STRPY	Q9jny8_streptococc	494	36	50.7	467	2	Q4HXK5_GIBZE	Q4hxx5_gibberella
422	36	50.7	313	2	Q9JN20_STRPY	Q9jnz0_streptococc	495	36	50.7	468	2	Q7UZF6_PROMP	Q7uzf6_prochloroco
423	36	50.7	313	2	Q9JP04_STRPY	Q9jpo4_streptococc	496	36	50.7	469	2	Q6LP56_PHOPR	Q6lp56_photobacter
424	36	50.7	313	2	Q9JP05_STRPY	Q9jpo5_streptococc	497	36	50.7	470	2	Q936V9_PROMA	Q936v9_prochloroco
425	36	50.7	313	2	Q9JP25_STRPY	Q9jps5_streptococc	498	36	50.7	475	2	O02258_CAEEL	O02258_caenorhabdi
426	36	50.7	313	2	Q7TTB6_BORBR	Q7ttb6_bordetella	499	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
427	36	50.7	316	2	Q9JN69_STRPY	Q9jne9_streptococc	500	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
428	36	50.7	318	2	Q9JN77_STRPY	Q9jnf7_streptococc	501	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
429	36	50.7	318	2	Q9JN77_STRPY	Q9jnx7_streptococc	502	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
430	36	50.7	327	2	Q9JN77_STRPY	Q9jnx7_streptococc	503	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
431	36	50.7	332	2	Q9JN77_STRPY	Q9jnx7_streptococc	504	36	50.7	496	1	NANT1_EC057	N8fd59_escherichia
432	36	50.7	332	2	Q6W219_RHISN	Q6w219_rhizobium s	505	36	50.7	496	2	Q57J00_SALCH	P59699_salmonella
433	36	50.7	334	2	Q6DBT8_SCHJA	Q6dbt8_schistosoma	506	36	50.7	496	2	Q5PLF0_SALCH	P59699_salmonella
434	36	50.7	334	2	Q7MYE3_9PSED	Q7mye3_pseudomonas	507	36	50.7	499	2	Q82GE0_STRAW	Q82ge0_streptomyce
435	36	50.7	335	2	Q8TYU3_METKA	Q8tyu3_methanopyru	508	36	50.7	502	2	Q82D12_STRAW	Q82d12_streptomyce
436	36	50.7	335	2	Q568J3_BRARE	Q568j3_brachydanio	509	36	50.7	504	2	Q9FC88_STRCO	Q9fc88_streptomyce
437	36	50.7	342	2	Q9JN75_STRPY	Q9jnx5_streptococc	510	36	50.7	510	2	Q6A9X4_PROAC	Q6a9x4_propionibac
438	36	50.7	343	2	Q6QAE3_ARATH	Q6gae3_arabidopsis	511	36	50.7	529	2	Q7X8Q6_ORYSA	Q7x8q6_oryza sativ
439	36	50.7	343	2	Q67ZB9_ARATH	Q67zr9_arabidopsis	512	36	50.7	532	2	O55IG7_CRYNE	O55ig7_cryptococcu
440	36	50.7	343	2	Q9C6U1_ARATH	Q9c6u1_arabidopsis	513	36	50.7	532	2	O5K808_CRYNE	O5k808_cryptococcu
441	36	50.7	343	2	Q6Z072_ORYSA	Q6z072_oryza sativ	514	36	50.7	533	2	Q7S8K7_NEUCR	Q7s8k7_neutospira
442	36	50.7	346	2	Q5BK32_RAT	Q5bk32_rattus norv	515	36	50.7	534	2	Q6A597_PROAC	Q6a597_propionibac
443	36	50.7	350	2	Q9JP22_STRPY	Q9jps2_streptococc	516	36	50.7	543	2	Q9HMM1_HALSA	Q9hmm1_halobacteri
444	36	50.7	357	2	Q6E6M4_9CARY	Q6e6m4_amaranthus	517	36	50.7	547	1	GUNC_BUTFI	G41i02_burkholderi
445	36	50.7	357	2	Q8VQC4_VIBAN	Q8vqc4_vibrio angu	518	36	50.7	557	2	Q4LSW9_9BURK	Q4lsw9_burkholderi
446	36	50.7	358	2	Q6E6M2_9RIAN	Q6e6m2_erigeron an	519	36	50.7	557	2	Q4LSW9_9BURK	Q4lsw9_burkholderi
447	36	50.7	360	2	Q6E6M1_9RIAN	Q6e6m1_erigeron an	520	36	50.7	557	2	Q62KG5_BURMA	Q62kg5_burkholderi
448	36	50.7	363	2	Q74KE4_LACUO	Q74ke4_lactobacill	521	36	50.7	557	2	Q63TK7_BURPS	Q63tk7_burkholderi
449	36	50.7	366	2	Q9JN19_STRPY	Q9jnin9_streptococc	522	36	50.7	570	2	Q759E0_ASHGO	Q759e0_ashya goss
450	36	50.7	368	2	Q4MS34_BACCE	Q4ms34_bacillus ce	523	36	50.7	580	2	Q6GQJ7_XENLA	Q6gqj7_xenopus lae
451	36	50.7	368	2	Q730A4_BACCI	Q730a4_bacillus ce	524	36	50.7	587	2	Q74DF6_GEOSL	Q74df6_geobacter s
452	36	50.7	368	2	Q817V8_BACCE	Q817v8_bacillus ce	525	36	50.7	656	2	Q7QTM5_GIALA	Q7qtm5_giardia lam
453	36	50.7	368	2	Q81LG1_BACAN	Q81lg1_bacillus an	526	36	50.7	699	1	EFQ_AQUAE	EFq428_aquifex aeo
454	36	50.7	368	2	Q6HD97_BACCH	Q6hd97_bacillus th	527	36	50.7	699	1	EFQ_AQUAE	EFq428_aquifex aeo
455	36	50.7	368	2	Q634B5_BACCH	Q634b5_bacillus ce	528	36	50.7	706	2	Q98N16_RHILHO	Q98n16_rhizobium l
456	36	50.7	371	2	Q9JN29_STRPY	Q9jnz9_streptococc	529	36	50.7	709	2	Q5N449_SYNPF	Q5n449_synechococc
457	36	50.7	374	2	Q9Y7V7_BOTCI	Q9y7v7_botrytis ci	530	36	50.7	710	2	Q936V8_PROMA	Q936v8_prochloroco
458	36	50.7	374	2	Q4G495_BOTCI	Q4g495_botrytis ci	531	36	50.7	710	2	Q7V3S3_PRONM	Q7v3s3_prochloroco
459	36	50.7	377	2	Q00012_ASPAC	Q00012_aspergillus	532	36	50.7	720	2	Q55440_SYNY3	Q55440_synechocyst
460	36	50.7	397	2	Q29236_ARCFU	Q29236_archaeoglob	533	36	50.7	725	1	GUNG_CLOCE	G37700_clostridium
461	36	50.7	402	2	Q7UVY0_RHOBA	Q7uvy0_rhodopirell	534	36	50.7	746	2	Q5AXP2_EMENI	Q5axp2_aspergillus
462	36	50.7	403	2	Q8E9P7_SHEON	Q8e9p7_shearella	535	36	50.7	753	2	Q4WR91_ASPFU	Q4wr91_aspergillus
463	36	50.7	404	2	Q9FLN1_SHEVI	Q9fln1_shearella	536	36	50.7	805	2	Q9SLS2_CITUN	Q9sls2_citrus unsh
464	36	50.7	408	2	Q45604_BACSU	Q45604_bacillus su	537	36	50.7	840	2	Q8AGN9_BACTN	Q8agn9_bacteroides
465	36	50.7	415	2	Q87V37_FSESM	Q87v37_pseudomonas	538	36	50.7	845	2	Q5LAE1_BACFN	Q5lae1_bacteroides
466	36	50.7	420	2	Q62CB3_HURMA	Q62cb3_burkholderi	539	36	50.7	845	2	Q64QS3_BACFR	Q64q3_bacteroides
467	36	50.7	422	1	CN050_HUMAN	Q96lq0_homo sapien	540	36	50.7	885	2	Q92NX4_RHIME	Q92nx4_rhizobium m
468	36	50.7	429	1	GUAA_CHLPN	Q9z913_chlamydia p	541	36	50.7	919	2	Q4WG65_ASPFU	Q4wg65_aspergillus
469	36	50.7	429	2	Q80TP7_MOUSE	Q80tp7_mus musculu	542	36	50.7	1021	2	Q7UFP2_RHOBA	Q7ufp2_rhodopirell

543	36	50.7	1041	2	Q6CBC6_YARLI	Q6cbc6	yarrowia li	616	35	49.3	245	2	Q9MZU7_9CETA	Q9mzu7	odocoileus
544	36	50.7	1050	2	Q5OXR5_ENTHI	Q5oxr5	entamoeba h	617	35	49.3	248	2	Q9HMU3_PSEAM	Q9hmw3	pseudomonas
545	36	50.7	1058	2	Q5QWZ5_IDILO	Q5qwz5	idiomarina	618	35	49.3	250	2	Q887I0_PSESM	Q887i0	pseudomonas
546	36	50.7	1177	2	Q5B0D9_EMENI	Q5bod9	aspergillus	619	35	49.3	256	1	PRI0_CEREN	P67987	cervus elap
547	36	50.7	1254	2	Q6RJW6_CANGA	Q6fjw6	candida gla	620	35	49.3	256	1	PRI0_CEREN	P67986	cervus elap
548	36	50.7	1264	2	Q4WAP8_ASPPU	Q4wap8	aspergillus	621	35	49.3	256	1	PRI0_ODOHE	P47852	odocoileus
549	36	50.7	1273	2	Q5VTU8_ANOGA	Q5vtu8	anopheles g	622	35	49.3	256	2	Q5XM82_CEREL	Q5xm82	cervus elap
550	36	50.7	1288	2	Q5VXG8_HUMAN	Q5vxg8	homo sapien	623	35	49.3	256	2	Q5XM83_CEREL	Q5xm83	cervus elap
551	36	50.7	1321	2	Q75129_HUMAN	Q75129	homo sapien	624	35	49.3	256	2	Q5XM84_CEREL	Q5xm84	cervus elap
552	36	50.7	1703	2	Q9NKQ9_LEIMA	Q9nkq9	leishmania	625	35	49.3	256	2	Q693S2_ALCAA	Q693s2	alces alces
553	36	50.7	1817	2	Q5TN74_ANOGA	Q5tn74	anopheles g	626	35	49.3	256	2	Q693S4_RANTA	Q693s4	rangifer ta
554	36	50.7	2109	2	Q8IAS7_PLAF7	Q8ias7	plasmodium	627	35	49.3	256	2	Q6VS46_ODOHE	Q6vsa6	odocoileus
555	36	50.7	6157	2	Q7UNV4_RHOBA	Q7unv4	rhodoptrell	628	35	49.3	256	2	Q7YSF3_DAMDA	Q7yef3	dama dama
556	35.5	50.0	238	2	Q97CD2_THEVO	Q97cd2	thermoplaem	629	35	49.3	256	2	Q863E8_9CETA	Q863e8	odocoileus
557	35.5	50.0	356	2	Q8MSH8_DROME	Q8msh8	drosohphila	630	35	49.3	256	2	Q863E9_9CETA	Q863e9	odocoileus
558	35.5	50.0	432	2	Q9W1R1_DROME	Q9w1r1	drosohphila	631	35	49.3	256	2	Q865Z5_9CETA	Q865z5	alces alces
559	35.5	50.0	497	2	Q8T162_METAC	Q8t162	methanosarc	632	35	49.3	256	2	Q865Z6_9CETA	Q865z6	alces alces
560	35.5	50.0	729	2	Q7OZG5_GIALA	Q7ozg5	giardia lam	633	35	49.3	256	2	Q6UWU7_ODOHE	Q6uuw7	odocoileus
561	35.5	50.0	831	2	Q4Y774_PLACH	Q4y774	plasmodium	634	35	49.3	256	2	Q6UWU8_9CETA	Q6uuw8	odocoileus
562	35.5	50.0	863	1	DPB6_BOVIN	P42659	bos taurus	635	35	49.3	256	2	Q5UAF3_RANTA	Q5uaf3	rangifer ta
563	35.5	50.0	1032	2	Q7JLZ2_CABEL	Q7j1z2	caenorhabdi	636	35	49.3	256	2	Q9MZU8_9CETA	Q9mzu8	odocoileus
564	35.5	50.0	1034	2	Q61J44_CABBR	Q61j44	caenorhabdi	637	35	49.3	256	2	Q6B507_CERNI	Q6b507	cervus nipp
565	35.5	50.0	1035	2	Q21079_CABER	Q21079	caenorhabdi	638	35	49.3	256	2	Q6DN38_CERNI	Q6dn38	cervus nipp
566	35.5	50.0	1040	1	Y043_CABEL	P34681	caenorhabdi	639	35	49.3	256	2	Q62670_CERNI	Q62670	cervus elap
567	35.5	50.0	1905	2	Q9XTP6_PLABE	Q9xtp6	plasmodium	640	35	49.3	256	2	Q549D4_CERNI	Q549d4	cervus elap
568	35	49.3	40	1	HBA2_UROHA	P18980	urosaatyx h	641	35	49.3	256	2	Q02841_ODOHE	Q02841	odocoileus
569	35	49.3	51	2	Q5BS46_SCHJA	Q5bs46	schistosoma	642	35	49.3	256	2	Q7J1Q1_9CETA	Q7j1q1	odocoileus
570	35	49.3	61	2	Q66X04_922Z2	Q66x04	uncultured	643	35	49.3	256	2	Q693S1_CAPCA	Q693s1	capreolus c
571	35	49.3	71	2	Q7S038_NEUCR	Q7s038	neurospora	644	35	49.3	260	2	Q887H9_PSESM	Q887h9	pseudomonas
572	35	49.3	84	2	Q42CVO_9VIRU	Q42cvo	bacterioph	645	35	49.3	261	2	Q5BM00_9TREM	Q5bm00	paragonimus
573	35	49.3	85	2	Q8UIAG_PYRPU	Q8uiag	pyrococcus	646	35	49.3	261	2	Q5BM01_9TREM	Q5bm01	paragonimus
574	35	49.3	86	2	Q8NIT7_NEUCR	Q8nit7	neurospora	647	35	49.3	264	2	Q9MZU6_ANTAM	Q9mzu6	antilocapra
575	35	49.3	94	2	Q8JUKM_9VIRU	Q8jukm	heliothis z	648	35	49.3	264	2	Q6E6L9_9ASTR	Q6e6l9	helianthus
576	35	49.3	96	2	Q858Z6_9CAUD	Q858z6	bacterioph	649	35	49.3	264	2	Q6E6M0_9ASTR	Q6e6m0	helianthus
577	35	49.3	96	2	Q38025_BPPEC	Q38025	bacterioph	650	35	49.3	264	2	Q4E6M3_ASITR	Q4e6m3	asimina tri
578	35	49.3	101	2	Q52GQ2_MAGGR	Q52gq2	magnaporthe	651	35	49.3	264	2	Q4ZXD6_PSESY	Q4zxd6	pseudomonas
579	35	49.3	118	2	Q9YF53_COLL1	Q9yf53	columba liv	652	35	49.3	265	2	Q8E6L8_SARPR	Q8e6l8	sarracenia
580	35	49.3	120	2	Q9CHY5_LACLA	Q9chy5	lactococcus	653	35	49.3	272	2	Q57IM5_SALCH	Q57im5	salmonella
581	35	49.3	122	2	Q5R0G3_IDILO	Q5r0g3	idiomarina	654	35	49.3	276	2	Q4IEW0_GIBZE	Q4iew0	gibberella
582	35	49.3	136	2	Q8VQ14_9BACT	Q8vq14	uncultured	655	35	49.3	282	2	Q73NX2_TREDE	Q73nx2	treponema d
583	35	49.3	145	2	Q7WBI1_BORPA	Q7wb1	bordetella	656	35	49.3	283	2	Q88MM2_PSEPK	Q88mm2	pseudomonas
584	35	49.3	145	2	Q7WV71_BORBR	Q7wv71	bordetella	657	35	49.3	285	2	Q6QVVB_VEROI	Q6qvva	verberna off
585	35	49.3	160	1	YRKB_BACSU	P54432	bacillus su	658	35	49.3	286	2	Q5DVT8_MIMPU	Q5dvt8	minosa pud
586	35	49.3	160	2	Q4MJW4_BACCE	Q4mjw4	bacillus ce	659	35	49.3	288	1	GIL2_ENTHI	Q51d00	entamoeba h
587	35	49.3	161	2	Q83M96_SHIFL	Q83m96	shigella fl	660	35	49.3	304	2	Q7TWV0_MYCBO	Q7twv0	mycobacteri
588	35	49.3	169	2	Q7MTQ5_PORGI	Q7mtq5	porphyromon	661	35	49.3	304	2	P96871_MYCTU	P96871	mycobacteri
589	35	49.3	172	2	Q46542_BAGNO	Q46542	bacteroides	662	35	49.3	311	2	Q9CCK8_MYCLE	Q9cck8	mycobacteri
590	35	49.3	182	2	Q4RT00_TETNG	Q4rt00	tetracodon n	663	35	49.3	319	2	Q67ER0_XENLA	Q67er0	xenopus lae
591	35	49.3	185	2	Q97694_CERNI	Q97694	cervus nipp	664	35	49.3	323	2	Q7XV16_ORYSA	Q7xv16	oryza sativ
592	35	49.3	188	2	Q6PBM8_BRARE	Q6pbm8	brachydanio	665	35	49.3	326	2	Q62010_CERCA	Q62010	ceratitidis c
593	35	49.3	191	2	Q4S3J49_TETNG	Q4s3j49	tetracodon n	666	35	49.3	326	2	Q9NFX5_CERCA	Q9nfx5	ceratitidis c
594	35	49.3	199	2	Q6NRC2_XENLA	Q6nrc2	xenopus lae	667	35	49.3	328	2	Q6WU80_LACRE	Q6wu80	lactobacill
595	35	49.3	201	2	Q9TJ72_CLOAB	Q9tj72	clostridium	668	35	49.3	328	2	Q7VLI1_9TRYP	Q7vli1	trypanosoma
596	35	49.3	201	2	Q4TIZ8_TETNG	Q4tiz8	tetracodon n	669	35	49.3	329	2	Q762L9_KLEPN	Q762l9	klebsiella
597	35	49.3	202	2	Q91406_9TELE	Q91406	salmo sp. i	670	35	49.3	334	2	Q5XL46_KLEPN	Q5xl46	klebsiella
598	35	49.3	204	2	Q97629_9CETA	Q97629	odocoileus	671	35	49.3	334	2	Q7XW18_ORYSA	Q7xw18	oryza sativ
599	35	49.3	204	2	Q9TSI8_9CETA	Q9tsi8	odocoileus	672	35	49.3	337	2	Q7XW18_ORYSA	Q7xw18	oryza sativ
600	35	49.3	204	2	Q9TSI8_9CETA	Q9tsi8	odocoileus	673	35	49.3	341	2	Q73914_BACCI	Q73914	bacillus ce
601	35	49.3	206	2	Q528V1_ORYSA	Q528v1	oryza sativ	674	35	49.3	342	2	Q83V29_PSEPL	Q83v29	pseudomonas
602	35	49.3	211	2	Q77787_ANTAM	Q77787	antilocapra	675	35	49.3	342	2	Q8RLH3_SALPU	Q8rlh3	salmonella
603	35	49.3	211	2	Q7SZ54_BRARE	Q7sz54	brachydanio	676	35	49.3	342	2	Q8RLH4_SALDU	Q8rlh4	salmonella
604	35	49.3	212	2	Q97698_CEREL	Q97698	cervus elap	677	35	49.3	342	2	Q8RLH5_SALGL	Q8rlh5	salmonella
605	35	49.3	220	2	Q02825_ODOHE	Q02825	odocoileus	678	35	49.3	346	2	Q5KQV4_KLEPN	Q5kqv4	klebsiella
606	35	49.3	220	2	Q73J72_ODOHE	Q73j72	odocoileus	679	35	49.3	351	2	P93018_ARATH	P93018	arabidopsis
607	35	49.3	224	2	Q6VG33_SIVCZ	Q6vg33	chimpanzee	680	35	49.3	355	2	Q4S366_TETNG	Q4s366	tetracodon n
608	35	49.3	226	2	Q6VML8_PSEPU	Q6vml8	pseudomonas	681	35	49.3	357	2	Q7SHB7_NEUCR	Q7shb7	neurospora
609	35	49.3	228	2	Q5FRK7_GLUOX	Q5frk7	gluconobact	682	35	49.3	362	2	Q4J9V4_SULAC	Q4j9v4	sulfolobus
610	35	49.3	229	2	Q5UWE5_HALMA	Q5uwe5	haloarcula	683	35	49.3	362	2	Q9HSN1_HALSA	Q9hsn1	halobacteri
611	35	49.3	235	2	Q97695_GIRCA	Q97695	giraffa cam	684	35	49.3	363	2	Q66AV6_YERPE	Q66av6	versinia pe
612	35	49.3	235	2	Q4FCM4_SCOMX	Q4fcm4	scophthalmu	685	35	49.3	363	2	Q8ZE24_YERPE	Q8ze24	versinia pe
613	35	49.3	240	2	Q6TRS2_USTMA	Q6trs2	ustilago ma	686	35	49.3	366	2	Q7UAG6_SHIFL	Q7uag6	shigella fl
614	35	49.3	240	2	Q4P8C1_USTMA	Q4p8c1	ustilago ma	687	35	49.3	366	2	Q83KV2_SHIFL	Q83kv2	shigella fl
615	35	49.3	244	2	Q6B506_CEREL	Q6b506	cervus elap	688	35	49.3	366	2	Q8XAS0_ECO57	Q8xas0	escherichia

689 Q8R9G5 THETN 368 2 Q8R9G5 thermoanaer 762 35 49.3 35
 690 Q5ZLB3 CHICK 368 2 Q5ZLB3 gall 763 35 49.3 35
 691 Q7WUH2 SALGL 377 2 Q7WUH2 salmonella 764 35 49.3 35
 692 QMPF SALTY 378 1 QMPF salmonella 765 35 49.3 35
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 697 Q8S9J2 ARATH 385 2 Q8S9J2 arabidopsis 770 35 49.3 35
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 699 Q4I919 GIBZE 388 2 Q4I919 gibberella 772 35 49.3 35
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 716 Q9X119 THEMA 431 2 Q9X119 thermotoga 789 35 49.3 35
 717 Q8DA83 VIBVU 434 2 Q8DA83 vibrio vuln 790 35 49.3 35
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 734 Q8FQAB COREF 476 2 Q8FQAB corynebacte 807 35 49.3 35
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 759 Q74ND5 NANEQ 537 2 Q74ND5 nanoarchaeu 832 35 49.3 35
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Q97M33 CLOSTRIDIUM 549 2 Q97M33 CLOAB 549 2 Q97M33 clostridium
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 Q99JX7 MUS MUSCULU 618 1 NXF1 MOUSE 618 1 NXF1 mouse
 Q8LJ95 ORYSA 627 2 Q8LJ95 ORYSA 627 2 Q8LJ95 oryza sativ
 Q9RG3 PSECL 637 2 Q9RG3 PSECL 637 2 Q9RG3 pseudomonas
 Q8G6M5 BIFLO 638 2 Q8G6M5 bifidobacte 638 2 Q8G6M5 bifidobacte
 Q9XEC8 ARATH 648 2 Q9XEC8 arabidopsis 648 2 Q9XEC8 arabidopsis
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 Q27798 METHANOBACT 666 2 Q27798 METHANOBACT 666 2 Q27798 methanobact
 Q86170 BACILLUS TH 682 1 C19BA BACUH 682 1 C19BA bacuh
 Q8UDAI AGRT5 696 2 Q8UDAI AGRT5 696 2 Q8UDAI agrobacteri
 Q9W191 DROSOPHILA 716 2 Q9W191 DROME 716 2 Q9W191 drosophila
 Q8DLB4 SYNEL 718 2 Q8DLB4 SYNEL 718 2 Q8DLB4 synechococc
 Q5MYA2 SYNEL 725 2 Q5MYA2 SYNEL 725 2 Q5MYA2 synechococc
 Q5MYA2 SYNEL 725 2 Q5MYA2 SYNEL 725 2 Q5MYA2 synechococc
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 Q4ZCG0 BACTERIOPHA 815 2 Q4ZCG0 BACTERIOPHA 815 2 Q4ZCG0 bacterioph
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 Q5K8S9 CRYNE 1004 2 Q5K8S9 CRYNE 1004 2 Q5K8S9 cryptococcu
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 LRP4 RAT 1905 1 LRP4 RAT 1905 1 LRP4 rattus norv

835	35	49.3	1905	2	Q5K7Z5_HUMAN	Q5ktz5	homo sapien	908	34	47.9	198	2	Q57B86_BRUAB	Q57bs6	brucella ab
836	35	49.3	1905	2	Q76LU2_RAT	Q76lu2	rattus norv	909	34	47.9	198	2	Q8FZ96_BRUSU	Q8fz96	bruceella su
837	35	49.3	1946	2	Q41IQ8_GIBZE	Q41iq8	gibberella	910	34	47.9	198	2	Q8YI19_BRUME	Q8yil9	bruceella me
838	35	49.3	1950	1	LRP4_HUMAN	Q75096	homo sapien	911	34	47.9	199	2	Q5XH87_XENTR	Q5xh87	xenopus tro
839	35	49.3	2134	2	Q6R3Z5_9PICO	Q6r3z5	avian encep	912	34	47.9	202	1	HOXM_ALCEU	P31909	alcaligenes
840	35	49.3	2134	2	Q6NQ42_9PICO	Q6nq42	avian encep	913	34	47.9	202	2	Q57PA2_SALCH	Q57pa2	salmonella
841	35	49.3	2134	2	Q9YLS9_9PICO	Q9yls9	avian encep	914	34	47.9	202	2	Q5FJDB_SALPA	Q5fjd8	salmonella
842	35	49.3	2214	2	Q20219_CAEEL	Q20219	caenorhabdi	915	34	47.9	202	2	Q8Z711_SALTY	Q8z711	salmonella
843	35	49.3	2222	2	Q619R0_CAEBR	Q619r0	caenorhabdi	916	34	47.9	202	2	Q8ZPH2_SALTY	Q8zph2	salmonella
844	35	49.3	2332	2	Q6ALH4_DSPPR	Q6alh4	desulfotale	917	34	47.9	202	2	Q8QMT6_COMPX	Q8qmt6	cowpox viru
845	35	49.3	2363	2	Q6ALH2_DSPPS	Q6alh2	desulfotale	918	34	47.9	203	1	VA17_VACCC	Q6s592	vaccinia vi
846	35	49.3	2504	2	Q4QP93_LEIMA	Q4qp93	leishmania	919	34	47.9	203	1	VA17_VACCV	P68593	vaccinia vi
847	35	49.3	2542	2	Q4QIH1_LEIMA	Q4qih1	leishmania	920	34	47.9	203	1	VA17_VACVV	P68593	vaccinia vi
848	35	49.3	2571	2	Q87Y04_BACSU	Q87y04	bacillus su	921	34	47.9	203	2	Q57Z26_9POXV	P68594	vaccinia vi
849	35	49.3	2589	2	Q7YY17_CRYPV	Q7yy17	cryptospori	922	34	47.9	203	2	Q6RZG5_9POXV	Q6rzg5	rabbitpox v
850	35	49.3	2661	2	Q5CKT8_CRYHO	Q5ckt8	cryptospori	923	34	47.9	203	2	Q76PV4_VAVR	Q76pv4	variola mln
851	35	49.3	2664	2	Q5CX88_CRYPV	Q5cx88	cryptospori	924	34	47.9	203	2	Q76ZQ1_9POXV	Q76zq1	vaccinia vi
852	35	49.3	2695	2	Q4Q3P5_LEIMA	Q4q3p5	leishmania	925	34	47.9	203	2	Q775Q8_CAMPS	Q775q8	camelopox vi
853	35	49.3	2910	2	Q6BFC5_PASTE	Q6bfc5	paramecium	926	34	47.9	203	2	Q77T13_VACCT	Q77t13	vaccinia vi
854	35	49.3	4810	2	Q4YRYS_PLABE	Q4yr55	plasmodium	927	34	47.9	203	2	Q8V2N8_CAMPN	Q8v2n8	camelopox vi
855	35	49.3	5071	2	P91905_CAEEL	P91905	caenorhabdi	928	34	47.9	203	2	Q8QDN7_COMPX	Q8qdn7	cowpox viru
856	35	49.3	5107	2	Q94279_CAEEL	Q94279	caenorhabdi	929	34	47.9	205	2	Q9G078_9CAUD	Q9g078	bacterioph
857	35	49.3	5207	2	Q6OWP5_CAEER	Q6owp5	caenorhabdi	930	34	47.9	206	2	Q6DV60_9ACTO	Q6dv60	streptomyc
858	35	49.3	6584	1	RIAB_CVPPU	Q91w06	p replicase	931	34	47.9	207	2	Q414W7_GIBZE	Q414w7	gibberella
859	34.5	48.6	153	2	Q87011_9VIRU	Q87011	subterranea	932	34	47.9	208	2	Q5E6J5_VIBF1	Q5e6j5	vibrio fib
860	34.5	48.6	177	2	Q8PX17_METMA	Q8px17	methanosarc	933	34	47.9	209	2	Q6F1H7_MESFL	Q6f1h7	mesoplasma
861	34.5	48.6	183	2	Q8TH17_METAC	Q8th17	methanosarc	934	34	47.9	220	2	Q4UMF5_XANCP	Q4uuf5	xanthomonas
862	34.5	48.6	335	2	Q6CVC2_KLULA	Q6cvc2	kluyveromyc	935	34	47.9	220	2	Q8P7P5_XANCP	Q8p7p5	xanthomonas
863	34.5	48.6	417	2	Q93U10_9BRAD	Q93u10	bradyrhizob	936	34	47.9	220	2	Q8PJ09_XANAC	Q8pj09	xanthomonas
864	34.5	48.6	428	2	Q4H7S3_9DEIO	Q4h7s9	deinococcus	937	34	47.9	226	2	Q8EHS1_SHEON	Q8ehs1	shewanella
865	34.5	48.6	443	1	HSJU_NITEU	Q82ap6	nitrosomona	938	34	47.9	232	2	P74171_SYNY3	P74171	synecocyst
866	34.5	48.6	712	2	Q9AQK7_VIBPA	Q9aqk7	vibrio para	939	34	47.9	236	2	Q4TBY7_TETNG	Q4tby7	tetradocyt
867	34.5	48.6	712	2	Q87FM3_VIBPA	Q87fm3	vibrio para	940	34	47.9	237	2	Q9JND1_STRPY	Q9jnd1	streptococ
868	34	47.9	15	2	Q7M0G8_9MURI	Q7m0g8	mus sp. cd3	941	34	47.9	238	2	Q9Y098_PRRAM	Q9y098	periplaneta
869	34	47.9	52	2	Q94EX7_NICTO	Q94ex7	nicotiana t	942	34	47.9	246	2	Q4ZP21_PSESY	Q4zp21	pseudomonas
870	34	47.9	52	2	Q94EX8_TOBAC	Q94ex8	nicotiana t	943	34	47.9	247	1	DDPX_SYNY3	P74268	synecocyst
871	34	47.9	52	2	Q94EX9_NICSY	Q94ex9	nicotiana s	944	34	47.9	247	2	Q87X15_PSESM	P74268	pseudomonas
872	34	47.9	52	2	Q94EY0_TOBAC	Q94ey0	nicotiana t	945	34	47.9	247	2	Q89MM7_BRAJA	Q89mm7	bradyrhizob
873	34	47.9	70	2	Q15809_PARCA	O15809	paramecium	946	34	47.9	248	2	Q4ZUUI_PSESY	Q4zuui	pseudomonas
874	34	47.9	82	2	Q6RGQ3_STRLA	Q6rgq3	streptomyc	947	34	47.9	249	1	Y84E_SCHPO	O14359	schizosacch
875	34	47.9	101	2	Q5UX42_HALMA	O5ux42	haloarcula	948	34	47.9	250	2	Q53R93_HUMAN	O53r93	homo sapien
876	34	47.9	104	2	Q89BV6_BRAJA	Q89bv6	bradyrhizob	949	34	47.9	251	2	P94940_METKA	P94940	methanopyru
877	34	47.9	108	2	Q7TT99_HAEDU	Q7tt99	haemophilus	950	34	47.9	252	2	Q5F0H0_NEUCR	Q5f0h0	neurospora
878	34	47.9	119	2	Q893T0_CLOTE	Q893t0	clostridium	951	34	47.9	254	2	Q7QXB3_ORYSA	Q7qxb3	oryza sativ
879	34	47.9	123	2	Q97GZ7_CLOAB	Q97gz7	clostridium	952	34	47.9	254	2	Q9AYK2_ORYSA	Q9ayk2	oryza sativ
880	34	47.9	129	2	Q7RUJ8_NEUCR	Q7ruj8	neurospora	953	34	47.9	255	2	Q8U324_PYRFU	Q8u324	pyrococcus
881	34	47.9	130	2	Q5UAL2_BOMMO	Q5ual2	bombyx mori	954	34	47.9	255	2	Q6VRY2_NEIME	Q6vry2	neisseria m
882	34	47.9	130	2	Q6EV20_PAPDA	Q6ev20	papilio dar	955	34	47.9	255	2	Q6VRZ1_NEIME	Q6vrz1	neisseria m
883	34	47.9	133	2	Q30005_ARCFU	O30005	archaeoglob	956	34	47.9	255	2	Q6VS04_NEIME	Q6vs04	neisseria m
884	34	47.9	136	2	Q8VQI5_9BACT	P83113	telmatobius	957	34	47.9	255	2	Q6VS07_NEIME	Q6vs07	neisseria m
885	34	47.9	137	1	HBA2_TELPE	P83113	telmatobius	958	34	47.9	255	2	Q6VS07_NEIME	Q6vs07	neisseria m
886	34	47.9	138	2	Q93D86_STRFU	Q93d86	streptococ	959	34	47.9	255	2	Q6VS09_NEIME	Q6vs09	neisseria m
887	34	47.9	144	2	Q6C7W2_YARLI	Q6c7w2	yarrowia li	960	34	47.9	259	2	Q6N8Z4_RHOPA	Q6n8z4	rhodospseudo
888	34	47.9	150	2	Q9HJ22_THEAC	Q9hj22	thermoplasma	961	34	47.9	260	2	Q4URB3_XANCP	Q4urb3	xanthomonas
889	34	47.9	157	2	Q981M5_RHILO	Q981m5	rhizobium l	962	34	47.9	260	2	Q8PC71_XANCP	Q8pc71	xanthomonas
890	34	47.9	157	2	Q8PNV8_XANAC	Q8pnv8	xanthomonas	963	34	47.9	261	2	Q9JND9_STRPY	Q9jnd9	streptococ
891	34	47.9	159	2	Q6CF10_YARLI	Q6cf10	yarrowia li	964	34	47.9	261	2	Q9JNW3_STRPY	Q9jnw3	streptococ
892	34	47.9	165	1	D8BE_CHRVU	Q48476	chromatium	965	34	47.9	262	2	Q9VIX5_DROME	Q9vix5	drosofila
893	34	47.9	169	1	CMEE_BRAJA	P45401	bradyrhizob	966	34	47.9	262	2	Q9JNN9_STRPY	Q9jnn9	streptococ
894	34	47.9	171	2	Q97Z02_SULSO	Q97z02	sulfolobus	967	34	47.9	262	2	Q9JNV4_STRPY	Q9jnv4	streptococ
895	34	47.9	171	2	Q8DB56_VIBVU	Q8db56	vibrio vuln	968	34	47.9	263	2	Q9AB49_CAUCR	Q9ab49	caulobacter
896	34	47.9	172	2	Q5TUN4_ANOGA	Q5tun4	anopheles g	969	34	47.9	264	2	Q9JNS2_STRPY	Q9jns2	streptococ
897	34	47.9	173	1	R1MM_FUSNN	Q8sgk8	fusobacteri	970	34	47.9	264	2	Q9JNS2_STRPY	Q9jns2	streptococ
898	34	47.9	173	2	Q7P718_FUSNV	Q7p718	fusobacteri	971	34	47.9	264	2	Q50E17_LACRE	Q50e17	lactobacill
899	34	47.9	173	2	Q4HL71_CAMLA	Q4hl71	campylobact	972	34	47.9	264	2	Q8R9H4_THETN	Q8r9h4	thermoanaer
900	34	47.9	176	2	Q7XUL9_ORYSA	Q7xul9	oryza sativ	973	34	47.9	265	2	Q9JNR3_STRPY	Q9jnr3	streptococ
901	34	47.9	182	2	Q5XTN6_BRARE	Q5xtn6	brachydanio	974	34	47.9	266	2	Q9JNC4_STRPY	Q9jnc4	streptococ
902	34	47.9	180	2	Q75ID8_ORYSA	Q75id8	oryza sativ	975	34	47.9	267	2	Q5FMM6_LACAC	Q5fmm6	lactobacill
903	34	47.9	184	2	Q87ML4_VIBPA	Q87ml4	vibrio para	976	34	47.9	268	2	Q9JNJ3_STRPY	Q9jnj3	streptococ
904	34	47.9	189	2	Q8L2K5_VIBVU	Q8l2k5	vibrio vuln	977	34	47.9	268	2	Q8UI22_AGRTS	Q8ui22	agrobacteri
905	34	47.9	190	2	Q7MIR6_VIBVU	Q7mir6	vibrio vuln	978	34	47.9	269	2	Q51SV1_WAGGR	Q51sv1	magnaporthe
906	34	47.9	192	2	Q4T815_TETNG	Q4t815	tetradocyt	979	34	47.9	269	2	Q4PR49_ORYSA	Q4pr49	oryza sativ
907	34	47.9	195	2	Q5V014_HALMA	Q5v014	haloarcula	980	34	47.9	269	2	Q9JP01_STRPY	Q9jp01	streptococ

981 34 47.9 270 2 Q7D237 agrobacteri
 982 34 47.9 270 2 Q50EL2 rhizobium f
 983 34 47.9 270 2 Q8XJ55 clostridium
 984 34 47.9 271 2 Q9JN11 streptococc
 985 34 47.9 271 2 Q9JN41 streptococc
 986 34 47.9 272 2 Q9JNA5 streptococc
 987 34 47.9 272 2 Q9JN06 streptococc
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 990 34 47.9 274 2 Q9JN06 streptococc
 991 34 47.9 275 2 Q9JN02 streptococc
 992 34 47.9 276 2 Q9JN18 streptococc
 993 34 47.9 276 2 Q9JN05 streptococc
 994 34 47.9 277 2 Q9JN05 streptococc
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 996 34 47.9 279 2 Q9JN01 streptococc
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 1000 34 47.9 279 2 Q9JN04 streptococc

ALIGNMENTS

RESULT 1
 Q6LZ19 METMP PRELIMINARY; PRT; 745 AA.
 AC Q6LZ19;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein precursor.
 GN OrderedLocustNames=MMP0638;
 OS Methanococcus maripaludis.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcus.
 OX NCBI_TaxID=39152;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S2 / LL;
 RX PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
 RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
 RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
 RA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
 RA Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
 RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
 RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
 RA "Complete genome sequence of the genetically tractable
 RT hydrogenotrophic methanogen Methanococcus maripaludis.";
 RL J. Bacteriol. 186:6956-6969 (2004).
 DR EMBL; BX957220; CAF30194.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 22 Potential.
 SQ SEQUENCE 745 AA; 84573 MW; 18D855215DEEB953 CRC64;

Query Match 77.5%; Score 55; DB 2; Length 745;
 Best Local Similarity 90.9%; Pred. No. 0.6;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YGGQSTVYMDA 13
 |||||
 Db 128 YGGQSTVYMDA 138

RESULT 2
 Q5B9S1 EMENI PRELIMINARY; PRT; 313 AA.
 AC Q5B9S1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.

GN ORFNames=AN2709.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepl Y., Collamore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACD01000047; EAA63111.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 313 AA; 33767 MW; 400489B1FE1B092B CRC64;

Query Match 50.6%; Score 43; DB 2; Length 313;
 Best Local Similarity 70.0%; Pred. No. 36;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
 |||||
 Db 138 DDYGGQSTYV 147

RESULT 3
 Q5AR04 EMENI PRELIMINARY; PRT; 381 AA.
 AC Q5AR04;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN9276.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepl Y., Collamore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Karatas A.,

RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Menes L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rhee C., Rogov P.,
 RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RL "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACD01000172; EAA66343.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 381 AA; 41698 MW; A2173C723D5D2BEE CRC64;
 Query Match 60.6%; Score 43; DB 2; Length 381;
 Best Local Similarity 70.0%; Pred. No. 44; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDYGGQSTTV 10
 Db 149 DDYGGMSAYL 158
 RESULT 4
 ID Q5V2G0_HALMA PRELIMINARY; PRT; 411 AA.
 AC Q5V2G0_
 DT 01-FEB-2005 (TRENBLrel. 29, Created)
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
 DE Heme biosynthesis protein.
 GN Name=nlrJ; OrderedLocusNames=rrnAC1363;
 OS Haloarcula marismortui (Haloaracterium marismortui)
 OC Archaea; Euryarchaeota; Halobacterium; Halobacteriales;
 OC Halobacteriaceae; Haloarcula.
 OX NCBI_TaxID=2238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 43049;
 RX PubMed=15520287; DOI=10.1101/gr.2700304; Pan M., Glusman G.,
 RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
 RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
 RA Date S.V., Marcotte E., Hood L., Ng W.V.;
 RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
 RT the Dead Sea.";
 RL Genome Res. 14:2221-2234(2004).
 DR EMBL; AY596297; AAV46292.1; -; Genomic DNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR InterPro; IPR006638; ELP3/WiB/NiEB.
 DR InterPro; IPR007197; Radical_SAM.
 DR Pfam; PF04055; Radical_SAM.
 DR SMART; SM00729; ELP3; 1.
 KW Complete proteome.
 SQ SEQUENCE 411 AA; 45166 MW; 4AFB3ABC56C6A989 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 411;
 Best Local Similarity 58.3%; Pred. No. 48;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 DYGGQSTVMDA 13
 Db 214 DYGGRGTEIVDA 225

RESULT 5
 ID Q83238 TREPA PRELIMINARY; PRT; 450 AA.
 AC Q83238_
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DE Preprotein translocase subunit (SecY).
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 GN OrderedLocusNames=TP0208;
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
 RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
 RA Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D.,
 RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
 RA Weidman J.P., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 DR EMBL; AE001203; AAC65198.1; -; Genomic_DNA.
 DR PIR; P71351; P71351.
 DR TIGR; TP0208;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015450; F:protein translocase activity; IEA.
 DR GO; GO:0009306; P:protein secretion; IEA.
 DR GO; GO:0006605; P:protein targeting; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR001220; Lectin_legB.
 DR InterPro; IPR002208; SecY.
 DR Pfam; PF00344; SecY; 1.
 DR PRINTS; PR00303; SECYTRNLCASE.
 DR TIGRfam; TIGR00967; 3a0501a007; 1.
 DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 KW Complete proteome; Protein transport; Translocation; Transmembrane;
 KW Transport.
 SQ SEQUENCE 450 AA; 50265 MW; 892BF3217F3B6E7E CRC64;
 Query Match 60.6%; Score 43; DB 2; Length 450;
 Best Local Similarity 87.5%; Pred. No. 52;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YGGQSTTV 10
 Db 253 YGGQSTVI 260
 RESULT 6
 ID Q4WBS1_ASPFU PRELIMINARY; PRT; 466 AA.
 AC Q4WBS1_
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Endo-1,4-beta-mannosidase, putative.
 GN ORFNames=Afu8g07030;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Nierman W., Fain A., Anderson M.J., Wortman J., Kim H.Stanley.,
 RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,

RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kunagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penalba M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000013; EAL85463.1; -; Genomic DNA.
SQ SEQUENCE 466 AA; 50293 MW; 5230BEF83786C827 CRC64;
Query Match 60.6%; Score 43; DB 2; Length 466;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 DDYGGQSTYV 10
||||| : ||
Db 238 DDYGGMAYV 247
RESULT 7
Q4WAF0 ASPFU PRELIMINARY; PRT; 477 AA.
ID Q4WAF0 ASPFU PRELIMINARY;
AC Q4WAF0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Endo-1,4-beta-mannosidase.
GN ORFNames=Afu701070;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OK NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley J.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kunagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penalba M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000015; EAL84786.1; -; Genomic DNA.
SQ SEQUENCE 477 AA; 52712 MW; 427E0B3F3B48ADA2 CRC64;
Query Match 60.6%; Score 43; DB 2; Length 477;
Best Local Similarity 70.0%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 DDYGGQSTYV 10
||||| : ||
Db 241 DDYGGMAYV 250
RESULT 8
NANT_YERPE STANDARD; PRT; 510 AA.
ID NANT_YERPE
AC QBZCH3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Putative sialic acid transporter (Sialic acid permease).
GN Name=nant; OrderedLocustNames=YPO3016, Y1465, YP2640;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OK NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans";
RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: May be a sugar-cation symporter involved in sialic acid
CC uptake (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (by similarity).
CC -!- INDUCTION: By N-acetylneuraminic acid (Probable).
CC -!- SIMILARITY: Belongs to the major facilitator superfamily. Sugar
CC transporter family. Sialic acid transporter (TC 2.A.1.12.1)
CC subfamily.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----

DR EMBL; AJ414154; CAC92259.1; -; Genomic DNA.
DR EMBL; AB013749; AA85036.1; -; Genomic DNA.
DR EMBL; AB017137; AA562832.1; -; Genomic DNA.

DR HAMAP; MF_01238; -; 1.

DR InterPro; IPR007114; MFS.

DR InterPro; IPR011701; MFS 1.

DR InterPro; IPR005829; Sug_transporter.

DR Pfam; PF07690; MFS 1; 1.

DR PROSITE; PS0850; MFS; 1.

DR PROSITE; PS0216; SUGAR_TRANSPORT_1; FALSE NEG.

DR PROSITE; PS0217; SUGAR_TRANSPORT_2; FALSE NEG.

KW Complete proteome; Inner membrane; Membrane; Sugar transport;

KW Transmembrane; Transport.

FT TRANSMEM 35 55 Potential.

FT TRANSMEM 72 92 Potential.

FT TRANSMEM 99 119 Potential.

FT TRANSMEM 120 140 Potential.

FT TRANSMEM 158 178 Potential.

FT TRANSMEM 180 200 Potential.

FT TRANSMEM 240 260 Potential.

FT TRANSMEM 262 282 Potential.

FT TRANSMEM 295 315 Potential.

FT TRANSMEM 330 350 Potential.

FT TRANSMEM 371 391 Potential.

FT TRANSMEM 392 412 Potential.

FT TRANSMEM 418 438 Potential.

FT TRANSMEM 449 469 Potential.

FT CONFLICT 182 182 L -> P (in Ref. 3).

SQ SEQUENCE 510 AA; 55278 MW; 74AFC49DFDCB5507 CRC64;

Query Match 60.6%; Score 43; DB 1; Length 510;

Best Local Similarity 58.3%; Pred. No. 60;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 DYGGQSTVYVMDA 13

DB 138 EYGSSTVYVES 149

Result 9

NANT YERPS STANDARD; PRT; 510 AA.

AC Q668K2;

DT 10-MAY-2005 (Rel. 47, Created)

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Putative sialic acid transporter (Sialic acid permease).

GN Name=nant; OrderedLocustNames=YPTB2736;

OS Yersinia pseudotuberculosis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=633;

RN [1]_TaxID=633;

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=IP32953 / Serotype 1;

RX PubMed=15358858; DOI=10.1073/pnas.0404012101;

RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,

RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,

RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,

RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,

RA Dierse A., Hauser L.J., Garcia E.;

RT "Insights into the evolution of Yersinia pestis through whole-genome

RT comparison with Yersinia pseudotuberculosis."

RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

CC -!- FUNCTION: May be a sugar-cation symporter involved in sialic acid

CC uptake (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (By similarity).

CC -!- INDUCTION: By N-acetylneuraminate (Probable).
CC -!- SIMILARITY: Belongs to the major facilitator superfamily. Sugar
CC transporter family. Sialic acid transporter (TC 2.A.1.12.1)
CC subfamily.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----

CC EMBL; BX936398; CAH21974.1; -; Genomic DNA.

CC HAMAP; MF_01238; -; 1.

CC InterPro; IPR011701; MFS 1.

CC InterPro; IPR005829; Sug_transporter.

CC Pfam; PF07690; MFS 1; 1.

DR PROSITE; PS0216; SUGAR_TRANSPORT_1; FALSE NEG.

DR PROSITE; PS0217; SUGAR_TRANSPORT_2; FALSE NEG.

KW Complete proteome; Inner membrane; Membrane; Sugar transport;

KW Transmembrane; Transport.

FT TRANSMEM 35 55 Potential.

FT TRANSMEM 72 92 Potential.

FT TRANSMEM 99 119 Potential.

FT TRANSMEM 120 140 Potential.

FT TRANSMEM 161 181 Potential.

FT TRANSMEM 183 203 Potential.

FT TRANSMEM 240 260 Potential.

FT TRANSMEM 262 282 Potential.

FT TRANSMEM 295 315 Potential.

FT TRANSMEM 330 350 Potential.

FT TRANSMEM 371 391 Potential.

FT TRANSMEM 392 412 Potential.

FT TRANSMEM 418 438 Potential.

FT TRANSMEM 449 469 Potential.

SQ SEQUENCE 510 AA; 55262 MW; 2858294759DDA448 CRC64;

Query Match 60.6%; Score 43; DB 1; Length 510;

Best Local Similarity 58.3%; Pred. No. 60;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 DYGGQSTVYVMDA 13

DB 138 EYGSSTVYVES 149

Result 10

QSW6G0 ORYSA PRELIMINARY; PRT; 520 AA.

ID QSW6G0 ORYSA PRELIMINARY; PRT; 520 AA.

AC QSW6G0;

DT 01-FEB-2005 (TREMBLrel. 29, Created)

DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)

DE Hypothetical protein OSJNB0006B22.2 (Hypothetical protein

DE OSJNB00059K16.9).

GN Name=OSJNB0006B22.2; Synonyms=OSJNB00059K16.9;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,

RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,

RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,

RA Hsiong J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,

RA Wu H.-P., Shaw J.-F., Yu Y., Rambo T., Currie J., Collura K.,

RA Soderlund C., Wing R.;

RT "Oryza sativa BAC OSJNB0006B22 genomic sequence."

RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

CC [2]

RP NUCLEOTIDE SEQUENCE.

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RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsuing J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F., Yu Y., Rambo T., Currie J., Collura K.,
RA Soderlund C., Wing R.;
RT "Oryza sativa BAC OSJNBb0059K16 genomic sequence.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RE EMBL; AC136224; AA04080.1; -; Genomic_DNA.
DR EMBL; AC134344; AA04120.1; -; Genomic_DNA.
DR GO; GO:0004553; F:hydrolase activity, Hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR Pfam; PF00150; Cellulase; I.
KW Hypothetical protein.
SQ SEQUENCE 520 AA; 56415 MW; 088F7CE0AF6B4BE2 CRC64;

Query Match 60.6%; Score 43; DB 2; Length 520;
Best Local Similarity 70.0%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
    |||||: ||
Db 211 DDYGGKAQYV 220

RESULT 11
ID Q53NM5 ORYSA PRELIMINARY; PRT; 230 AA.
AC Q53NM5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Hamilton J.,
RA Jones K., Tallon L., Feldblyum T., Tsitrin T., Bera J., Kim M.,
RA Jin S., Fedorsh D., Vuong H., Overton II L., Reardon M., Weaver B.,
RA Johri S., Lewis M., Utterback T., Van Aken S., Wortman J., Haas B.,
RA Koo H., Zismann V., Hsiao J., Iobst S., de Vazeilles A., White O.,
RA Salzberg S., Fraser C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC134045; AAX95343.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 230 AA; 26594 MW; 9CBCE8A602ABF91 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 230;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
    |||||: ||
Db 22 DDYGGASSY 30

RESULT 12
ID Q9LW44 ARATH PRELIMINARY; PRT; 311 AA.
AC Q9LW44;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE (1-4)-beta-mannan endohydrolase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. 1. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016878; BAB01021.1; -; Genomic_DNA.
DR HSSP; Q99036; 1QNR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 311 AA; 34984 MW; 90E2EE368D27ABCD CRC64;

Query Match 59.2%; Score 42; DB 2; Length 311;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
    |||||: ||
Db 78 DDYGGKKQYV 87

RESULT 13
ID Q9SG95 ARATH PRELIMINARY; PRT; 408 AA.
AC Q9SG95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative (1-4)-beta-mannan endohydrolase.
GN Name=T7M13.2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Rønning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011708; AAF19559.1; -; Genomic_DNA.
DR HSSP; Q99036; 1QNR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00150; Cellulase; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 408 AA; 45376 MW; 86C48FA7D311BA15 CRC64;

Query Match 59.2%; Score 42; DB 2; Length 408;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
    |||||: ||

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Db      134 DDYGGKKQTV 143

RESULT 14
QSVVQ1 NOCEA
ID QSVVQ1_NOCEA PRELIMINARY; PRT; 82 AA.
AC QSVVQ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=nf28930;
OS Nocardia farcinica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD57740.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 82 AA; 8823 MW; C9213724E8C9B6B8 CRC64;

Query Match 57.7%; Score 41; DB 2; Length 82;
Best Local Similarity 61.5%; Pred. No. 20; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 DDYGGQSTYVMDA 13
    |||||
Db      44 DDYGGALYVAGA 56

RESULT 15
Q6FR37 CANGA
ID Q6FR37_CANGA PRELIMINARY; PRT; 551 AA.
AC Q6FR37;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome I complete sequence.
GN OrderedLocusNames=CAGL0101210g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolesrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala P., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA "Genome evolution in yeasts.";
RT Nature 430:35-44(2004)
DR EMBL; CR380955; CAG60244.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 551 AA; 63532 MW; 639D2E7A75853C0E CRC64;

Query Match 57.7%; Score 41; DB 2; Length 631;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YGGQSTYVM 11
    :|||
Db      574 FGGQSTYIL 582

RESULT 17
Q6FUB1 CANGA
ID Q6FUB1_CANGA PRELIMINARY; PRT; 666 AA.
AC Q6FUB1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P15424 Saccharomyces cerevisiae YDR194c MSS116.
GN OrderedLocusNames=CAGL0F05577g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolesrame A., Boyer J., Cattolico L., Confanieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

```

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.-M., Nikolajski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RA "Genome evolution in yeasts.";
 RL Nature 430:33-44(2004).
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 DR EMBL; CR380952; CAG59137.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR000629; DEAD_box_
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KW ATP-binding; Complete proteome; Helicase; Hydrolase;
 KW Nucleotide-binding; RNA-binding
 SQ SEQUENCE 666 AA; 76320 MW; B79E1E88156C9130 CRC64;

 Query Match 57.7%; Score 41; DB 2; Length 666;
 Best Local Similarity 77.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 DDYGGQSTY 9
 Db 71 DDYRGQNTY 79

 RESULT 18
 Q73HF1 WOLPM PRELIMINARY; PRT; 778 AA.
 AC Q73HF1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glycosyl transferase, group 1 family protein / moaa/nifb/pqg family
 DE protein.
 OS OrderedLocusNames=WD0613;
 GN Wolbachia pipientis wMel.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Wolbachieae; Wolbachia.
 OK NCBI_TaxID=66077;
 CC -1-
 CC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
 RX Wu M., Sun L.V., Vanathavan J.J., Riegler M., DeBoy R.T.,
 RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
 RA Wiegand C., Madupou R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
 RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
 RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
 RA "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
 RA a streamlined genome overrun by mobile genetic elements.";
 RL PLoS Biol. 2:327-341(2004).
 DR EMBL; AE017258; AAS14314.1; -; Genomic_DNA.
 DR TIGR; WD0613; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco.trans_1.
 DR InterPro; IPR001197; RadicalSAM.
 DR Pfam; PF00534; Glycos.trans_1; 1.
 DR Pfam; PF04055; RadicalSAM; 1.

KW Complete proteome; Transferase.
 SQ SEQUENCE 778 AA; 89990 MW; 3022C3DB4F6FC65D CRC64;

 Query Match 57.7%; Score 41; DB 2; Length 778;
 Best Local Similarity 63.6%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Qy 2 DYGGQSTYVMD 12
 Db 355 DYGGWAEYVRD 365
 ||||: |||
 ||||: |||

 RESULT 19
 Q9TYX3 CAEL PRELIMINARY; PRT; 909 AA.
 ID Q9TYX3 CAEL PRELIMINARY;
 AC Q9TYX3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Egl-1 suppressor/dio uptake defective/raf enhancer protein 1 (EOR-1).
 DE 1).
 GN Name=eor-1; ORFNames=RL1E3.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol NZ;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15355793; DOI=10.1016/j.ydbio.2004.06.022;
 RA Hoepfner D.J., Spector M.S., Ratliff T.M., Kinchen J.M., Granat S.,
 RA Lin S.C., Bhushri S.S., Conradt B., Herman M.A., Hengartner M.O.;
 RT "eor-1 and eor-2 are required for cell-specific apoptotic death in C.
 RT elegans.";
 RL Dev. Biol. 274:125-138(2004).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22123406; PubMed=12130541; DOI=10.1101/gad.998402;
 RA Howard R.M., Sundaram M.V.;
 RT "C. elegans EOR-1/PLZF and EOR-2 positively regulate Ras and Wnt
 RT signaling and function redundantly with LIN-25 and the SUR-2 Mediator
 RT component.";
 RL Genes Dev. 16:1815-1827(2002).
 CC -1- INTERACTION:
 CC Q22534:gei-16; NbExp=1; IntAct=EBI-322274, EBI-327642;
 DR EMBL; AF100669; AAK39268.1; -; Genomic_DNA.
 DR EMBL; AF502568; AAM74151.1; -; mRNA.
 DR EMBL; AF519108; AAM74222.1; -; mRNA.
 DR PIR; T33749; T33749.
 DR HSP; P07248; 2ADR.
 DR Interact; Q9TYX3; -.
 DR Ensembl; RL1E3.6; Caenorhabditis elegans.
 DR WormBase; WBGene00001324; eor-1.
 DR WormPep; RL1E3.6; CE19548.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF00096; zf-C2H2; 6.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00355; Znf_C2H2; 9.
 DR PROSITE; PS00097; BTB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.


```
DR PROSITE, PS50157; ZINC_FINGER_C2H2_2; 6.
SQ Complete proteome.
KW SEQUENCE 909 AA; 103916 MW; 72A869D747B733F6 CRC64;

Query Match
Best Local Similarity 57.7%; Score 41; DB 2; Length 909;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
    :|||||
Db 736 NDYGGPSTY 744

RESULT 20
O39818 9PICO
ID O39818 9PICO PRELIMINARY; PRT; 2247 AA.
AC O39818
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Polyprotein.
OS Equine rhinitis A virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=47000;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96165505; PubMed=8577774; DOI=10.1073/pnas.93.3.990;
RA Li P., Browning G.F., Suddert M.J., Crabb B.S.; foot-and-mouth disease
RT "Equine rhinovirus 1 is more closely related to foot-and-mouth disease
RT virus than to other picornaviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:990-995 (1996).
DR EMBL; L43052; AAB61952.1; -; Genomic_RNA.
DR HSP; O88590; 1TWF.
DR MEROPS; C28.002; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; F:transcription; IEA.
DR GO; GO:0019079; F:viral genome replication; IEA.
DR GO; GO:0016032; F:viral life cycle; IEA.
DR GO; GO:0019082; F:viral protein processing; IEA.
DR InterPro; IPR000199; Pept_C3_picorn.
DR InterPro; IPR004004; Pept_Calici.
DR InterPro; IPR008739; Peptidase_C28.
DR InterPro; IPR001676; Rhv.
DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_PSD.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF05408; Peptidase_C28; 1.
DR Pfam; PF00548; Peptidase_C3; 1.
DR Pfam; PF00680; RGRP_1; 1.
DR Pfam; PF00073; Rhv; 2.
DR Pfam; PF00910; RNA_helicase; 1.
DR PRINTS; PR00918; CALICVIRUSNS.
DR ProDom; PD001125; Pept_C3_picorn; 1.
KW Polyprotein.
SQ SEQUENCE 2247 AA; 249303 MW; FDCP65A0P2C55B7F CRC64;

Query Match
Best Local Similarity 57.7%; Score 41; DB 2; Length 2247;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
    :|:|:|:|:|
Db 1293 DQYNGQVVVMDA 1305

RESULT 21
Q4MOQ3 9BURK
ID Q4MOQ3 9BURK PRELIMINARY; PRT; 410 AA.
AC Q4MOQ3
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Glycosyl transferase, group 1.
GN ORFNames=Bcen2424DRAFT_6877;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Irani S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AALH01000001; EAM21975.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 410 AA; 45551 MW; A956D45B993E230F CRC64;

Query Match
Best Local Similarity 75.0%; Score 40.5; DB 2; Length 410;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 DY-GGQSTYVMD 12
    :|:|:|:|:|
Db 37 DYGGQSTYVMD 48

RESULT 22
Q6VRX5 NEILA
ID Q6VRX5 NEILA PRELIMINARY; PRT; 130 AA.
AC Q6VRX5
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative lipoprotein (fragment).
OS Neisseria lactamica.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=486;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UR5;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barriak V., Farley J.E., Howell A.,
RA Knaut M., Ooi P., Smith R.F., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100 (2004).
DR EMBL; AY330415; AAR84490.1; -; Genomic_DNA.
KW Lipoprotein.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 13922 MW; 0483035A487DA834 CRC64;
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Query Match          56.3%; Score 40; DB 2; Length 130;
Best Local Similarity 58.3%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 39 DDAGGKLTYYTD 50

RESULT 23
Q7N8E0 PHOLL PRELIMINARY; PRT; 238 AA.
AC Q7N8E0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to putative fibrial chaperone.
GN OrderedLocusNames=plu0787;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TT01;
RA MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssiuet G., Gaudriault S.,
RA Medigue C., Lanols A., Powell K., Siquier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boenare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571861; CAEI3082.1; -; Genomic_DNA.
DR HSSP; P31697; 1KTU.
DR Photolista; plu0787; -;
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0051082; F:unfolding protein binding; IEA.
DR GO; GO:0007047; P:cell wall organization and biogenesis; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001829; Pili_chaperone.
DR Pfam; PF02753; Pili_assembly_C; 1.
DR PRINTS; PR00969; CHAPERONPILI.
DR ProDom; PD001447; Pili_chaperone; 1.
DR Complete proteome.
DR ProDom; PD001447; Pili_chaperone; 1.
KW Complete proteome.
SQ SEQUENCE 238 AA; 25674 MW; E6F4239673B4470C CRC64;

Query Match          56.3%; Score 40; DB 2; Length 238;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
Db 225 NDFGGESTY 233

RESULT 24
Q63U18 BURPS PRELIMINARY; PRT; 249 AA.
AC Q63U18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative fibrial chaperone.
GN OrderedLocusNames=BPSU1799;
OS Burkholderia pseudomallei (pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243;
RA PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens C., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571965; CAH35798.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0051082; F:unfolding protein binding; IEA.
DR GO; GO:0007047; P:cell wall organization and biogenesis; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001829; Pili_chaperone.
DR Pfam; PF02753; Pili_assembly_C; 1.
DR PRINTS; PR00969; CHAPERONPILI.
DR ProDom; PD001447; Pili_chaperone; 1.
DR PROSITE; PS00635; PILI_CHAPERONE; 1.
KW Chaperone; Complete proteome.
SQ SEQUENCE 249 AA; 27035 MW; 09DDE38FEBE7A411 CRC64;

Query Match          56.3%; Score 40; DB 2; Length 249;
Best Local Similarity 64.3%; Pred. No. 98;
Matches 9; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DDYGGQST--YVMD 12
Db 227 DDYGGQVTEYVTC 240

RESULT 25
Q6VS10 NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipoprotein (fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M98-250572;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330380; AAR84455.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN <1 254 lipoprotein.
FT NON TER 1
SQ SEQUENCE 254 AA; 27130 MW; 46C7C8C0CF7859A2 CRC64;

Query Match          56.3%; Score 40; DB 2; Length 254;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 159 DDAGGKLTYYTD 170

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RESULT 26
Q6VS11 NEIME
ID Q6VS11 NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS11
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMB;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330379; AAR84454.1; -; Genomic_DNA.
DR EMBL; AY330379; AAR84454.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON TER 1 1 putative lipoprotein.
SQ SEQUENCE 254 AA; 27157 MW; 47D8CA10CF7856C4 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:|
DB 159 DDAGGKLYTID 170

RESULT 27
Q6VS12 NEIME
ID Q6VS12 NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS12
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L5-M981;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330378; AAR84453.1; -; Genomic_DNA.
DR EMBL; AY330378; AAR84453.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON TER 1 1 putative lipoprotein.
SQ SEQUENCE 254 AA; 27071 MW; FB7111E45C8868E7 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:|
DB 159 DDAGGKLYTID 170

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RESULT 28
Q6VS14 NEIME
ID Q6VS14 NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS14
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-253248, M98-250809, and 8704446;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330376; AAR84451.1; -; Genomic_DNA.
DR EMBL; AY330377; AAR84452.1; -; Genomic_DNA.
DR EMBL; AY330375; AAR84450.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON TER 1 1 putative lipoprotein.
SQ SEQUENCE 254 AA; 27131 MW; 9007A6E327D3CD06 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:|
DB 159 DDAGGKLYTID 170

RESULT 29
Q6VS19 NEIME
ID Q6VS19 NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS19
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-252976, M97-251854, CDC-1521, M98-250622, M98-250716, and
RC 2996;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330371; AAR84446.1; -; Genomic_DNA.
DR EMBL; AY330372; AAR84447.1; -; Genomic_DNA.
DR EMBL; AY330373; AAR84448.1; -; Genomic_DNA.
DR EMBL; AY330374; AAR84449.1; -; Genomic_DNA.
DR EMBL; AY330414; AAR84489.1; -; Genomic_DNA.
DR EMBL; AY330370; AAR84445.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON TER 1 1 putative lipoprotein.
SQ SEQUENCE 254 AA; 27129 MW; 46C7C8C0CF785414 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;

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Best Local Similarity 58.3%; Pred. No. 1e+02; Mismatches 2; Indels 3; Gaps 0;
Matches 7; Conservative

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 159 DDAGGKLTYYTID 170

RESULT 30

Q6VS24_NEIME
ID Q6VS24_NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L8-M978, M97-252988, M97-252697, 6557, and CDC-1492;
RA PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330366; AAR84441.1; -; Genomic DNA.
DR EMBL; AY330367; AAR84442.1; -; Genomic DNA.
DR EMBL; AY330368; AAR84443.1; -; Genomic DNA.
DR EMBL; AY330369; AAR84444.1; -; Genomic DNA.
DR EMBL; AY330365; AAR84440.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER
SQ SEQUENCE 254 AA; 27186 MW; 99398528EDA7CB8 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;

Best Local Similarity 58.3%; Pred. No. 1e+02; Mismatches 2; Indels 3; Gaps 0;
Matches 7; Conservative

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 159 DDAGGKLTYYTID 170

RESULT 31

Q6VS26_NEIME
ID Q6VS26_NEIME PRELIMINARY; PRT; 254 AA.
AC Q6VS26;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC-1610;
RA PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330364; AAR84439.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER
SQ SEQUENCE 254 AA; 27096 MW; 510331287DDDF3BF CRC64;

SQ SEQUENCE 254 AA; 27152 MW; 9939852847AD6B8 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 254;
Best Local Similarity 58.3%; Pred. No. 1e+02; Mismatches 2; Indels 3; Gaps 0;
Matches 7; Conservative

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 159 DDAGGKLTYYTID 170

RESULT 32

Q6VRX9_NEIME
ID Q6VRX9_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-250571;
RA PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330411; AAR84486.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER
SQ SEQUENCE 255 AA; 26994 MW; F36A739359A8FEF4 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02; Mismatches 2; Indels 3; Gaps 0;
Matches 7; Conservative

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 160 DDAGGKLTYYTID 171

RESULT 33

Q6VRY1_NEIME
ID Q6VRY1_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRY1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC-1343;
RA PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330409; AAR84484.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER
SQ SEQUENCE 255 AA; 27096 MW; 510331287DDDF3BF CRC64;

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Query Match      56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 34
Q6VRV3_NEIME
ID Q6VRV3_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRV3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC-852;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330407; AAR84482.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER <1 255 putative lipoprotein.
SQ SEQUENCE 255 AA; 27003 MW; 452DFD9689F64590 CRC64;

Query Match      56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 35
Q6VRY8_NEIME
ID Q6VRY8_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRY8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-253524; M97-251885, M97-251926, M98-250670, and 880049;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330402; AAR84477.1; -; Genomic DNA.
DR EMBL; AY330403; AAR84478.1; -; Genomic DNA.
DR EMBL; AY330404; AAR84479.1; -; Genomic DNA.
DR EMBL; AY330405; AAR84480.1; -; Genomic DNA.
DR EMBL; AY330401; AAR84476.1; -; Genomic DNA.
KW Lipoprotein.

Query Match      56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 36
Q6VRZ0_NEIME
ID Q6VRZ0_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRZ0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M982;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330400; AAR84475.1; -; Genomic_DNA.
KW Lipoprotein.
FT CHAIN
FT NON_TER <1 255 lipoprotein.
SQ SEQUENCE 255 AA; 27009 MW; 45APF3967573A57E CRC64;

Query Match      56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 37
Q6VRZ6_NEIME
ID Q6VRZ6_NEIME PRELIMINARY; PRT; 255 AA.
AC Q6VRZ6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-252097, 870227, H355, H44.76, 8529, CDC-2367, and CDC-937;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330394; AAR84469.1; -; Genomic DNA.
DR EMBL; AY330395; AAR84470.1; -; Genomic DNA.
DR EMBL; AY330396; AAR84471.1; -; Genomic DNA.
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DR EMBL; AY330397; AAR84472.1; -; Genomic DNA.
DR EMBL; AY330398; AAR84473.1; -; Genomic DNA.
DR EMBL; AY330410; AAR84485.1; -; Genomic DNA.
DR EMBL; AY330393; AAR84468.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN <1 255 putative lipoprotein.
FT NON TER 1
SQ SEQUENCE 255 AA; 26964 MW; F36A738FA4693EF4 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 255;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|||: ||: |
Db 160 DDAGGKLTYYID 171

RESULT 38
Q6VS27_NEIME
ID Q6VS27_NEIME PRELIMINARY; PRT; 257 AA.
AC Q6VS27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M97-252153;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;
RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330363; AAR84438.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN <1 257 putative lipoprotein.
FT NON TER 1
SQ SEQUENCE 257 AA; 27205 MW; 8BDE14D2B8E87119 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 257;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|||: ||: |
Db 162 DDAGGKLTYYID 173

RESULT 39
Q6VRY4_NEIME
ID Q6VRY4_NEIME PRELIMINARY; PRT; 260 AA.
AC Q6VRY4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipoprotein (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC-1573;
RX PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
RA Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
RA Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
RA Zagursky R., Zhang Y., Zlotnick G.W.;

RT "Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
RL Infect. Immun. 72:2088-2100(2004).
DR EMBL; AY330361; AAR84436.1; -; Genomic DNA.
KW Lipoprotein.
FT CHAIN <1 261 lipoprotein.
FT NON TER 1
SQ SEQUENCE 261 AA; 27640 MW; 5F5FB9B4CD932D66 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 261;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|||: ||: |
Db 166 DDAGGKLTYYID 177

RESULT 41
Q6QCB7_NEIME
ID Q6QCB7_NEIME PRELIMINARY; PRT; 274 AA.
AC Q6QCB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Lipoprotein GNA1870.
GN Name=gna1870.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M3390, and N98/254;
RX PubMed=15100304;
RA Welsch J.A., Rossi R., Comanducci M., Granoff D.M.;
RT "Protective activity of monoclonal antibodies to genome-derived
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RT neisserial antigen 1870, a Neisseria meningitidis candidate vaccine.";
RL J. Immunol. 172:5606-5615 (2004).
DR EMBL; AY548376; AAS56919.1; -; Genomic DNA.
DR EMBL; AY548375; AAS56918.1; -; Genomic_DNA.
KW Lipoprotein.
SQ SEQUENCE 274 AA; 29256 MW; 9A778025C70CDF6B CRC64;

Query Match 56.3%; Score 40; DB 2; Length 274;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
DB 179 DDAGGKLYTID 190

RESULT 42
Q6QCB9 NEIME
ID Q6QCB9_NEIME PRELIMINARY; PRT; 274 AA.
AC Q6QCB9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Lipoprotein GNA1870.
GN Name=gna1870;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M6190;
RX PubMed=15100304;
RA Welsch J.A., Rossi R., Comanducci M., Granoff D.M.;
RT "Protective activity of monoclonal antibodies to genome-derived
RT neisserial antigen 1870, a Neisseria meningitidis candidate vaccine.";
RL J. Immunol. 172:5606-5615 (2004).
DR EMBL; AY548374; AAS56917.1; -; Genomic_DNA.
KW Lipoprotein.
SQ SEQUENCE 274 AA; 29194 MW; 5C206D1A59BB9ABE CRC64;

Query Match 56.3%; Score 40; DB 2; Length 274;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
DB 179 DDAGGKLYTID 190

RESULT 43
Q6QCC0 NEIME
ID Q6QCC0_NEIME PRELIMINARY; PRT; 274 AA.
AC Q6QCC0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Lipoprotein GNA1870.
GN Name=gna1870;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4243;
RX PubMed=15100304;
RA Welsch J.A., Rossi R., Comanducci M., Granoff D.M.;
RT "Protective activity of monoclonal antibodies to genome-derived
RT neisserial antigen 1870, a Neisseria meningitidis candidate vaccine.";
RL J. Immunol. 172:5606-5615 (2004).
DR EMBL; AY548373; AAS56916.1; -; Genomic_DNA.
KW Lipoprotein.
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SQ SEQUENCE 274 AA; 29148 MW; 4380CE9C2C7D525C CRC64;

Query Match 56.3%; Score 40; DB 2; Length 274;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
DB 179 DDAGGKLYTID 190

RESULT 44
Q6QCC2 NEIME
ID Q6QCC2_NEIME PRELIMINARY; PRT; 274 AA.
AC Q6QCC2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Lipoprotein GNA1870.
GN Name=gna1870;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CU385, BZ83, and H44/76;
RX PubMed=15100304;
RA Welsch J.A., Rossi R., Comanducci M., Granoff D.M.;
RT "Protective activity of monoclonal antibodies to genome-derived
RT neisserial antigen 1870, a Neisseria meningitidis candidate vaccine.";
RL J. Immunol. 172:5606-5615 (2004).
DR EMBL; AY548371; AAT01290.1; -; Genomic DNA.
DR EMBL; AY548372; AAS56915.1; -; Genomic_DNA.
DR EMBL; AY548370; AAT01289.1; -; Genomic_DNA.
KW Lipoprotein.
SQ SEQUENCE 274 AA; 28989 MW; 5DDCF683CF877E2A CRC64;

Query Match 56.3%; Score 40; DB 2; Length 274;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
DB 179 DDAGGKLYTID 190

RESULT 45
Q8DRG2 STRR6
ID Q8DRG2_STRR6 PRELIMINARY; PRT; 276 AA.
AC Q8DRG2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ABC transporter substrate-binding protein-amino acid transport.
GN Name=ABC-SBP; OrderedLocNames=spr0146;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Albom W.B. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peary R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
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RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
RE EMBL; AE008398; AAK98950.1; -; Genomic_DNA.
DR PIR; B97890; B97890.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006162; Pfam; PF00497; SBP_bac_3.
DR InterPro; IPR001311; SBP_glu_receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPb; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 276 AA; 30627 MW; A882851F7EE1A13E CRC64;

Query Match 56.3%; Score 40; DB 2; Length 276;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
Db 141 DDIGGKSTEVVQA 153

RESULT 46
Q97T12_STRPN
ID Q97T12_STRPN PRELIMINARY; PRT; 276 AA.
AC Q97T12;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ABC transporter, substrate-binding protein.
GN OrderedLocusNames=SP0148;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC BAA-334 / TIGR4;
RE MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E.K., Khouri H.M., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
RL Science 293:498-506(2001).
RE EMBL; AE007331; AAK74330.1; -; Genomic_DNA.
DR PIR; A95017; A95017.
DR TIGR; SP0148; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006162; Pfam; PF00497; SBP_bac_3.
DR InterPro; IPR001311; SBP_glu_receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPb; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 276 AA; 30579 MW; 31117F6017186AE0 CRC64;

Query Match 56.3%; Score 40; DB 2; Length 276;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 DDYGGQSTYVMDA 13
Db 141 DDIGGKSTEVVQA 153

RESULT 47
Q9JXV4_NEIMB
ID Q9JXV4_NEIMB PRELIMINARY; PRT; 320 AA.
AC Q9JXV4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NMB1870;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MC58 / Serogroup B;
RE MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittoni H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scariato V., Masignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
RE EMBL; AE002098; AAF42204.1; -; Genomic_DNA.
DR PIR; D81032; D81032.
DR TIGR; NMB1870; -.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 320 AA; 34286 MW; 8CA166BCAC1B005C CRC64;

Query Match 56.3%; Score 40; DB 2; Length 320;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 225 DDAGGKLTYYTD 236

RESULT 48
Q6BUN7_DEBHA
ID Q6BUN7_DEBHA PRELIMINARY; PRT; 335 AA.
AC Q6BUN7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P40442 Saccharomyces cerevisiae Y11169c related to glucan 1.
GN OrderedLocusNames=DEHA001595g;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RE PubMed=15229592; DOI=10.1038/nature02579;
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,

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RA Despons L., Fabre E., Fairhead C., Perry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpell C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382139; CAG90040.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35286 MW; AC75E44A1C5E1711 CRC64;

Query Match          56.3%; Score 40; DB 2; Length 335;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DYGGQSTY 9
Db      |||||
39 DYGGTSTY 46

RESULT 49
Q5B7X2 EMENI PRELIMINARY; PRT; 383 AA.
AC Q5B7X2.
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN3358.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nuebaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaife D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
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RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACD01000055; EAA63326.1; -; Genomic_DNA.
KW Hypothetical protein.
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RA Kiene R.P., Henriksen J.R., King G.M., Belas R., Fuqua C.,
RA Brinkac L.M., Lewis M., Johri S., Weaver B., Pai G., Eisen J.A.,
RA Rahe E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Rasko D.A.,
RA Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J.,
RA Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,
RA Haft D.H., Selengut J., Ward N.;
RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the
RT marine environment.";
RL Nature 432:910-913(2004).
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GenCore version 5.1.1.8
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OM protein - protein search, using sw model

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Title: US-10-808-538-3

Perfect score: 71

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Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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161	33	46.5	117	2	US-09-016-061-6	Sequence 6, Appl	234	32	45.1	28	1	US-09-076-721-18	Sequence 18, Appl
162	33	46.5	126	2	US-09-248-796A-25746	Sequence 25746, A	235	32	45.1	31	1	US-08-244-701B-15	Sequence 15, Appl
163	33	46.5	129	2	US-09-530-139-24	Sequence 24, Appl	236	32	45.1	31	2	US-09-076-721-15	Sequence 15, Appl
164	33	46.5	159	2	US-09-248-796A-16325	Sequence 16325, A	237	32	45.1	39	2	US-09-962-756-193	Sequence 193, App
165	33	46.5	195	2	US-08-810-836B-8	Sequence 8, Appl	238	32	45.1	69	2	US-09-621-976-6668	Sequence 6668, Ap
166	33	46.5	222	1	US-08-090-048-1	Sequence 1, Appl	239	32	45.1	74	2	US-09-621-976-5052	Sequence 5052, Ap
167	33	46.5	222	1	US-08-292-550-1	Sequence 1, Appl	240	32	45.1	83	2	US-10-037-311B-7	Sequence 7, Appl
168	33	46.5	222	1	US-07-927-661A-1	Sequence 1, Appl	241	32	45.1	95	2	US-09-043-514-2	Sequence 2, Appl
169	33	46.5	241	2	US-08-813-453B-63	Sequence 63, Appl	242	32	45.1	96	2	US-08-851-362D-27	Sequence 27, Appl
170	33	46.5	255	2	US-09-248-796A-17593	Sequence 17593, A	243	32	45.1	97	2	US-10-194-975-29	Sequence 29, Appl
171	33	46.5	282	2	US-09-134-001C-5052	Sequence 5052, Ap	244	32	45.1	97	2	US-10-194-975-31	Sequence 31, Appl
172	33	46.5	314	2	US-09-551-826D-6	Sequence 6, Appl	245	32	45.1	97	2	US-09-534-717-616	Sequence 616, App
173	33	46.5	316	2	US-09-551-826D-2	Sequence 2, Appl	246	32	45.1	104	2	US-09-143-571-27	Sequence 27, Appl

247	32	45.1	111	2	US-09-823-746-10	Sequence 10, Appl	320	45.1	530	2	US-09-252-991A-23666	Sequence 23666, A
248	32	45.1	116	2	US-08-545-809A-135	Sequence 135, Appl	321	45.1	552	2	US-09-252-991A-24600	Sequence 24600, A
249	32	45.1	116	2	US-09-515-697-135	Sequence 135, Appl	322	45.1	557	2	US-09-252-991A-18216	Sequence 18216, A
250	32	45.1	117	2	US-08-851-362D-44	Sequence 44, Appl	323	45.1	563	2	US-08-362-525-12	Sequence 12, Appl
251	32	45.1	117	2	US-09-540-236-3305	Sequence 3305, Appl	324	45.1	616	1	US-08-545-745-2	Sequence 2, Appl
252	32	45.1	118	1	US-08-326-362-2	Sequence 2, Appl	325	45.1	659	2	US-09-189-462-4	Sequence 4, Appl
253	32	45.1	118	1	US-08-101-669D-29	Sequence 29, Appl	326	45.1	659	2	US-09-196-270-5	Sequence 5, Appl
254	32	45.1	118	1	US-08-472-788A-29	Sequence 29, Appl	327	45.1	659	2	US-09-863-040-4	Sequence 4, Appl
255	32	45.1	118	1	US-08-477-531B-29	Sequence 29, Appl	328	45.1	659	2	US-09-248-796A-20931	Sequence 20931, A
256	32	45.1	118	1	US-08-082-842A-29	Sequence 29, Appl	329	45.1	712	2	US-09-059-584-51	Sequence 51, Appl
257	32	45.1	122	2	US-08-983-607-30	Sequence 30, Appl	330	45.1	717	1	US-08-435-925C-2	Sequence 2, Appl
258	32	45.1	142	1	US-08-556-823-10	Sequence 10, Appl	331	45.1	741	2	US-09-605-703B-1584	Sequence 1584, Ap
259	32	45.1	153	2	US-09-502-540-16278	Sequence 16278, A	332	45.1	756	2	US-09-252-991A-30809	Sequence 30809, A
260	32	45.1	158	2	US-09-433-248A-4	Sequence 4, Appl	333	45.1	771	2	US-10-104-047-2427	Sequence 2427, Ap
261	32	45.1	163	2	US-09-270-767-33325	Sequence 33325, A	334	45.1	816	2	US-09-543-681A-4599	Sequence 4599, Ap
262	32	45.1	163	2	US-09-270-767-48542	Sequence 48542, A	335	45.1	843	2	US-09-361-631-1	Sequence 1, Appl
263	32	45.1	163	2	US-10-104-047-2013	Sequence 2013, Ap	336	45.1	843	2	US-09-361-631-2	Sequence 2, Appl
264	32	45.1	172	2	US-09-949-016-9380	Sequence 9380, Ap	337	45.1	867	2	US-09-248-796A-19207	Sequence 19207, A
265	32	45.1	181	2	US-09-252-991A-27683	Sequence 27683, A	338	45.1	888	1	US-07-718-575-6	Sequence 6, Appl
266	32	45.1	222	2	US-09-252-991A-30586	Sequence 30586, A	339	45.1	888	1	US-08-481-206-6	Sequence 6, Appl
267	32	45.1	223	2	US-09-080-983-13	Sequence 13, Appl	340	45.1	888	1	US-08-687-379-10	Sequence 10, Appl
268	32	45.1	223	2	US-09-613-486-13	Sequence 13, Appl	341	45.1	888	1	US-08-687-379-12	Sequence 12, Appl
269	32	45.1	232	2	US-09-248-796A-15087	Sequence 15087, A	342	45.1	888	1	US-08-486-269A-6	Sequence 6, Appl
270	32	45.1	240	2	US-09-651-656-1	Sequence 1, Appl	343	45.1	888	2	US-08-257-029-2	Sequence 2, Appl
271	32	45.1	240	2	US-09-650-855-1	Sequence 1, Appl	344	45.1	888	2	US-08-257-029-4	Sequence 4, Appl
272	32	45.1	244	2	US-10-002-344A-276	Sequence 276, Appl	345	45.1	888	2	US-08-896-063-2	Sequence 2, Appl
273	32	45.1	246	1	US-07-843-125-11	Sequence 11, Appl	346	45.1	888	2	US-08-896-063-4	Sequence 4, Appl
274	32	45.1	247	2	US-09-902-540-11435	Sequence 11435, A	347	45.1	894	2	US-09-949-016-5997	Sequence 5997, Ap
275	32	45.1	251	2	US-09-248-796A-26488	Sequence 26488, A	348	45.1	901	2	US-09-134-001C-5351	Sequence 5351, Ap
276	32	45.1	253	1	US-08-242-188-2	Sequence 2, Appl	349	45.1	911	2	US-09-949-016-8717	Sequence 8717, Ap
277	32	45.1	253	1	US-08-509-261A-2	Sequence 2, Appl	350	45.1	924	2	US-09-949-016-8718	Sequence 8718, Ap
278	32	45.1	253	1	US-08-660-626-8	Sequence 8, Appl	351	45.1	934	1	US-08-457-176-2	Sequence 2, Appl
279	32	45.1	253	1	US-08-692-892-2	Sequence 2, Appl	352	45.1	934	1	US-08-457-175-2	Sequence 2, Appl
280	32	45.1	253	1	US-08-713-939A-2	Sequence 2, Appl	353	45.1	934	2	US-08-709-784-1	Sequence 1, Appl
281	32	45.1	253	1	US-08-868-162A-22	Sequence 22, Appl	354	45.1	934	2	US-09-651-656-3	Sequence 3, Appl
282	32	45.1	253	2	US-09-031-168-8	Sequence 8, Appl	355	45.1	934	2	US-09-650-855-3	Sequence 3, Appl
283	32	45.1	253	2	US-09-128-416-20	Sequence 20, Appl	356	45.1	934	2	US-09-708-200-13	Sequence 13, Appl
284	32	45.1	253	2	US-09-036-579-2	Sequence 2, Appl	357	45.1	934	2	US-09-788-657-19	Sequence 19, Appl
285	32	45.1	253	2	US-09-823-494-20	Sequence 20, Appl	358	45.1	934	2	US-09-712-691-11	Sequence 11, Appl
286	32	45.1	253	2	US-09-550-374-2	Sequence 2, Appl	359	45.1	934	2	US-09-538-092-1120	Sequence 1120, Ap
287	32	45.1	253	2	US-09-431-887-1	Sequence 1, Appl	360	45.1	934	2	US-09-707-468C-11	Sequence 11, Appl
288	32	45.1	253	2	US-09-943-906-2	Sequence 2, Appl	361	45.1	934	2	US-10-641-068-19	Sequence 19, Appl
289	32	45.1	253	2	US-09-669-516C-8	Sequence 8, Appl	362	45.1	935	2	US-09-512-250C-33	Sequence 33, Appl
290	32	45.1	253	2	US-09-919-172-57	Sequence 57, Appl	363	45.1	939	2	US-10-029-065-4	Sequence 4, Appl
291	32	45.1	253	2	US-09-976-594-72	Sequence 72, Appl	364	45.1	939	2	US-10-029-065-2	Sequence 2, Appl
292	32	45.1	253	2	US-09-904-987-3	Sequence 3, Appl	365	45.1	940	2	US-09-512-250C-2	Sequence 2, Appl
293	32	45.1	253	2	US-09-248-796A-19227	Sequence 19227, A	366	45.1	963	2	US-09-394-272-12	Sequence 12, Appl
294	32	45.1	253	2	US-10-435-602-2	Sequence 2, Appl	367	45.1	963	2	US-09-394-272-13	Sequence 13, Appl
295	32	45.1	260	2	US-09-270-767-35171	Sequence 35171, A	368	45.1	1010	2	US-09-512-250C-31	Sequence 31, Appl
296	32	45.1	260	2	US-09-270-767-50388	Sequence 50388, A	369	45.1	1042	2	US-09-512-250C-32	Sequence 32, Appl
297	32	45.1	263	2	US-09-134-000C-5721	Sequence 5721, Ap	370	45.1	1045	1	US-08-553-436A-6	Sequence 6, Appl
298	32	45.1	282	2	US-09-270-767-56753	Sequence 56753, A	371	45.1	1045	2	US-09-394-272-7	Sequence 7, Appl
299	32	45.1	293	2	US-09-252-991A-23350	Sequence 23350, A	372	45.1	1049	2	US-09-394-272-10	Sequence 10, Appl
300	32	45.1	328	2	US-09-489-039A-7290	Sequence 7290, Ap	373	45.1	1053	2	US-09-394-272-6	Sequence 6, Appl
301	32	45.1	333	2	US-09-025-819-29	Sequence 29, Appl	374	45.1	1054	1	US-08-356-354-4	Sequence 4, Appl
302	32	45.1	333	2	US-09-808-126-29	Sequence 29, Appl	375	45.1	1054	1	US-08-778-656-4	Sequence 4, Appl
303	32	45.1	333	2	US-09-803-951-29	Sequence 29, Appl	376	45.1	1054	2	US-09-394-272-3	Sequence 3, Appl
304	32	45.1	355	2	US-09-248-796A-16861	Sequence 16861, A	377	45.1	1054	2	US-09-376-045-4	Sequence 4, Appl
305	32	45.1	358	2	US-09-483-039A-12539	Sequence 12539, A	378	45.1	1056	2	US-09-394-272-1	Sequence 1, Appl
306	32	45.1	365	2	US-08-875-811-53	Sequence 53, Appl	379	45.1	1057	2	US-08-853-948B-2	Sequence 2, Appl
307	32	45.1	366	2	US-08-875-811-55	Sequence 55, Appl	380	45.1	1057	2	US-09-697-367-23	Sequence 23, Appl
308	32	45.1	370	2	US-09-252-991A-30880	Sequence 30880, A	381	45.1	1057	2	US-09-394-272-2	Sequence 2, Appl
309	32	45.1	377	2	US-09-270-767-59051	Sequence 59051, A	382	45.1	1057	2	US-09-918-909A-29	Sequence 29, Appl
310	32	45.1	380	2	US-09-248-796A-15048	Sequence 15048, A	383	45.1	1059	2	US-09-697-367-16	Sequence 16, Appl
311	32	45.1	388	1	US-08-382-505-2	Sequence 2, Appl	384	45.1	1059	2	US-09-394-272-5	Sequence 5, Appl
312	32	45.1	400	2	US-09-949-016-6685	Sequence 6685, Ap	385	45.1	1059	2	US-09-918-909A-16	Sequence 16, Appl
313	32	45.1	406	2	US-09-949-016-10207	Sequence 10207, A	386	45.1	1068	1	US-08-429-054A-11	Sequence 11, Appl
314	32	45.1	413	2	US-09-902-540-12315	Sequence 12315, A	387	45.1	1068	1	US-08-718-777-7	Sequence 7, Appl
315	32	45.1	429	2	US-09-252-991A-31588	Sequence 31588, A	388	45.1	1068	2	US-09-051-341-7	Sequence 8, Appl
316	32	45.1	482	2	US-09-538-092-486	Sequence 486, Appl	389	45.1	1068	2	US-08-429-053-11	Sequence 11, Appl
317	32	45.1	487	2	US-09-252-991A-17620	Sequence 17620, A	390	45.1	1081	2	US-09-394-272-4	Sequence 4, Appl
318	32	45.1	504	2	US-09-602-787A-500	Sequence 500, App	391	45.1				
319	32	45.1	513	2	US-09-270-767-41529	Sequence 41529, A	392	45.1				

393	32	45.1	1083	2	US-09-394-272-11	Sequence 11, Appl	466	31	43.7	299	2	US-09-303-518D-22	Sequence 22, Appl
394	32	45.1	1084	2	US-09-394-272-9	Sequence 9, Appl	467	31	43.7	300	2	US-09-303-518D-24	Sequence 24, Appl
395	32	45.1	1120	2	US-09-792-024-86	Sequence 86, Appl	468	31	43.7	301	2	US-09-270-767-37497	Sequence 37497, A
396	32	45.1	1222	2	US-09-266-942-37	Sequence 37, Appl	469	31	43.7	301	2	US-09-270-767-52714	Sequence 52714, A
397	32	45.1	1222	2	US-10-193-764-37	Sequence 37, Appl	470	31	43.7	302	2	US-09-107-532A-5280	Sequence 5280, Ap
398	32	45.1	1228	2	US-09-206-942-34	Sequence 34, Appl	471	31	43.7	304	2	US-09-303-518D-28	Sequence 28, Appl
399	32	45.1	1228	2	US-10-193-764-34	Sequence 34, Appl	472	31	43.7	308	1	US-08-164-292B-18	Sequence 18, Appl
400	32	45.1	1245	1	US-08-801-263A-3	Sequence 3, Appl	473	31	43.7	308	1	US-08-576-626A-36	Sequence 36, Appl
401	32	45.1	1245	1	US-08-801-263A-6	Sequence 6, Appl	474	31	43.7	308	2	US-08-845-623-18	Sequence 18, Appl
402	32	45.1	1245	1	US-08-801-263A-10	Sequence 10, Appl	475	31	43.7	308	2	US-08-815-927-18	Sequence 18, Appl
403	32	45.1	1245	1	US-09-102-248-3	Sequence 3, Appl	476	31	43.7	308	2	US-09-103-330-18	Sequence 18, Appl
404	32	45.1	1245	2	US-09-102-248-6	Sequence 6, Appl	477	31	43.7	308	2	US-09-435-242-18	Sequence 18, Appl
405	32	45.1	1245	2	US-09-102-248-10	Sequence 10, Appl	478	31	43.7	308	2	US-09-513-999C-4832	Sequence 4832, Ap
406	32	45.1	1245	2	US-09-367-764-3	Sequence 3, Appl	479	31	43.7	312	2	US-09-631-616-10	Sequence 10, Appl
407	32	45.1	1245	2	US-09-367-764-6	Sequence 6, Appl	480	31	43.7	315	2	US-09-248-796A-19865	Sequence 19865, A
408	32	45.1	1245	2	US-09-367-764-10	Sequence 10, Appl	481	31	43.7	325	2	US-09-248-796A-17218	Sequence 17218, A
409	32	45.1	2182	1	US-08-487-826B-16	Sequence 16, Appl	482	31	43.7	326	2	US-10-272-490-12	Sequence 12, Appl
410	32	45.1	3122	2	US-10-237-551-201	Sequence 201, App	483	31	43.7	348	2	US-09-949-016-11617	Sequence 11617, A
411	32	45.1	3122	2	US-10-237-551-250	Sequence 250, App	484	31	43.7	350	1	US-07-868-353A-14	Sequence 14, Appl
412	31	43.7	16	1	US-08-318-200-13	Sequence 13, Appl	485	31	43.7	350	1	US-08-407-804-23	Sequence 23, Appl
413	31	43.7	17	2	US-09-192-854-139	Sequence 139, App	486	31	43.7	350	2	US-09-124-807-23	Sequence 23, Appl
414	31	43.7	17	2	US-09-511-939-248	Sequence 248, App	487	31	43.7	355	2	US-09-442-349A-107	Sequence 107, App
415	31	43.7	20	2	US-08-992-877-65	Sequence 65, Appl	488	31	43.7	356	2	US-09-152-060-65	Sequence 65, Appl
416	31	43.7	61	2	US-09-540-236-3067	Sequence 3067, Ap	489	31	43.7	356	2	US-09-852-797-65	Sequence 65, Appl
417	31	43.7	64	2	US-09-513-999C-7584	Sequence 7584, Ap	490	31	43.7	356	2	US-09-853-161-65	Sequence 65, Appl
418	31	43.7	68	2	US-09-902-540-15409	Sequence 15409, A	491	31	43.7	356	2	US-10-058-993-65	Sequence 65, Appl
419	31	43.7	71	2	US-09-248-796A-21710	Sequence 21710, A	492	31	43.7	358	2	US-09-949-016-11528	Sequence 11528, A
420	31	43.7	87	2	US-09-621-976-4127	Sequence 4127, Ap	493	31	43.7	359	2	US-09-902-540-11932	Sequence 11932, A
421	31	43.7	98	2	US-09-270-767-37488	Sequence 37488, A	494	31	43.7	362	2	US-09-248-796A-26034	Sequence 26034, A
422	31	43.7	98	2	US-09-270-767-48705	Sequence 48705, A	495	31	43.7	376	2	US-09-949-016-9185	Sequence 9185, Ap
423	31	43.7	103	2	US-09-513-999C-5823	Sequence 5823, Ap	496	31	43.7	378	2	US-09-299-843A-66	Sequence 66, Appl
424	31	43.7	111	2	US-09-899-896-7	Sequence 7, Appl	497	31	43.7	378	2	US-09-088-337B-66	Sequence 66, Appl
425	31	43.7	114	2	US-09-344-587-9	Sequence 9, Appl	498	31	43.7	382	2	US-09-252-991A-29696	Sequence 29696, A
426	31	43.7	116	2	US-09-325-932A-47	Sequence 47, Appl	499	31	43.7	382	2	US-09-949-016-11596	Sequence 11596, A
427	31	43.7	119	2	US-09-232-290-50	Sequence 50, Appl	500	31	43.7	385	2	US-09-311-021-78	Sequence 78, Appl
428	31	43.7	120	1	US-08-478-039-98	Sequence 98, Appl	501	31	43.7	387	2	US-09-569-771B-25	Sequence 25, Appl
429	31	43.7	120	1	US-08-476-349A-98	Sequence 98, Appl	502	31	43.7	393	2	US-09-569-771B-26	Sequence 26, Appl
430	31	43.7	121	2	US-08-487-761-11	Sequence 11, Appl	503	31	43.7	405	2	US-09-489-039A-7341	Sequence 7341, Ap
431	31	43.7	125	2	US-09-266-805-7	Sequence 7, Appl	504	31	43.7	412	2	US-09-540-236-2209	Sequence 2209, Ap
432	31	43.7	131	2	US-09-303-518D-20	Sequence 20, Appl	505	31	43.7	413	2	US-09-248-796A-23092	Sequence 23092, A
433	31	43.7	137	2	US-09-640-211A-1175	Sequence 1175, Ap	506	31	43.7	421	2	US-09-000-040-1	Sequence 1, Appl
434	31	43.7	143	2	US-09-270-767-37886	Sequence 37886, Ap	507	31	43.7	422	2	US-09-071-035-484	Sequence 484, App
435	31	43.7	143	2	US-09-270-767-53118	Sequence 53103, A	508	31	43.7	422	2	US-10-206-576-484	Sequence 484, App
436	31	43.7	159	2	US-09-270-767-35518	Sequence 35518, A	509	31	43.7	424	2	US-09-826-509-455	Sequence 455, App
437	31	43.7	159	2	US-09-270-767-50735	Sequence 50735, A	510	31	43.7	435	2	US-09-248-796A-16669	Sequence 16669, A
438	31	43.7	162	2	US-09-134-000C-6697	Sequence 6697, Ap	511	31	43.7	437	1	US-08-620-605D-4	Sequence 4, Appl
439	31	43.7	168	2	US-09-248-796A-23779	Sequence 23779, A	512	31	43.7	438	2	US-09-902-540-16624	Sequence 16624, A
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441	31	43.7	185	2	US-09-252-991A-26776	Sequence 26776, A	514	31	43.7	442	6	5310667-6	Patent No. 5310667
442	31	43.7	194	2	US-09-570-856B-23	Sequence 23, Appl	515	31	43.7	444	6	5310667-3	Patent No. 5310667
443	31	43.7	198	2	US-09-248-796A-19363	Sequence 19363, A	516	31	43.7	445	2	US-09-902-540-16491	Sequence 16491, A
444	31	43.7	201	2	US-08-816-346-6	Sequence 6, Appl	517	31	43.7	446	2	Sequence 13677, A	Sequence 6746, Ap
445	31	43.7	203	2	US-09-335-411-6	Sequence 41, Appl	518	31	43.7	448	2	US-09-134-000C-6746	Sequence 482, App
446	31	43.7	203	2	US-09-328-352-4293	Sequence 4293, Ap	519	31	43.7	449	2	US-09-071-035-482	Sequence 482, App
447	31	43.7	204	2	US-09-902-540-12794	Sequence 12794, A	520	31	43.7	449	2	US-10-206-576-482	Sequence 5714, Ap
448	31	43.7	216	2	US-09-134-000C-4803	Sequence 4803, Ap	521	31	43.7	450	2	US-09-134-000C-5714	Sequence 5714, Ap
449	31	43.7	227	2	US-09-605-703B-818	Sequence 818, App	522	31	43.7	455	2	US-09-107-532A-6473	Sequence 6473, Ap
450	31	43.7	229	2	US-09-543-681A-5339	Sequence 5339, Ap	523	31	43.7	457	1	US-08-278-635B-3	Sequence 3, Appl
451	31	43.7	229	2	US-09-489-039A-12956	Sequence 12956, A	524	31	43.7	457	2	US-08-471-961-3	Sequence 3, Appl
452	31	43.7	229	2	US-09-640-211A-749	Sequence 749, App	525	31	43.7	457	2	US-09-345-109C-3	Sequence 3, Appl
453	31	43.7	230	2	US-09-252-991A-22207	Sequence 22207, A	526	31	43.7	457	2	US-09-595-990A-2	Sequence 2, Appl
454	31	43.7	231	2	US-09-270-767-42822	Sequence 42822, A	527	31	43.7	457	2	US-08-991-143A-2	Sequence 2, Appl
455	31	43.7	236	2	US-09-543-681A-6430	Sequence 6430, Ap	528	31	43.7	458	2	US-08-464-258B-3	Sequence 3, Appl
456	31	43.7	244	2	US-09-543-681A-7039	Sequence 7039, Ap	529	31	43.7	458	2	US-08-487-596-16	Sequence 16, Appl
457	31	43.7	247	2	US-09-248-796A-15872	Sequence 15872, A	530	31	43.7	458	2	US-08-484-722-4	Sequence 4, Appl
458	31	43.7	252	2	US-09-431-887-32	Sequence 32, Appl	531	31	43.7	458	2	US-08-660-451A-16	Sequence 16, Appl
459	31	43.7	256	2	US-09-431-887-31	Sequence 31, Appl	532	31	43.7	458	2	US-09-949-016-5986	Sequence 5986, Ap
460	31	43.7	257	2	US-09-431-887-29	Sequence 29, Appl	533	31	43.7	458	2	US-09-703-951A-16	Sequence 16, Appl
461	31	43.7	265	2	US-09-742-693-30	Sequence 30, Appl	534	31	43.7	460	2	US-09-917-254-79	Sequence 79, Appl
462	31	43.7	268	2	US-09-134-000C-4427	Sequence 4427, Ap	535	31	43.7	461	2	US-09-252-991A-18060	Sequence 18060, A
463	31	43.7	270	2	US-09-902-540-14359	Sequence 14359, A	536	31	43.7	464	1	US-09-005-232A-4	Sequence 4, Appl
464	31	43.7	279	2	US-09-543-681A-5096	Sequence 5096, Ap	537	31	43.7	468	2	US-08-487-596-8	Sequence 8, Appl
465	31	43.7	287	2	US-09-303-518D-26	Sequence 26, Appl	538	31	43.7	468	2	US-08-660-451A-8	Sequence 8, Appl

539	31	43.7	468	2	US-09-703-951A-8	Sequence 8, Appli	612	31	43.7	813	2	US-09-701-711-4	Sequence 4, Appli
540	31	43.7	471	2	US-09-152-060-102	Sequence 102, App	613	31	43.7	815	2	US-09-371-307-88	Sequence 88, Appli
541	31	43.7	471	2	US-09-852-797-102	Sequence 102, App	614	31	43.7	952	2	US-09-248-796A-20878	Sequence 20878, A
542	31	43.7	471	2	US-09-853-161-102	Sequence 102, App	615	31	43.7	967	2	US-08-816-346-56	Sequence 56, Appli
543	31	43.7	471	2	US-10-058-993-102	Sequence 102, App	616	31	43.7	967	2	US-09-335-411-56	Sequence 56, Appli
544	31	43.7	477	2	US-09-075-375F-4	Sequence 4, Appli	617	31	43.7	968	2	US-08-816-346-2	Sequence 2, Appli
545	31	43.7	480	2	US-09-252-991A-24951	Sequence 24951, A	618	31	43.7	968	2	US-09-335-411-2	Sequence 2, Appli
546	31	43.7	482	2	US-09-248-796A-17800	Sequence 17800, A	619	31	43.7	977	2	US-09-252-991A-28261	Sequence 28261, A
547	31	43.7	483	2	US-09-027-166-9	Sequence 9, Appli	620	31	43.7	987	2	US-09-903-540-10740	Sequence 10740, A
548	31	43.7	483	2	US-09-049-672A-5	Sequence 5, Appli	621	31	43.7	998	1	US-08-415-788-7	Sequence 7, Appli
549	31	43.7	489	2	US-09-545-814-29	Sequence 29, Appl	622	31	43.7	1023	2	US-09-514-907A-6	Sequence 6, Appli
550	31	43.7	492	2	US-09-635-872A-19	Sequence 19, Appl	623	31	43.7	1023	2	US-09-896-994-6	Sequence 6, Appli
551	31	43.7	492	2	US-09-636-077A-19	Sequence 19, Appl	624	31	43.7	1023	2	US-10-040-722-2	Sequence 2, Appli
552	31	43.7	492	2	US-09-636-060C-19	Sequence 19, Appl	625	31	43.7	1026	2	US-10-040-722-4	Sequence 4, Appli
553	31	43.7	492	2	US-09-986-552-19	Sequence 19, Appl	626	31	43.7	1026	2	US-09-949-016-7526	Sequence 7526, Ap
554	31	43.7	492	2	US-09-636-596C-19	Sequence 19, Appl	627	31	43.7	1029	1	US-08-415-788-3	Sequence 3, Appli
555	31	43.7	492	2	US-10-023-894-20	Sequence 20, Appl	628	31	43.7	1171	2	US-09-248-796A-16043	Sequence 16043, A
556	31	43.7	492	2	US-10-306-686-19	Sequence 19, Appl	629	31	43.7	1208	2	US-09-540-236-3604	Sequence 3604, Ap
557	31	43.7	492	2	US-09-895-072-19	Sequence 19, Appl	630	31	43.7	1212	2	US-09-090-535-1	Sequence 1, Appli
558	31	43.7	492	2	US-10-023-888-20	Sequence 20, Appl	631	31	43.7	1212	2	US-09-090-535-2	Sequence 2, Appli
559	31	43.7	494	2	US-10-290-579A-175	Sequence 175, App	632	31	43.7	1212	2	US-09-090-535-3	Sequence 3, Appli
560	31	43.7	502	2	US-09-328-352-5891	Sequence 5891, Ap	633	31	43.7	1212	2	US-09-090-535-4	Sequence 4, Appli
561	31	43.7	502	2	US-09-270-767-45124	Sequence 45124, A	634	31	43.7	1525	2	US-09-396-651B-1	Sequence 1, Appli
562	31	43.7	508	2	US-09-270-767-4233	Sequence 4233, A	635	31	43.7	1665	2	US-09-543-681A-4476	Sequence 4476, Ap
563	31	43.7	515	2	US-09-635-872A-6	Sequence 6, Appli	636	31	43.7	2285	2	US-09-252-991A-17790	Sequence 17790, A
564	31	43.7	515	2	US-09-636-077A-6	Sequence 6, Appli	637	30.5	43.0	315	1	US-08-378-761A-73	Sequence 73, Appli
565	31	43.7	515	2	US-09-636-060C-6	Sequence 6, Appli	638	30.5	43.0	315	1	US-08-485-286-73	Sequence 73, Appli
566	31	43.7	515	2	US-09-986-552-6	Sequence 6, Appli	639	30.5	43.0	315	2	US-08-816-977-2	Sequence 2, Appli
567	31	43.7	515	2	US-09-636-596C-6	Sequence 6, Appli	640	30.5	43.0	315	2	US-09-489-039A-13103	Sequence 13103, A
568	31	43.7	515	2	US-10-023-894-18	Sequence 18, Appl	641	30.5	43.0	315	2	US-09-334-477-2	Sequence 2, Appli
569	31	43.7	515	2	US-10-306-686-6	Sequence 6, Appli	642	30.5	43.0	323	2	US-08-816-977-21	Sequence 21, Appli
570	31	43.7	515	2	US-09-895-072-6	Sequence 6, Appli	643	30.5	43.0	323	2	US-09-334-477-21	Sequence 21, Appli
571	31	43.7	515	2	US-10-023-888-18	Sequence 18, Appl	644	30.5	43.0	326	2	US-08-816-977-37	Sequence 37, Appli
572	31	43.7	519	2	US-09-248-796A-20368	Sequence 20368, A	645	30.5	43.0	326	2	US-09-334-477-37	Sequence 37, Appli
573	31	43.7	521	1	US-08-878-563A-3	Sequence 3, Appli	646	30.5	43.0	333	2	US-09-270-767-61810	Sequence 61810, A
574	31	43.7	521	2	US-09-270-117-3	Sequence 3, Appli	647	30.5	43.0	590	1	US-08-756-317-12	Sequence 12, Appli
575	31	43.7	521	2	US-09-046-572-5	Sequence 5, Appli	648	30.5	43.0	672	2	US-09-270-767-46242	Sequence 46242, A
576	31	43.7	526	2	US-09-438-185A-37	Sequence 37, Appl	649	30.5	43.0	690	2	US-08-816-977-47	Sequence 47, Appli
577	31	43.7	532	3	US-10-104-047-3224	Sequence 3224, Ap	650	30.5	43.0	690	2	US-09-334-477-47	Sequence 47, Appli
578	31	43.7	559	2	US-09-545-814-14	Sequence 14, Appl	651	30.5	43.0	708	2	US-08-816-977-33	Sequence 33, Appli
579	31	43.7	574	2	US-09-252-991A-30868	Sequence 30868, A	652	30.5	43.0	708	2	US-09-334-477-33	Sequence 33, Appli
580	31	43.7	583	2	US-09-545-814-2	Sequence 2, Appli	653	30	42.3	14	1	US-08-765-179B-4	Sequence 4, Appli
581	31	43.7	583	2	US-09-545-814-5	Sequence 5, Appli	654	30	42.3	15	2	US-09-025-769B-179	Sequence 179, App
582	31	43.7	593	2	US-09-252-991A-21665	Sequence 21665, A	655	30	42.3	15	2	US-09-490-070A-179	Sequence 179, App
583	31	43.7	600	2	US-09-543-681A-6004	Sequence 6004, Ap	656	30	42.3	15	2	US-09-490-153-179	Sequence 179, App
584	31	43.7	620	2	US-09-252-991A-19796	Sequence 19796, A	657	30	42.3	15	2	US-09-490-324-179	Sequence 179, App
585	31	43.7	635	2	US-09-545-814-32	Sequence 32, Appl	658	30	42.3	15	2	US-10-194-975-105	Sequence 105, App
586	31	43.7	655	2	US-09-311-626B-14	Sequence 14, Appl	659	30	42.3	17	2	US-08-783-853A-9	Sequence 9, Appli
587	31	43.7	684	2	US-09-518-550-45	Sequence 45, Appl	660	30	42.3	17	2	US-09-344-050-9	Sequence 9, Appli
588	31	43.7	703	2	US-09-543-681A-7429	Sequence 7429, Ap	661	30	42.3	17	2	US-09-497-997C-31	Sequence 31, Appli
589	31	43.7	706	2	US-09-252-991A-32448	Sequence 32448, A	662	30	42.3	21	2	US-09-180-570A-5	Sequence 5, Appli
590	31	43.7	753	2	US-09-543-681A-5022	Sequence 5022, Ap	663	30	42.3	21	2	US-09-497-997C-19	Sequence 19, Appli
591	31	43.7	770	2	US-09-107-532A-4388	Sequence 4388, Ap	664	30	42.3	22	1	US-08-705-660-31	Sequence 31, Appli
592	31	43.7	773	1	US-08-019-870-1	Sequence 1, Appli	665	30	42.3	22	2	US-08-989-045-31	Sequence 31, Appli
593	31	43.7	773	1	US-08-019-870-6	Sequence 6, Appli	666	30	42.3	22	2	US-09-497-997C-4	Sequence 4, Appli
594	31	43.7	774	1	US-07-747-901A-3	Sequence 3, Appli	667	30	42.3	22	2	US-09-497-997C-20	Sequence 20, Appli
595	31	43.7	774	1	US-07-935-312-3	Sequence 3, Appli	668	30	42.3	22	2	US-09-315-355A-31	Sequence 31, Appli
596	31	43.7	774	1	US-08-019-870-3	Sequence 3, Appli	669	30	42.3	25	1	US-08-053-131-100	Sequence 100, App
597	31	43.7	774	1	US-08-019-870-5	Sequence 5, Appli	670	30	42.3	25	1	US-08-645-641-100	Sequence 100, App
598	31	43.7	774	1	US-08-019-870-8	Sequence 8, Appli	671	30	42.3	25	1	US-07-853-408B-100	Sequence 100, App
599	31	43.7	774	1	US-08-019-870-11	Sequence 11, Appli	672	30	42.3	25	1	US-08-096-762-100	Sequence 100, App
600	31	43.7	774	1	US-07-731-157A-7	Sequence 7, Appli	673	30	42.3	25	1	US-08-308-865-100	Sequence 100, App
601	31	43.7	774	1	US-08-314-309A-21	Sequence 21, Appl	674	30	42.3	25	2	US-09-042-353-297	Sequence 297, App
602	31	43.7	774	1	US-08-633-760-44	Sequence 44, Appl	675	30	42.3	25	2	US-08-758-417A-145	Sequence 145, App
603	31	43.7	774	1	US-08-633-760-46	Sequence 46, Appl	676	30	42.3	25	4	PCT-US92-10983-100	Sequence 100, App
604	31	43.7	774	1	US-08-633-760-48	Sequence 48, Appl	677	30	42.3	26	1	US-08-053-131-88	Sequence 88, Appli
605	31	43.7	774	1	US-08-633-760-50	Sequence 50, Appl	678	30	42.3	26	1	US-08-645-641-88	Sequence 88, Appli
606	31	43.7	774	1	US-08-633-760-52	Sequence 52, Appl	679	30	42.3	26	1	US-08-471-780C-17	Sequence 17, Appli
607	31	43.7	774	1	US-08-541-780-7	Sequence 7, Appli	680	30	42.3	26	1	US-07-853-408B-88	Sequence 88, Appli
608	31	43.7	775	2	US-09-305-640-2	Sequence 2, Appli	681	30	42.3	26	1	US-08-467-282B-17	Sequence 17, Appli
609	31	43.7	811	2	US-09-614-912-22	Sequence 22, Appli	682	30	42.3	26	1	US-08-096-762-88	Sequence 88, Appli
610	31	43.7	813	2	US-09-540-236-3472	Sequence 3472, Ap	683	30	42.3	26	1	US-08-471-282A-17	Sequence 17, Appli
611	31	43.7	813	2	US-09-701-711-2	Sequence 2, Appli	684	30	42.3	26	1	US-08-466-710C-17	Sequence 17, Appli

685	30	42.3	26	1	US-08-308-865-88	Sequence 88, Appl	758	30	42.3	34	4	PCT-US92-10983-87	Sequence 87, Appl
686	30	42.3	26	2	US-08-468-739C-17	Sequence 17, Appl	759	30	42.3	35	2	US-09-199-290-6	Sequence 6, Appl
687	30	42.3	26	2	US-09-042-353-285	Sequence 285, App	760	30	42.3	35	2	US-09-821-616-6	Sequence 6, Appl
688	30	42.3	26	2	US-08-758-417A-133	Sequence 133, App	761	30	42.3	35	2	US-09-270-767-60639	Sequence 60639, A
689	30	42.3	26	2	US-09-293-769A-17	Sequence 17, Appl	762	30	42.3	48	1	US-08-209-747-14	Sequence 14, Appl
690	30	42.3	26	4	PCT-US92-10983-88	Sequence 88, Appl	763	30	42.3	48	1	US-08-458-298-14	Sequence 14, Appl
691	30	42.3	26	4	US-08-053-131-80	Sequence 80, Appl	764	30	42.3	49	2	US-09-497-997C-10	Sequence 10, Appl
692	30	42.3	27	1	US-08-645-641-80	Sequence 80, Appl	765	30	42.3	51	1	US-08-392-625-31	Sequence 31, Appl
693	30	42.3	27	1	US-07-853-408B-80	Sequence 80, Appl	766	30	42.3	51	1	US-08-466-961A-31	Sequence 31, Appl
694	30	42.3	27	1	US-08-096-762-80	Sequence 80, Appl	767	30	42.3	51	1	US-08-436-874-2	Sequence 2, Appl
695	30	42.3	27	1	US-08-308-865-80	Sequence 80, Appl	768	30	42.3	51	4	PCT-US94-08194-2	Sequence 2, Appl
696	30	42.3	27	2	US-09-042-353-277	Sequence 277, App	769	30	42.3	67	2	US-09-270-767-58535	Sequence 58535, A
697	30	42.3	27	2	US-08-758-417A-125	Sequence 125, App	770	30	42.3	74	2	US-09-248-796A-27233	Sequence 27233, A
698	30	42.3	27	4	PCT-US92-10983-80	Sequence 80, Appl	771	30	42.3	75	2	US-08-783-853A-48	Sequence 48, Appl
699	30	42.3	28	1	US-08-053-131-90	Sequence 90, Appl	772	30	42.3	75	2	US-09-344-050-48	Sequence 48, Appl
700	30	42.3	28	1	US-08-053-131-95	Sequence 95, Appl	773	30	42.3	92	2	US-08-783-853A-84	Sequence 84, Appl
701	30	42.3	28	1	US-08-645-641-90	Sequence 90, Appl	774	30	42.3	92	2	US-09-344-050-84	Sequence 84, Appl
702	30	42.3	28	1	US-08-645-641-95	Sequence 95, Appl	775	30	42.3	93	2	US-09-513-999C-4986	Sequence 4986, Ap
703	30	42.3	28	1	US-08-244-701B-16	Sequence 16, Appl	776	30	42.3	97	2	US-08-851-362D-33	Sequence 33, Appl
704	30	42.3	28	1	US-07-853-408B-90	Sequence 90, Appl	777	30	42.3	101	2	US-09-605-703B-1644	Sequence 1644, Ap
705	30	42.3	28	1	US-07-853-408B-95	Sequence 95, Appl	778	30	42.3	102	1	US-08-273-146-65	Sequence 65, Appl
706	30	42.3	28	1	US-08-096-762-90	Sequence 90, Appl	779	30	42.3	106	2	US-09-949-016-9100	Sequence 9100, Ap
707	30	42.3	28	1	US-08-096-762-95	Sequence 95, Appl	780	30	42.3	107	2	US-09-497-997C-26	Sequence 26, Appl
708	30	42.3	28	1	US-08-308-865-90	Sequence 90, Appl	781	30	42.3	109	1	US-08-379-057-32	Sequence 32, Appl
709	30	42.3	28	1	US-08-308-865-95	Sequence 95, Appl	782	30	42.3	110	2	US-10-014-012-217	Sequence 217, App
710	30	42.3	28	2	US-08-042-353-287	Sequence 287, App	783	30	42.3	112	2	US-08-783-853A-20	Sequence 20, Appl
711	30	42.3	28	2	US-08-042-353-292	Sequence 292, App	784	30	42.3	112	2	US-09-344-050-20	Sequence 20, Appl
712	30	42.3	28	2	US-08-758-417A-135	Sequence 135, App	785	30	42.3	113	2	US-08-974-899-6	Sequence 6, Appl
713	30	42.3	28	2	US-08-758-417A-140	Sequence 140, App	786	30	42.3	113	2	US-09-795-798-6	Sequence 5, Appl
714	30	42.3	28	2	US-09-076-721-16	Sequence 16, Appl	787	30	42.3	113	2	US-09-232-290-57	Sequence 57, Appl
715	30	42.3	28	4	PCT-US92-10983-90	Sequence 90, Appl	788	30	42.3	113	2	US-09-434-870-4	Sequence 4, Appl
716	30	42.3	28	4	PCT-US92-10983-95	Sequence 95, Appl	789	30	42.3	113	2	US-08-908-469-11	Sequence 11, Appl
717	30	42.3	29	1	US-08-053-131-72	Sequence 72, Appl	790	30	42.3	115	1	US-08-379-057-31	Sequence 31, Appl
718	30	42.3	29	1	US-08-645-641-72	Sequence 72, Appl	791	30	42.3	115	2	US-09-513-999C-5898	Sequence 5898, Ap
719	30	42.3	29	1	US-07-853-408B-72	Sequence 72, Appl	792	30	42.3	115	2	US-09-269-332-89	Sequence 89, Appl
720	30	42.3	29	1	US-08-096-762-72	Sequence 72, Appl	793	30	42.3	115	2	US-09-534-717-35	Sequence 35, Appl
721	30	42.3	29	1	US-08-308-865-72	Sequence 72, Appl	794	30	42.3	115	2	US-09-534-717-35	Sequence 35, Appl
722	30	42.3	29	2	US-08-042-353-269	Sequence 269, App	795	30	42.3	115	2	US-09-534-717-39	Sequence 39, Appl
723	30	42.3	29	2	US-08-758-417A-117	Sequence 117, App	796	30	42.3	115	2	US-09-534-717-41	Sequence 41, Appl
724	30	42.3	29	4	PCT-US92-10983-72	Sequence 72, Appl	797	30	42.3	116	1	US-07-634-278-5	Sequence 5, Appl
725	30	42.3	30	2	US-09-336-093-4	Sequence 4, Appl	798	30	42.3	116	1	US-07-634-278-73	Sequence 73, Appl
726	30	42.3	30	2	US-09-557-465D-4	Sequence 4, Appl	799	30	42.3	116	1	US-07-634-278-57	Sequence 57, Appl
727	30	42.3	30	2	US-09-497-997C-7	Sequence 7, Appl	800	30	42.3	116	1	US-08-477-728-5	Sequence 5, Appl
728	30	42.3	30	2	US-09-720-003C-5	Sequence 5, Appl	801	30	42.3	116	1	US-08-477-728-57	Sequence 57, Appl
729	30	42.3	30	2	US-10-144-549-21	Sequence 21, Appl	802	30	42.3	116	1	US-08-477-728-73	Sequence 73, Appl
730	30	42.3	31	1	US-08-053-131-81	Sequence 81, Appl	803	30	42.3	116	1	US-08-474-040-5	Sequence 5, Appl
731	30	42.3	31	1	US-08-645-641-81	Sequence 81, Appl	804	30	42.3	116	1	US-08-474-040-57	Sequence 57, Appl
732	30	42.3	31	1	US-08-244-701B-13	Sequence 13, Appl	805	30	42.3	116	1	US-08-474-040-73	Sequence 73, Appl
733	30	42.3	31	1	US-07-853-408B-81	Sequence 81, Appl	806	30	42.3	116	1	US-08-487-200-5	Sequence 5, Appl
734	30	42.3	31	1	US-08-096-762-81	Sequence 81, Appl	807	30	42.3	116	1	US-08-487-200-57	Sequence 57, Appl
735	30	42.3	31	1	US-08-308-865-81	Sequence 81, Appl	808	30	42.3	116	1	US-08-487-200-73	Sequence 73, Appl
736	30	42.3	31	2	US-09-042-353-278	Sequence 278, App	809	30	42.3	116	1	US-08-488-113B-169	Sequence 169, App
737	30	42.3	31	2	US-08-758-417A-126	Sequence 126, App	810	30	42.3	116	1	US-08-477-484B-169	Sequence 169, App
738	30	42.3	31	2	US-08-525-539A-15	Sequence 15, Appl	811	30	42.3	116	1	US-08-107-669D-55	Sequence 55, Appl
739	30	42.3	31	2	US-09-076-721-13	Sequence 13, Appl	812	30	42.3	116	1	US-08-472-788A-86	Sequence 86, Appl
740	30	42.3	31	2	US-09-497-997C-9	Sequence 9, Appl	813	30	42.3	116	1	US-08-477-531B-55	Sequence 55, Appl
741	30	42.3	31	4	PCT-US92-10983-81	Sequence 81, Appl	814	30	42.3	116	1	US-08-646-360-169	Sequence 169, App
742	30	42.3	33	2	US-09-497-997C-23	Sequence 23, Appl	815	30	42.3	116	1	US-08-082-842A-86	Sequence 86, Appl
743	30	42.3	34	1	US-08-053-131-75	Sequence 75, Appl	816	30	42.3	116	1	US-08-652-816A-14	Sequence 14, Appl
744	30	42.3	34	1	US-08-053-131-87	Sequence 87, Appl	817	30	42.3	116	2	US-08-934-841-1	Sequence 1, Appl
745	30	42.3	34	1	US-08-645-641-75	Sequence 75, Appl	818	30	42.3	116	2	US-09-393-409-1	Sequence 1, Appl
746	30	42.3	34	1	US-08-645-641-87	Sequence 87, Appl	819	30	42.3	116	2	US-08-397-411-3	Sequence 3, Appl
747	30	42.3	34	1	US-07-853-408B-75	Sequence 75, Appl	820	30	42.3	116	2	US-08-839-765-169	Sequence 169, App
748	30	42.3	34	1	US-08-096-762-87	Sequence 87, Appl	821	30	42.3	116	2	US-09-136-389-169	Sequence 169, App
749	30	42.3	34	1	US-08-096-762-75	Sequence 75, Appl	822	30	42.3	116	2	US-08-484-537-5	Sequence 5, Appl
750	30	42.3	34	1	US-08-096-762-87	Sequence 87, Appl	823	30	42.3	116	2	US-08-484-537-57	Sequence 57, Appl
751	30	42.3	34	1	US-08-308-865-75	Sequence 75, Appl	824	30	42.3	116	2	US-08-484-537-73	Sequence 73, Appl
752	30	42.3	34	1	US-08-308-865-87	Sequence 87, Appl	825	30	42.3	116	2	US-09-610-838-169	Sequence 169, App
753	30	42.3	34	1	US-09-042-353-272	Sequence 272, App	826	30	42.3	116	2	US-09-711-485-169	Sequence 169, App
754	30	42.3	34	2	US-09-042-353-284	Sequence 284, App	827	30	42.3	116	2	US-08-537-871A-18	Sequence 18, Appl
755	30	42.3	34	2	US-08-758-417A-120	Sequence 120, App	828	30	42.3	117	1	US-07-942-245-36	Sequence 36, Appl
756	30	42.3	34	2	US-08-758-417A-132	Sequence 132, App	829	30	42.3	117	2	US-08-752-693A-3	Sequence 3, Appl
757	30	42.3	34	4	PCT-US92-10983-75	Sequence 75, Appl	830	30	42.3	117	2	US-08-752-693A-4	Sequence 4, Appl

831	30	42.3	117	2	US-09-157-370-1	Sequence 1, Appl	904	30	42.3	119	2	US-09-490-070A-65	Sequence 65, Appl
832	30	42.3	117	2	US-09-025-769B-22	Sequence 22, Appl	905	30	42.3	119	2	US-08-478-684G-11	Sequence 11, Appl
833	30	42.3	117	2	US-09-025-769B-22	Sequence 22, Appl	906	30	42.3	119	2	US-09-490-153-21	Sequence 21, Appl
834	30	42.3	117	2	US-08-525-539A-78	Sequence 78, Appl	907	30	42.3	119	2	US-09-490-153-26	Sequence 26, Appl
835	30	42.3	117	2	US-09-490-070A-22	Sequence 22, Appl	908	30	42.3	119	2	US-09-490-153-39	Sequence 39, Appl
836	30	42.3	117	2	US-09-490-070A-24	Sequence 24, Appl	909	30	42.3	119	2	US-09-490-153-65	Sequence 65, Appl
837	30	42.3	117	2	US-09-802-083-2	Sequence 2, Appl	910	30	42.3	119	2	US-09-254-180C-18	Sequence 18, Appl
838	30	42.3	117	2	US-09-490-153-22	Sequence 22, Appl	911	30	42.3	119	2	US-09-254-180C-19	Sequence 19, Appl
839	30	42.3	117	2	US-09-490-153-24	Sequence 24, Appl	912	30	42.3	119	2	US-09-467-903-5	Sequence 5, Appl
840	30	42.3	117	2	US-09-720-493-2	Sequence 2, Appl	913	30	42.3	119	2	US-09-490-324-21	Sequence 21, Appl
841	30	42.3	117	2	US-09-490-324-22	Sequence 22, Appl	914	30	42.3	119	2	US-09-490-324-26	Sequence 26, Appl
842	30	42.3	117	2	US-09-490-324-24	Sequence 24, Appl	915	30	42.3	119	2	US-09-490-324-39	Sequence 39, Appl
843	30	42.3	117	2	US-10-330-613A-13	Sequence 13, Appl	916	30	42.3	119	2	US-09-490-324-65	Sequence 65, Appl
844	30	42.3	117	4	PCR-US93-11611-6	Sequence 6, Appl	917	30	42.3	119	2	US-10-330-613A-25	Sequence 25, Appl
845	30	42.3	117	4	PCR-US93-11611-7	Sequence 7, Appl	918	30	42.3	119	2	US-09-602-812A-4	Sequence 4, Appl
846	30	42.3	118	2	US-08-513-968-80	Sequence 80, Appl	919	30	42.3	119	2	US-09-602-812A-6	Sequence 6, Appl
847	30	42.3	118	2	US-09-199-149-5	Sequence 5, Appl	920	30	42.3	120	1	US-07-942-245-35	Sequence 35, Appl
848	30	42.3	118	2	US-08-851-362D-47	Sequence 47, Appl	921	30	42.3	120	1	US-08-497-312-28	Sequence 28, Appl
849	30	42.3	118	2	US-09-025-769B-25	Sequence 25, Appl	922	30	42.3	120	1	US-07-934-373C-2	Sequence 2, Appl
850	30	42.3	118	2	US-09-530-139-22	Sequence 22, Appl	923	30	42.3	120	1	US-07-934-373C-6	Sequence 6, Appl
851	30	42.3	118	2	US-09-490-070A-25	Sequence 25, Appl	924	30	42.3	120	1	US-07-934-373C-42	Sequence 42, Appl
852	30	42.3	118	2	US-09-490-153-25	Sequence 25, Appl	925	30	42.3	120	1	US-07-934-373C-44	Sequence 44, Appl
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855	30	42.3	119	1	US-07-634-278-65	Sequence 65, Appl	928	30	42.3	120	1	US-08-428-197-28	Sequence 28, Appl
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857	30	42.3	119	1	US-08-477-728-65	Sequence 65, Appl	930	30	42.3	120	1	US-08-428-197-22	Sequence 22, Appl
858	30	42.3	119	1	US-08-477-728-89	Sequence 89, Appl	931	30	42.3	120	1	US-08-428-197-26	Sequence 26, Appl
859	30	42.3	119	1	US-07-988-925-11	Sequence 11, Appl	932	30	42.3	120	1	US-08-428-197-28	Sequence 28, Appl
860	30	42.3	119	1	US-08-331-398A-46	Sequence 46, Appl	933	30	42.3	120	1	US-08-428-197-30	Sequence 30, Appl
861	30	42.3	119	1	US-08-478-039-65	Sequence 65, Appl	934	30	42.3	120	1	US-08-428-197-32	Sequence 32, Appl
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863	30	42.3	119	1	US-08-474-040-65	Sequence 65, Appl	936	30	42.3	120	2	US-08-437-642B-2	Sequence 2, Appl
864	30	42.3	119	1	US-08-474-040-89	Sequence 89, Appl	937	30	42.3	120	2	US-08-437-642B-6	Sequence 6, Appl
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866	30	42.3	119	1	US-08-487-200-89	Sequence 89, Appl	939	30	42.3	120	2	US-08-437-642B-44	Sequence 44, Appl
867	30	42.3	119	1	US-08-476-349A-65	Sequence 65, Appl	940	30	42.3	120	2	US-09-171-945-55	Sequence 55, Appl
868	30	42.3	119	1	US-08-476-349A-100	Sequence 100, Appl	941	30	42.3	120	2	US-09-171-945-75	Sequence 75, Appl
869	30	42.3	119	1	US-08-360-125-5	Sequence 5, Appl	942	30	42.3	120	2	US-09-171-945-79	Sequence 79, Appl
870	30	42.3	119	1	US-08-450-578-5	Sequence 5, Appl	943	30	42.3	120	2	US-09-171-945-81	Sequence 81, Appl
871	30	42.3	119	1	US-08-362-780-11	Sequence 11, Appl	944	30	42.3	120	2	US-09-171-945-85	Sequence 85, Appl
872	30	42.3	119	1	US-08-331-397B-46	Sequence 46, Appl	945	30	42.3	120	2	US-09-171-945-89	Sequence 89, Appl
873	30	42.3	119	1	US-09-017-628-5	Sequence 5, Appl	946	30	42.3	120	2	US-09-171-945-91	Sequence 91, Appl
874	30	42.3	119	1	US-08-759-804A-46	Sequence 46, Appl	947	30	42.3	120	2	US-09-025-769B-35	Sequence 35, Appl
875	30	42.3	119	1	US-09-014-880-5	Sequence 5, Appl	948	30	42.3	120	2	US-09-025-769B-36	Sequence 36, Appl
876	30	42.3	119	2	US-08-933-983-81	Sequence 81, Appl	949	30	42.3	120	2	US-09-025-769B-38	Sequence 38, Appl
877	30	42.3	119	2	US-08-484-537-65	Sequence 65, Appl	950	30	42.3	120	2	US-09-025-769B-40	Sequence 40, Appl
878	30	42.3	119	2	US-08-484-537-89	Sequence 89, Appl	951	30	42.3	120	2	US-09-025-769B-57	Sequence 57, Appl
879	30	42.3	119	2	US-09-227-693-46	Sequence 46, Appl	952	30	42.3	120	2	US-09-025-769B-59	Sequence 59, Appl
880	30	42.3	119	2	US-09-025-769B-21	Sequence 21, Appl	953	30	42.3	120	2	US-09-025-769B-67	Sequence 67, Appl
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882	30	42.3	119	2	US-09-025-769B-39	Sequence 39, Appl	955	30	42.3	120	2	US-08-871-488A-19	Sequence 19, Appl
883	30	42.3	119	2	US-09-025-769B-65	Sequence 65, Appl	956	30	42.3	120	2	US-08-146-206C-2	Sequence 2, Appl
884	30	42.3	119	2	US-08-450-363-5	Sequence 5, Appl	957	30	42.3	120	2	US-08-146-206C-6	Sequence 6, Appl
885	30	42.3	119	2	US-09-648-067A-13	Sequence 13, Appl	958	30	42.3	120	2	US-09-705-686-6	Sequence 6, Appl
886	30	42.3	119	2	US-09-648-067A-15	Sequence 15, Appl	959	30	42.3	120	2	US-09-705-686-6	Sequence 6, Appl
887	30	42.3	119	2	US-09-647-468-30	Sequence 30, Appl	960	30	42.3	120	2	US-09-490-070A-35	Sequence 35, Appl
888	30	42.3	119	2	US-09-647-468-40	Sequence 40, Appl	961	30	42.3	120	2	US-09-490-070A-36	Sequence 36, Appl
889	30	42.3	119	2	US-09-647-468-42	Sequence 42, Appl	962	30	42.3	120	2	US-09-490-070A-38	Sequence 38, Appl
890	30	42.3	119	2	US-09-647-468-50	Sequence 50, Appl	963	30	42.3	120	2	US-09-490-070A-40	Sequence 40, Appl
891	30	42.3	119	2	US-09-647-468-52	Sequence 52, Appl	964	30	42.3	120	2	US-09-490-070A-57	Sequence 57, Appl
892	30	42.3	119	2	US-09-647-468-58	Sequence 58, Appl	965	30	42.3	120	2	US-09-490-070A-59	Sequence 59, Appl
893	30	42.3	119	2	US-09-647-468-60	Sequence 60, Appl	966	30	42.3	120	2	US-09-490-070A-63	Sequence 63, Appl
894	30	42.3	119	2	US-09-647-468-64	Sequence 64, Appl	967	30	42.3	120	2	US-09-490-070A-67	Sequence 67, Appl
895	30	42.3	119	2	US-09-647-468-70	Sequence 70, Appl	968	30	42.3	120	2	US-09-840-459-85	Sequence 85, Appl
896	30	42.3	119	2	US-09-647-468-72	Sequence 72, Appl	969	30	42.3	120	2	US-09-490-153-35	Sequence 35, Appl
897	30	42.3	119	2	US-09-647-468-76	Sequence 76, Appl	970	30	42.3	120	2	US-09-490-153-36	Sequence 36, Appl
898	30	42.3	119	2	US-09-647-468-78	Sequence 78, Appl	971	30	42.3	120	2	US-09-490-153-38	Sequence 38, Appl
899	30	42.3	119	2	US-09-647-468-82	Sequence 82, Appl	972	30	42.3	120	2	US-09-490-153-40	Sequence 40, Appl
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903	30	42.3	119	2	US-09-490-070A-39	Sequence 39, Appl	976	30	42.3	120	2	US-09-490-153-67	Sequence 67, Appl

977 30 42.3 120 2 US-09-705-392A-2 Sequence 2, Appl
978 30 42.3 120 2 US-09-705-392A-6 Sequence 6, Appl
979 30 42.3 120 2 US-09-705-392A-28 Sequence 28, Appl
980 30 42.3 120 2 US-09-705-392A-30 Sequence 30, Appl
981 30 42.3 120 2 US-09-705-392A-32 Sequence 32, Appl
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983 30 42.3 120 2 US-09-705-392A-36 Sequence 36, Appl
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985 30 42.3 120 2 US-09-705-398-2 Sequence 2, Appl
986 30 42.3 120 2 US-09-705-398-6 Sequence 6, Appl
987 30 42.3 120 2 US-09-232-290-39 Sequence 39, Appl
988 30 42.3 120 2 US-09-490-324-35 Sequence 35, Appl
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996 30 42.3 120 2 US-10-194-975-114 Sequence 114, App
997 30 42.3 120 2 US-09-910-059-55 Sequence 55, Appl
998 30 42.3 120 2 US-09-910-059-75 Sequence 75, Appl
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ALIGNMENTS

RESULT 1
US-09-155-106-3 Query Match 100.0%; Score 71; DB 2; Length 13;
; Sequence 3, Application US/09155106 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
; Patent No. 6730300 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-3

Query Match 100.0%; Score 71; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
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Db 1 DDYGGQSTYVMDA 13

RESULT 2
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-18

Query Match 100.0%; Score 71; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
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Db 99 DDYGGQSTYVMDA 111

RESULT 3
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; Sequence 19, Application US/09155106 Best Local Similarity 100.0%; Pred. No. 0.00023;
; Patent No. 6730300 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19

Query Match 100.0%; Score 71; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 99 DDYGGQSTYVMDA 111

RESULT 4

US-09-155-106-20
; Sequence 20, Application US/09155106
; Patent No. 6730300

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-20

Query Match

Best Local Similarity 100.0%; Score 71; DB 2; Length 122;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13

| | | | | | | | | |

Db 99 DDYGGQSTYVMDA 111

RESULT 5

US-09-155-106-26
; Sequence 26, Application US/09155106
; Patent No. 6730300

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-26

Query Match 100.0%; Score 71; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13

| | | | | | | | | |

Db 99 DDYGGQSTYVMDA 111

RESULT 6

US-09-155-106-32
; Sequence 32, Application US/09155106
; Patent No. 6730300

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-32

Query Match

Best Local Similarity 100.0%; Score 71; DB 2; Length 122;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13

| | | | | | | | | |

Db 99 DDYGGQSTYVMDA 111

RESULT 7

US-09-107-532A-5551

; Sequence 5551, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD/ROM ISO9660

; COMPUTER: PC

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; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5551:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 416 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (8) LOCATION 1...416
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5551:
US-09-107-532A-5551

Query Match          57.7%; Score 41; DB 2; Length 416;
Best Local Similarity 53.8%; Pred. No. 67;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGGQSTYVMDA 13
Db      103 ENYDGESTIVLDA 115

RESULT 8
US-09-091-219-25
; Sequence 25, Application US/09091219
; Patent No. 6171592
; GENERAL INFORMATION:
;   APPLICANT: STUDDERT, Michael J.
;   APPLICANT: CRABB, Brendan S.
;   APPLICANT: FENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; CURRENT APPLICATION NUMBER: US/09/091,219
; EARLIER FILING DATE: 1998-10-05
; EARLIER FILING DATE: 1996-12-18
; EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2232
; TYPE: PRT
; ORGANISM: equine rhinovirus 1
US-09-091-219-25

Query Match          57.7%; Score 41; DB 2; Length 2232;
Best Local Similarity 53.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DDYGGQSTYVMDA 13
Db      1293 DGYNGQAVVIMDA 1305

RESULT 9
US-09-660-541-25
; Sequence 25, Application US/09660541
; Patent No. 6531136
; GENERAL INFORMATION:
;   APPLICANT: STUDDERT, Michael J.
;   APPLICANT: CRABB, Brendan S.
;   APPLICANT: FENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/660,541
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/091,219
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-12-18
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2232
; TYPE: PRT
; ORGANISM: equine rhinovirus 1
US-09-660-541-25

Query Match          57.7%; Score 41; DB 2; Length 2232;
Best Local Similarity 53.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DDYGGQSTYVMDA 13
Db      1293 DGYNGQAVVIMDA 1305

RESULT 11
US-09-660-541-2
; Sequence 2, Application US/09660541
; Patent No. 6531136
; GENERAL INFORMATION:
;   APPLICANT: STUDDERT, Michael J.
```

```

; APPLICANT: CRABB, Brendan S.
; APPLICANT: FENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/660,541
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/091,219
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN7201
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2247
; TYPE: PRT
; ORGANISM: equine rhinovirus 1
US-09-660-541-2

```

```

Query Match      57.7%; Score 41; DB 2; Length 2247;
Best Local Similarity 53.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 DDYGGQSTYVMDA 13
DB 1293 DGYNGQAVVIMDA 1305

```

```

RESULT 12
; Sequence 4832, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4832
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4832

```

```

Query Match      56.3%; Score 40; DB 2; Length 183;
Best Local Similarity 61.5%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 DDYGGQSTYVMDA 13
DB 48 DDIGKSTEVQA 60

```

```

RESULT 13
US-09-266-464-3
; Sequence 3, Application US/09266464
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/266,464
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
US-09-266-464-3

```

```

Query Match      54.9%; Score 39; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 DDYGGQSTYVMD 12
DB 3 DDYGESESTSSME 14

```

```

RESULT 14
US-09-952-385-3
; Sequence 3, Application US/09952385
; Patent No. 6689570
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
US-09-952-385-3

```

```

Query Match      54.9%; Score 39; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 DDYGGQSTYVMD 12
DB 3 DDYGESESTSSME 14

```

```

RESULT 15
US-09-966-755-3
; Sequence 3, Application US/09966755
; Patent No. 6884574
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/966,755
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
US-09-966-755-3

Query Match 54.9%; Score 39; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
||||:|||||
Db 3 DDYGSESTSSME 14

RESULT 16

US-09-522-752-3
; Sequence 3, Application US/09522752
; Patent No. 6936248
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: 1855.1064-003
; CURRENT APPLICATION NUMBER: US/09/522,752
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: US 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-Terminal Peptide of Human GPR-9-6
US-09-522-752-3

Query Match 54.9%; Score 39; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
||||:|||||
Db 3 DDYGSESTSSME 14

RESULT 17

US-09-266-464-2
; Sequence 2, Application US/09266464
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LK98-16
; CURRENT APPLICATION NUMBER: US/09/266,464
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-266-464-2

Query Match 54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
||||:|||||

Db 3 DDYGSESTSSME 14

RESULT 18

US-09-170-496D-24
; Sequence 24, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-24

Query Match 54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
||||:|||||
Db 3 DDYGSESTSSME 14

RESULT 19

US-09-170-496D-176
; Sequence 176, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-176

Query Match 54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
||||:|||||
Db 3 DDYGSESTSSME 14

RESULT 20

US-09-952-385-2
; Sequence 2, Application US/09952385
; Patent No. 6689570
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION

```
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-952-385-2

Query Match          54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   ||||:|:|:|:
Db 3 DDYGESTSSME 14

RESULT 21
US-09-966-755-2
; Sequence 2, Application US/09966755
; Patent No. 6884574
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/966,755
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-755-2

Query Match          54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   ||||:|:|:|:
Db 3 DDYGESTSSME 14

RESULT 22
US-09-522-752-2
; Sequence 2, Application US/09522752
; Patent No. 6936248
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: 1855.1064-003
; CURRENT APPLICATION NUMBER: US/09/522,752
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: US 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 357

; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 09/266,464
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-952-385-2

Query Match          54.9%; Score 39; DB 2; Length 357;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   ||||:|:|:|:
Db 3 DDYGESTSSME 14

RESULT 23
US-09-826-509-481
; Sequence 481, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 481
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-481

Query Match          54.9%; Score 39; DB 2; Length 369;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   ||||:|:|:|:
Db 15 DDYGESTSSME 26

RESULT 24
US-09-721-341-6
; Sequence 6, Application US/09721341
; Patent No. 6828108
; GENERAL INFORMATION:
; APPLICANT: Goelling, Jennifa
; APPLICANT: Dairaghi, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-000710US
; CURRENT APPLICATION NUMBER: US/09/721,341
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/686,020
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
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; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor (CCR9)
US-09-721-341-6

Query Match          54.9%; Score 39; DB 2; Length 369;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
    |||| :||| :
Db 15 DDYGSESTSSME 26

RESULT 25
US-09-721-495B-6
; Sequence 6, Application US/09721495B
; Patent No. 6835547
; GENERAL INFORMATION:
; APPLICANT: Goeling, Jennifa
; APPLICANT: Dairaghi, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Talbot, Dale
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc. Receptor
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-0007210US
; CURRENT APPLICATION NUMBER: US/09/721.495B
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/686,019
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor CCR9
US-09-721-495B-6

Query Match          54.9%; Score 39; DB 2; Length 369;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
    |||| :||| :
Db 15 DDYGSESTSSME 26

RESULT 26
US-09-949-016-11223
; Sequence 11223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11223
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11223

Query Match          54.9%; Score 39; DB 2; Length 371;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
    |||| :||| :
Db 17 DDYGSESTSSME 28

RESULT 27
US-09-513-999C-4828
; Sequence 4828, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4828
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-4828

Query Match          53.5%; Score 38; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
    |||| :|
Db 102 DDYGGYNNY 110

RESULT 28
US-09-513-999C-4831
; Sequence 4831, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
```

; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4831
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4831

Query Match 53.5%; Score 38; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
||| :
Db 102 DDYGGYNNY 110

RESULT 29
US-09-152-060-116
; Sequence 116, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 118
; SEQ ID NO 116
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-116

Query Match 53.5%; Score 38; DB 2; Length 223;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
||| :
Db 136 DDYGGYNNY 144

RESULT 30
US-09-852-797-116
; Sequence 116, Application US/09852797
; Patent No. 6878806
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-116

Query Match 53.5%; Score 38; DB 2; Length 223;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
||| :
Db 136 DDYGGYNNY 144

RESULT 31
US-09-853-161-116
; Sequence 116, Application US/09853161
; Patent No. 6919433
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765


```
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-116

Query Match      53.5%; Score 38; DB 2; Length 223;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGGQSTY 9
      ||||| : |
Db     136 DDYGYNNY 144

RESULT 32
US-10-058-993-116
; Sequence 116, Application US/10058993
; Patent No. 6951924
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-116

Query Match      53.5%; Score 38; DB 2; Length 223;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGGQSTY 9
      ||||| : |
Db     136 DDYGYNNY 144

RESULT 33
US-09-949-016-9966
; Sequence 9966, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9966
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9966

Query Match      53.5%; Score 38; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGGQSTY 9
      ||||| : |
Db     77 DDYGYNNY 85

RESULT 34
US-09-949-016-9967
; Sequence 9967, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9967
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9967

Query Match      53.5%; Score 38; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDYGGQSTY 9
      ||||| : |
Db     77 DDYGYNNY 85
```

```
RESULT 35
US-09-949-016-7015
; Sequence 7015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7015
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7015

Query Match 53.5%; Score 38; DB 2; Length 331;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
DB 136 DDYGGYNNY 144

RESULT 36
US-09-134-078-61
; Sequence 61, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELEPHONE: 858/677-1465
; TELEFAX: 858/677-1456
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-61

Query Match 53.5%; Score 38; DB 2; Length 680;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTYV 10
DB 147 DDFGGMNQYV 156

RESULT 37
US-09-134-078-25
; Sequence 25, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-25

Query Match 53.5%; Score 38; DB 2; Length 680;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTYV 10
DB 147 DDFGGMNQYV 156

RESULT 38
US-08-684-005-2
; Sequence 2, Application US/08684005
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; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-61

Query Match 53.5%; Score 38; DB 2; Length 663;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTYV 10
DB 130 DDFGGMNQYV 139

RESULT 37
US-09-134-078-25
; Sequence 25, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-134-078-25

Query Match 53.5%; Score 38; DB 2; Length 680;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTYV 10
DB 147 DDFGGMNQYV 156

RESULT 38
US-08-684-005-2
; Sequence 2, Application US/08684005
```

```
; Patent No. 6682918
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Buikema, William J.
; APPLICANT: Bauer, Christopher C.
; TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,005
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARSB:508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 806 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-684-005-2

Query Match 53.5%; Score 38; DB 2; Length 806;
Best Local Similarity 63.6%; Pred. No. 4.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DYGGQSTVMD 12
Db 292 DTGGQVVYVLD 302

RESULT 39
US-08-568-459A-12
; Sequence 12, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids

; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-568-459A-12

Query Match 53.5%; Score 38; DB 1; Length 2710;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
Db 102 DEYGGQCTH 110

RESULT 40
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-487-826B-12
Query Match 53.5%; Score 38; DB 1; Length 2710;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
Db 102 DEYGGQCTH 110
|:|||||:

RESULT 41
US-09-210-288-12
; Sequence 12, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12
Query Match 53.5%; Score 38; DB 2; Length 2710;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
Db 102 DEYGGQCTH 110
|:|||||:

RESULT 42
US-10-153-273-12
; Sequence 12, Application US/10153273
; Patent No. 6962987
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12
Query Match 53.5%; Score 38; DB 2; Length 2710;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
Db 102 DEYGGQCTH 110
|:|||||:

RESULT 43
US-08-487-826B-14
; Sequence 14, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
```

```
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Welles, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3060 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-826B-14

Query Match 53.5%; Score 38; DB 1; Length 3060;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DDYGGQSTY 9
Db 100 DEYGGQCTH 108

RESULT 44
US-08-983-607-38
; Sequence 38, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient
; ORGANISM: immunized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lympho-
; INDIVIDUAL ISOLATE: cytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: FUSE5 fusion phage construct
; CLONE: V575
; FEATURE:
; NAME/KEY: heavy chain
US-08-983-607-38

Query Match 52.1%; Score 37; DB 2; Length 123;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 YGGOSTYVMD 12
Db 103 YGGNSDIQMD 112

RESULT 45
PCT-US94-03744-4
; Sequence 4, Application PC/TUS9403744
; GENERAL INFORMATION:
; APPLICANT: PETRI, WILLIAM A.
; APPLICANT: MCCOY, JAMES J.
; APPLICANT: MANN, BARBARA J.
; TITLE OF INVENTION: 35/31 KDA SUBUNIT OF THE
; TITLE OF INVENTION: ENTAMOERA
; TITLE OF INVENTION: HISTOLYTICA ADHERENCE LECTIN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03744
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,679
; FILING DATE: 09-APR-1993
; ATTORNEY/AGENT INFORMATION:
```

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29148-20005.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-03744-4

Query Match 52.1%; Score 37; DB 4; Length 288;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:||||
DB 95 DDKNGDQRYVMD 106

RESULT 46
US-08-476-008-56
Sequence 56, Application US/08476008
Patent No. 5627061
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-008-56

Query Match 52.1%; Score 37; DB 1; Length 444;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GQGSTYVMD 12
|||:||||
DB 115 GGNATYVLD 123

RESULT 47
US-08-306-063-56
Sequence 56, Application US/08306063
Patent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-306-063-56

Query Match 52.1%; Score 37; DB 1; Length 444;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GQGSTYVMD 12
|||:||||
DB 115 GGNATYVLD 123

```
RESULT 48
US-08-833-485-56
; Sequence 56, Application US/08833485
; Patent No. 5804425
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,485
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-485-56

Query Match 52.1%; Score 37; DB 1; Length 444;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GQSTYVMD 12
|||:|
Db 115 GGNATYVLD 123

RESULT 49
US-09-243-374-5
; Sequence 5, Application US/09243374B
; Patent No. 6225114
; GENERAL INFORMATION:
; APPLICANT: Eichholtz, David Alan
; APPLICANT: Gasser, Charles Scott
; APPLICANT: Kishore, Ganesh M
; TITLE OF INVENTION: Glyphosate-tolerant 5-enolpyruvyl-3-phosphoshikimate
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```
; TITLE OF INVENTION: synthases
; FILE REFERENCE: EPSP synthases
; CURRENT APPLICATION NUMBER: US/09/243,374B
; CURRENT FILING DATE: 1999-02-01
; EARLIER APPLICATION NUMBER: 07/590,647
; EARLIER FILING DATE: 1990-09-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-09-243-374-5

Query Match 52.1%; Score 37; DB 2; Length 444;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GQSTYVMD 12
|||:|
Db 115 GGNATYVLD 123

RESULT 50
US-09-137-440-56
; Sequence 56, Application US/09137440
; Patent No. 6248876
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,440
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/833,485
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
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```

;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
US-09-137-440-56

Query Match      52.1%; Score 37; DB 2; Length 444;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GQGSTYVMD 12
      |||:|
Db      115 GGNATVLD 123

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OM protein - protein search, using sw model

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Title: US-10-808-538-3

Perfect score: 71

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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259	37	52.1	570	6	US-11-050-645-5	Sequence 5, Appli	332	37	52.1	823	4	US-10-425-114-72813	Sequence 72813, A
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261	37	52.1	593	4	US-10-425-114-50109	Sequence 50109, A	334	37	52.1	849	4	US-10-425-115-315003	Sequence 315003, A
262	37	52.1	596	4	US-10-425-114-62525	Sequence 62525, A	335	37	52.1	854	4	US-10-437-963-1149401	Sequence 1149401, A
263	37	52.1	596	4	US-10-437-963-104991	Sequence 104991, A	336	37	52.1	860	4	US-10-437-963-114440	Sequence 114440, A
264	37	52.1	619	4	US-10-425-114-68121	Sequence 68121, A	337	37	52.1	864	4	US-10-437-963-183335	Sequence 183335, A
265	37	52.1	628	4	US-10-424-599-244151	Sequence 244151, A	338	37	52.1	1028	4	US-10-425-115-228803	Sequence 228803, A
266	37	52.1	639	4	US-10-425-114-58450	Sequence 58450, A	339	37	52.1	1126	5	US-10-732-923-12828	Sequence 12828, A
267	37	52.1	645	5	US-10-732-923-3162	Sequence 3162, Ap	340	37	52.1	4904	6	US-11-097-143-13539	Sequence 13539, A
268	37	52.1	651	4	US-10-425-114-43911	Sequence 43911, A	341	37	52.1	19725	4	US-10-084-846A-4	Sequence 4, Appli
269	37	52.1	652	4	US-10-425-114-46682	Sequence 46682, A	342	36.5	51.4	21	5	US-10-661-156-551	Sequence 551, App
270	37	52.1	664	4	US-10-425-115-270765	Sequence 270765, A	343	36.5	51.4	145	4	US-10-094-749-1957	Sequence 1957, Ap
271	37	52.1	670	4	US-10-425-114-49869	Sequence 49869, A	344	36.5	51.4	184	4	US-10-437-963-156653	Sequence 156653, A
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273	37	52.1	677	5	US-10-989-228-38	Sequence 38, Appl	346	36	50.7	17	4	US-10-327-598-471	Sequence 471, App
274	37	52.1	678	4	US-10-437-963-183341	Sequence 183341, A	347	36	50.7	17	4	US-10-327-598-473	Sequence 473, App
275	37	52.1	683	4	US-10-425-114-68384	Sequence 68384, A	348	36	50.7	17	4	US-10-327-598-482	Sequence 482, App
276	37	52.1	749	4	US-10-425-114-56196	Sequence 56196, A	349	36	50.7	18	3	US-09-928-213A-2	Sequence 2, Appli
277	37	52.1	777	5	US-10-481-032A-124	Sequence 124, App	350	36	50.7	21	5	US-10-661-156-584	Sequence 584, App
278	37	52.1	777	5	US-10-481-032A-6091	Sequence 6091, A	351	36	50.7	67	3	US-09-867-550-158	Sequence 158, App
279	37	52.1	786	4	US-10-481-032A-128	Sequence 128, App	352	36	50.7	88	5	US-10-450-763-33067	Sequence 33067, A
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281	37	52.1	798	4	US-10-437-963-109848	Sequence 109848, A	354	36	50.7	147	5	US-10-916-840-52	Sequence 52, Appl
282	37	52.1	798	5	US-10-481-032A-126	Sequence 126, App	355	36	50.7	162	4	US-10-437-963-134940	Sequence 134940, A
283	37	52.1	802	4	US-10-080-114A-2	Sequence 2, Appli	356	36	50.7	175	4	US-10-437-963-124592	Sequence 124592, A
284	37	52.1	802	4	US-10-080-114A-5	Sequence 5, Appli	357	36	50.7	206	4	US-10-408-765A-385	Sequence 385, App
285	37	52.1	802	4	US-10-767-701-47013	Sequence 47013, A	358	36	50.7	215	3	US-09-925-302-465	Sequence 465, App
286	37	52.1	802	4	US-10-425-115-295611	Sequence 295611, A	359	36	50.7	215	3	US-09-925-302-465	Sequence 465, App
287	37	52.1	802	4	US-10-425-115-295612	Sequence 295612, A	360	36	50.7	215	4	US-10-264-049-2504	Sequence 2504, Ap
288	37	52.1	802	5	US-10-739-930-7579	Sequence 7579, Ap	361	36	50.7	230	4	US-10-071-485-102	Sequence 102, App
289	37	52.1	803	5	US-10-928-992-192	Sequence 192, App	362	36	50.7	230	5	US-10-985-581-102	Sequence 102, App
290	37	52.1	804	5	US-10-417-375-81	Sequence 81, Appl	363	36	50.7	235	4	US-10-071-485-93	Sequence 93, Appl
291	37	52.1	805	4	US-10-137-036-77	Sequence 77, Appl	364	36	50.7	235	5	US-10-985-581-93	Sequence 93, Appl
292	37	52.1	805	4	US-10-217-939-28	Sequence 28, Appl	365	36	50.7	239	4	US-10-767-701-44653	Sequence 44653, A
293	37	52.1	805	4	US-10-393-840-44	Sequence 44, Appl	366	36	50.7	240	4	US-10-071-485-91	Sequence 91, Appl
294	37	52.1	805	4	US-10-393-840-144	Sequence 144, App	367	36	50.7	240	5	US-10-985-581-91	Sequence 91, Appl
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297	37	52.1	805	4	US-10-702-319A-77	Sequence 77, Appl	370	36	50.7	267	5	US-10-985-581-2	Sequence 2, Appli
298	37	52.1	806	4	US-10-003-405-2	Sequence 2, Appli	371	36	50.7	273	4	US-10-374-535-18	Sequence 18, Appl
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305	37	52.1	808	4	US-10-289-757-169	Sequence 169, App	378	36	50.7	429	4	US-10-312-273-227	Sequence 227, App
306	37	52.1	808	5	US-10-955-745-74	Sequence 74, Appl	379	36	50.7	429	4	US-10-289-762-189	Sequence 189, App
307	37	52.1	808	5	US-10-955-745-75	Sequence 75, Appl	380	36	50.7	429	4	US-10-282-122A-54850	Sequence 54850, A
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310	37	52.1	809	4	US-10-437-963-167348	Sequence 167348, A	383	36	50.7	445	4	US-10-013-477-13	Sequence 13, Appl
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314	37	52.1	811	4	US-10-425-115-265750	Sequence 265750, A	387	36	50.7	468	5	US-10-985-581-67	Sequence 67, Appl
315	37	52.1	812	4	US-10-424-599-241731	Sequence 241731, A	388	36	50.7	470	6	US-11-097-143-8883	Sequence 8883, Ap
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317	37	52.1	814	5	US-10-955-745-76	Sequence 76, Appl	390	36	50.7	479	5	US-10-450-763-35274	Sequence 35274, A
318	37	52.1	815	4	US-10-289-757-170	Sequence 170, App	391	36	50.7	481	4	US-10-437-963-168785	Sequence 168785, A
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395	36	50.7	540	4	US-10-437-963-170599	Sequence 170599, A	468	35	49.3	682	4	US-10-782-570-16	Sequence 16, Appl
396	36	50.7	541	4	US-10-071-485-85	Sequence 85, Appl	469	35	49.3	682	5	US-10-783-417-14	Sequence 14, Appl
397	36	50.7	541	5	US-10-985-581-85	Sequence 85, Appl	470	35	49.3	682	5	US-10-781-979-21	Sequence 21, Appl
398	36	50.7	557	4	US-10-1282-122A-48000	Sequence 48000, A	471	35	49.3	700	4	US-10-369-493-10142	Sequence 10142, A
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401	36	50.7	686	4	US-10-072-012-795	Sequence 795, App	474	35	49.3	1000	6	US-11-097-143-13989	Sequence 13989, A
402	36	50.7	711	4	US-10-071-485-90	Sequence 90, Appl	475	35	49.3	1231	4	US-10-282-122A-77799	Sequence 77799, A
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404	36	50.7	720	4	US-10-217-700-14	Sequence 14, Appl	477	35	49.3	1553	4	US-10-415-188-5	Sequence 5, Appl
405	36	50.7	720	4	US-10-369-493-2848	Sequence 2848, Ap	478	35	49.3	1573	4	US-10-369-493-6867	Sequence 6867, Ap
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411	35	49.3	32	5	US-10-946-647-181	Sequence 181, App	484	35	49.3	1596	4	US-10-221-278-711	Sequence 711, App
412	35	49.3	32	5	US-10-946-647-540	Sequence 540, App	485	35	49.3	1637	4	US-10-291-172-335	Sequence 335, App
413	35	49.3	65	4	US-10-424-599-256935	Sequence 256935, A	486	35	49.3	1637	4	US-10-221-278-335	Sequence 335, App
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417	35	49.3	123	4	US-10-723-434-89	Sequence 89, Appl	490	35	49.3	2214	4	US-10-369-493-6737	Sequence 6737, Ap
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422	35	49.3	243	5	US-10-683-547-6	Sequence 6, Appl	495	34	47.9	21	5	US-10-661-156-505	Sequence 505, App
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425	35	49.3	256	4	US-10-109-551-6	Sequence 6, Appl	498	34	47.9	33	4	US-10-668-767-119	Sequence 119, App
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461	35	49.3	516	4	US-10-477-369-61	Sequence 61, Appl	534	34	47.9	255	4	US-10-652-870-180	Sequence 180, App
462	35	49.3	534	5	US-10-732-923-23777	Sequence 23777, A	535	34	47.9	255	4	US-10-652-870-218	Sequence 218, App
463	35	49.3	538	4	US-10-369-493-6293	Sequence 6293, Ap	536	34	47.9	255	4	US-10-652-870-222	Sequence 222, App
464	35	49.3	627	4	US-10-437-963-120488	Sequence 120488, A	537	34	47.9	256	4	US-09-880-748-907	Sequence 907, App
465	35	49.3	638	4	US-10-282-122A-52387	Sequence 52387, A	538	34	47.9	256	4	US-10-293-418-907	Sequence 907, App

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540	34	47.9	256	4	US-10-652-870-178	Sequence 178, App	613	34	47.9	878	4	US-10-722-050-2	Sequence 2, Appl
541	34	47.9	256	4	US-10-652-870-220	Sequence 220, App	614	34	47.9	882	4	US-10-282-122A-47274	Sequence 47274, A
542	34	47.9	257	4	US-10-369-493-11794	Sequence 11794, A	615	34	47.9	907	3	US-09-328-599A-1	Sequence 1, Appl
543	34	47.9	257	4	US-10-369-493-14201	Sequence 14201, A	616	34	47.9	1101	3	US-10-156-761-11157	Sequence 11157, A
544	34	47.9	257	4	US-10-369-493-14530	Sequence 14530, A	617	34	47.9	1155	4	US-10-282-122A-53419	Sequence 53419, A
545	34	47.9	257	4	US-10-369-493-15048	Sequence 15048, A	618	34	47.9	1301	6	US-11-097-143-20904	Sequence 20904, A
546	34	47.9	262	6	US-11-097-143-25818	Sequence 25818, A	619	34	47.9	1859	5	US-10-745-237-140	Sequence 140, App
547	34	47.9	265	4	US-10-425-114-37125	Sequence 37125, A	620	34	47.9	4868	4	US-10-668-767-57	Sequence 57, Appl
548	34	47.9	280	5	US-10-488-786B-16	Sequence 16, Appl	621	34	47.9	5100	4	US-10-668-767-146	Sequence 146, App
549	34	47.9	280	5	US-10-488-786B-21	Sequence 21, Appl	622	34	47.9	5101	4	US-10-668-767-6	Sequence 4, Appl
550	34	47.9	282	4	US-10-374-535-3	Sequence 3, Appl	623	34	47.9	5104	4	US-10-668-767-6	Sequence 6, Appl
551	34	47.9	284	4	US-10-437-963-170166	Sequence 170166, A	624	34	47.9	5107	6	US-11-097-143-22563	Sequence 22563, A
552	34	47.9	287	6	US-11-097-143-25821	Sequence 25821, A	625	34	47.9	5109	4	US-10-668-767-10	Sequence 10, Appl
553	34	47.9	304	4	US-10-425-114-49002	Sequence 49002, A	626	34	47.9	5112	4	US-10-668-767-125	Sequence 125, App
554	34	47.9	308	5	US-10-474-792-648	Sequence 648, App	627	34	47.9	5112	4	US-10-668-767-126	Sequence 126, App
555	34	47.9	319	4	US-10-369-493-18816	Sequence 18816, A	628	34	47.9	5113	4	US-10-668-767-121	Sequence 121, App
556	34	47.9	322	4	US-10-369-493-11269	Sequence 11269, A	629	34	47.9	5126	4	US-10-668-767-56	Sequence 56, Appl
557	34	47.9	328	4	US-10-214-766-23	Sequence 1269, A	630	34	47.9	5126	4	US-10-668-767-123	Sequence 123, App
558	34	47.9	339	3	US-09-882-227-524	Sequence 23, Appl	631	34	47.9	5126	4	US-10-668-767-124	Sequence 124, App
559	34	47.9	339	4	US-10-425-114-55855	Sequence 524, App	632	34	47.9	5127	4	US-10-668-767-8	Sequence 8, Appl
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561	34	47.9	339	4	US-10-335-977-6402	Sequence 6402, Ap	634	34	47.9	5127	4	US-10-668-767-122	Sequence 122, App
562	34	47.9	346	3	US-09-917-378-8	Sequence 8, Appl	635	34	47.9	5128	4	US-10-668-767-128	Sequence 128, App
563	34	47.9	350	4	US-10-335-977-6403	Sequence 6403, Ap	636	34	47.9	5134	4	US-10-668-767-130	Sequence 130, App
564	34	47.9	356	3	US-09-791-961-3	Sequence 3, Appl	637	34	47.9	5142	4	US-10-668-767-2	Sequence 2, Appl
565	34	47.9	356	4	US-10-637-280-3	Sequence 3, Appl	638	34	47.9	5142	4	US-10-668-767-144	Sequence 144, App
566	34	47.9	357	4	US-10-112-857-18	Sequence 18, Appl	639	33.5	47.2	324	4	US-10-425-115-346743	Sequence 346743, A
567	34	47.9	382	3	US-09-795-693-23	Sequence 23, Appl	640	33.5	47.2	913	4	US-10-282-122A-51223	Sequence 51223, A
568	34	47.9	382	4	US-10-156-239-23	Sequence 23, Appl	641	33.5	47.2	1436	6	US-11-097-143-24630	Sequence 24630, A
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570	34	47.9	393	5	US-10-739-930-9981	Sequence 9981, Ap	643	33	46.5	17	4	US-10-305-231-102	Sequence 146, App
571	34	47.9	399	4	US-10-425-115-293767	Sequence 293767, A	644	33	46.5	17	4	US-10-723-434-146	Sequence 472, App
572	34	47.9	399	6	US-11-097-143-22206	Sequence 22206, A	645	33	46.5	32	3	US-09-864-761-39634	Sequence 39634, A
573	34	47.9	415	4	US-10-424-599-159631	Sequence 159631, A	646	33	46.5	32	3	US-10-424-599-218081	Sequence 218081, A
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577	34	47.9	428	4	US-10-424-599-266292	Sequence 266292, A	650	33	46.5	55	4	US-10-450-763-56425	Sequence 56425, A
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586	34	47.9	465	5	US-10-816-276-19	Sequence 19, Appl	658	33	46.5	100	4	US-10-424-599-218081	Sequence 218081, A
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590	34	47.9	472	6	US-11-097-143-36474	Sequence 36474, A	662	33	46.5	107	4	US-10-424-599-189294	Sequence 189294, A
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592	34	47.9	516	4	US-10-214-766-24	Sequence 24, Appl	664	33	46.5	117	2	US-08-790-540A-2	Sequence 2, Appl
593	34	47.9	520	6	US-11-051-955-27	Sequence 27, Appl	665	33	46.5	117	2	US-08-790-540A-6	Sequence 6, Appl
594	34	47.9	520	4	US-10-214-766-25	Sequence 25, Appl	666	33	46.5	117	2	US-08-791-391A-2	Sequence 2, Appl
595	34	47.9	535	4	US-10-424-599-210578	Sequence 210578, A	667	33	46.5	117	2	US-08-791-391A-6	Sequence 6, Appl
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597	34	47.9	589	3	US-09-962-855-4	Sequence 4, Appl	669	33	46.5	117	3	US-09-900-590-6	Sequence 6, Appl
598	34	47.9	589	3	US-09-963-131-213	Sequence 131, App	670	33	46.5	117	4	US-10-078-757B-56	Sequence 56, Appl
599	34	47.9	589	4	US-10-369-493-12286	Sequence 12286, A	671	33	46.5	117	4	US-10-305-231-2	Sequence 2, Appl
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601	34	47.9	605	4	US-10-755-889-72	Sequence 72, Appl	673	33	46.5	117	4	US-10-452-440-2	Sequence 2, Appl
602	34	47.9	634	4	US-10-282-122A-52070	Sequence 52070, A	674	33	46.5	117	4	US-10-452-440-6	Sequence 6, Appl
603	34	47.9	638	4	US-10-282-122A-78426	Sequence 78426, A	675	33	46.5	117	4	US-10-463-847-2	Sequence 2, Appl
604	34	47.9	658	3	US-09-328-599A-2	Sequence 2, Appl	676	33	46.5	117	4	US-10-463-847-6	Sequence 6, Appl
605	34	47.9	680	4	US-10-389-566-1402	Sequence 1402, Ap	677	33	46.5	117	5	US-10-959-871-2	Sequence 2, Appl
606	34	47.9	681	4	US-10-282-122A-71657	Sequence 71657, A	678	33	46.5	120	4	US-10-959-871-6	Sequence 6, Appl
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611	34	47.9	799	4	US-10-437-963-176984	Sequence 176984, A	683	33	46.5	125	4	US-10-632-706-48	Sequence 48, Appl
							684	33	46.5	129	3	US-09-530-139-24	Sequence 24, Appl

685	33	46.5	130	4	US-10-078-757B-44	Sequence 44, Appl	758	33	46.5	345	4	US-10-415-325-23	Sequence 23, Appl
686	33	46.5	131	4	US-10-282-122A-49822	Sequence 49822, A	759	33	46.5	345	4	US-10-415-325-24	Sequence 24, Appl
687	33	46.5	132	4	US-10-424-599-258438	Sequence 28438, A	760	33	46.5	345	4	US-10-415-325-25	Sequence 25, Appl
688	33	46.5	133	4	US-10-425-115-287045	Sequence 287045, A	761	33	46.5	354	5	US-10-732-923-7690	Sequence 7690, Ap
689	33	46.5	139	4	US-10-424-599-251765	Sequence 251765, A	762	33	46.5	356	5	US-10-732-923-7434	Sequence 7434, Ap
690	33	46.5	141	4	US-10-155-886-61	Sequence 61, Appl	763	33	46.5	360	4	US-10-437-963-11838	Sequence 11838, A
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692	33	46.5	143	4	US-10-469-304-17	Sequence 17, Appl	765	33	46.5	364	4	US-10-437-963-164683	Sequence 164683, A
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697	33	46.5	163	4	US-10-437-963-164682	Sequence 164682, A	770	33	46.5	379	4	US-10-424-599-221308	Sequence 221308, A
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701	33	46.5	188	4	US-10-767-701-40866	Sequence 40866, A	774	33	46.5	384	4	US-10-231-265-806	Sequence 806, App
702	33	46.5	195	3	US-09-810-836B-8	Sequence 8, Appl	775	33	46.5	384	4	US-10-291-265-807	Sequence 807, App
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705	33	46.5	195	4	US-10-225-066A-560	Sequence 560, App	778	33	46.5	394	3	US-09-815-142-11188	Sequence 11188, A
706	33	46.5	195	4	US-10-374-780A-2438	Sequence 2438, Ap	779	33	46.5	394	4	US-10-282-122A-58421	Sequence 10338, A
707	33	46.5	195	4	US-10-424-599-148712	Sequence 148712, A	780	33	46.5	402	4	US-10-156-761-10338	Sequence 8360, Ap
708	33	46.5	195	4	US-10-437-963-164689	Sequence 164689, A	781	33	46.5	404	4	US-10-156-761-8360	Sequence 72281, A
709	33	46.5	195	5	US-10-495-918-94	Sequence 94, Appl	782	33	46.5	406	4	US-10-282-122A-72281	Sequence 210704, A
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712	33	46.5	198	4	US-10-225-066A-560	Sequence 560, App	785	33	46.5	415	4	US-10-425-114-72426	Sequence 168830, A
713	33	46.5	207	4	US-10-286-237-2800	Sequence 2800, Ap	786	33	46.5	417	4	US-10-437-963-126830	Sequence 143, App
714	33	46.5	211	4	US-10-232-342-2	Sequence 2, Appl	787	33	46.5	420	5	US-10-485-710-143	Sequence 6, Appl
715	33	46.5	221	4	US-10-394-575-63	Sequence 63, Appl	788	33	46.5	424	5	US-10-380-437-6	Sequence 53, Appl
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717	33	46.5	226	5	US-10-450-763-49241	Sequence 49241, A	790	33	46.5	425	3	US-09-925-301-1274	Sequence 1, Appl
718	33	46.5	241	3	US-09-813-453A-63	Sequence 63, Appl	791	33	46.5	426	3	US-09-966-781A-1	Sequence 111386, A
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720	33	46.5	242	4	US-10-425-115-301381	Sequence 301381, A	793	33	46.5	427	3	US-09-850-982B-2	Sequence 51441, A
721	33	46.5	260	4	US-10-155-886-20	Sequence 20, Appl	794	33	46.5	432	3	US-10-425-114-51441	Sequence 208, App
722	33	46.5	262	4	US-10-437-963-172456	Sequence 172456, A	795	33	46.5	432	3	US-09-764-898-208	Sequence 3198, Ap
723	33	46.5	274	4	US-10-425-115-188394	Sequence 188394, A	796	33	46.5	435	3	US-10-128-714-3198	Sequence 1, Appl
724	33	46.5	275	5	US-10-732-923-750	Sequence 750, App	797	33	46.5	441	3	US-09-142-613-1	Sequence 9, Appl
725	33	46.5	277	4	US-10-425-115-300053	Sequence 300053, A	798	33	46.5	441	5	US-10-311-444-9	Sequence 57153, A
726	33	46.5	282	4	US-10-724-972A-6562	Sequence 6562, Ap	799	33	46.5	442	4	US-10-425-114-57153	Sequence 57153, A
727	33	46.5	288	5	US-10-485-710-106	Sequence 106, App	800	33	46.5	444	3	US-09-861-696-51	Sequence 51, Appl
728	33	46.5	288	5	US-10-485-710-141	Sequence 141, App	801	33	46.5	444	3	US-09-861-696-52	Sequence 52, Appl
729	33	46.5	290	4	US-10-437-963-146947	Sequence 146947, A	802	33	46.5	444	3	US-09-464-099A-51	Sequence 51, Appl
730	33	46.5	306	4	US-10-425-115-211068	Sequence 211068, A	803	33	46.5	444	3	US-09-464-099A-52	Sequence 52, Appl
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737	33	46.5	322	3	US-09-789-831-6	Sequence 6, Appl	810	33	46.5	445	5	US-10-732-923-20234	Sequence 20234, A
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743	33	46.5	337	3	US-09-815-242-13953	Sequence 13953, A	816	33	46.5	450	4	US-10-239-588-2	Sequence 2, Appl
744	33	46.5	337	4	US-10-282-122A-75542	Sequence 75542, A	817	33	46.5	450	4	US-10-239-588-4	Sequence 4, Appl
745	33	46.5	337	5	US-10-647-649-1	Sequence 1, Appl	818	33	46.5	453	4	US-10-425-115-243205	Sequence 243205, A
746	33	46.5	344	4	US-10-437-963-196435	Sequence 196435, A	819	33	46.5	454	4	US-10-425-115-243205	Sequence 243205, A
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748	33	46.5	345	3	US-09-789-831-5	Sequence 5, Appl	821	33	46.5	454	5	US-10-310-154-669	Sequence 669, App
749	33	46.5	345	4	US-10-060-036-183	Sequence 183, App	822	33	46.5	458	4	US-10-732-923-584	Sequence 584, App
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833	33	46.5	516	6	US-11-051-955-26	Sequence 26, Appl	906	33	46.5	931	3	US-09-949-654-2	Sequence 2, Appl
834	33	46.5	517	4	US-10-239-588-6	Sequence 6, Appl	907	33	46.5	941	4	US-10-205-823-80	Sequence 80, Appl
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841	33	46.5	531	4	US-10-128-714-8158	Sequence 8158, App	914	33	46.5	1011	4	US-10-156-761-8999	Sequence 8999, App
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850	33	46.5	571	4	US-10-051-909-34	Sequence 34, Appl	923	33	46.5	1627	4	US-10-637-544-6	Sequence 6, Appl
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866	33	46.5	645	4	US-10-723-606-12	Sequence 12, Appl	939	32	45.1	16	3	US-09-972-656-52	Sequence 52, Appl
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898	33	46.5	908	3	US-09-376-045-6	Sequence 6, Appl	971	32	45.1	96	3	US-09-187-693-43	Sequence 43, Appl
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997 32 45.1 101 4 US-10-424-599-280008 Sequence 280008,
998 32 45.1 104 3 US-09-934-909-27 Sequence 27, Appl
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1000 32 45.1 108 5 US-10-727-155-282 Sequence 282, App

ALIGNMENTS

RESULT 1
US-09-155-106-3
; Sequence 3, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/155,106
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: PCT/US97/04696
; PRIORITY APPLICATION DATA:
; FILING DATE: 20-MAR-1996
; APPLICATION NUMBER: US 60/013,708
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-808-538-3

Query Match 100.0%; Score 71; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DDYGGQSTYVMDA 13

RESULT 2
US-10-808-538-3
; Sequence 3, Application US/10808538

; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 25-Mar-2004
; APPLICATION NUMBER: US/10/808,538
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
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; STRANDEDNESS: <Unknown>
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US-10-808-538-3

Query Match 100.0%; Score 71; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DDYGGQSTYVMDA 13

RESULT 3
US-09-155-106-18
; Sequence 18, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/155,106
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid

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; STRANDEDNESS:
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; MOLECULE TYPE: protein
US-09-155-106-18

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Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 99 DDYGGQSTYVMDA 111

RESULT 4
US-09-155-106-19
; Sequence 19, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-19

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Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
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Db 99 DDYGGQSTYVMDA 111

RESULT 5
US-09-155-106-20
; Sequence 20, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-20

Query Match      100.0%; Score 71; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
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Db 99 DDYGGQSTYVMDA 111

RESULT 6
US-09-155-106-26
; Sequence 26, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-26

Query Match      100.0%; Score 71; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
    |||||
Db 99 DDYGGQSTYVMDA 111

RESULT 7
US-09-155-106-32
; Sequence 32, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Immunomedics, Inc.
FILING DATE: 19-MAR-1997
PRIORITY APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-155-106-32

Query Match 100.0%; Score 71; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
Db 99 DDYGGQSTYVMDA 111

RESULT 8

US-10-808-538-18
Sequence 18, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-808-538-18
Query Match 100.0%; Score 71; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
Db 99 DDYGGQSTYVMDA 111

RESULT 9

US-10-808-538-19
Sequence 19, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-808-538-19

Query Match 100.0%; Score 71; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
Db 99 DDYGGQSTYVMDA 111

RESULT 10

US-10-808-538-20
Sequence 20, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/808,538
;; FILING DATE: 25-Mar-2004
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155,106
;; FILING DATE: 17-NOV-1998
;; APPLICATION NUMBER: PCT/US97/04696
;; FILING DATE: 19-MAR-1997
;; APPLICATION NUMBER: US 60/013,708
;; FILING DATE: 20-MAR-1996
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-808-538-20

Query Match 100.0%; Score 71; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 DDYGGQSTYVMDA 13
|||
DB 99 DDYGGQSTYVMDA 111

RESULT 11
US-10-808-538-26
; Sequence 26, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-808-538-26

Query Match 100.0%; Score 71; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
|||
DB 99 DDYGGQSTYVMDA 111

RESULT 12
US-10-808-538-32
; Sequence 32, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-808-538-32

Query Match 100.0%; Score 71; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00093; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1 DDYGGQSTYVMDA 13
|||
DB 99 DDYGGQSTYVMDA 111

RESULT 13
US-10-327-598-476
; Sequence 476, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 476

; LENGTH: 17
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-476

Query Match 60.6%; Score 43; DB 4; Length 17;
Best Local Similarity 72.7%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YGGQSTYVMDA 13
||| ||| ||
Db 4 YGGSSTYYADA 14

RESULT 14

US-10-425-115-202484
; Sequence 202484, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 202484
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116256C.1.pep
US-10-425-115-202484

Query Match 60.6%; Score 43; DB 4; Length 77;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
||| ||| ||
Db 24 DDFGQKAYV 33

RESULT 15

US-10-327-598-886
; Sequence 886, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: For Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 886
; LENGTH: 134
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-886

Query Match 60.6%; Score 43; DB 4; Length 134;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YGGQSTYVMDA 13
||| ||| ||
Db 72 YGGSSTYYADA 82

RESULT 16

US-10-424-599-220900
; Sequence 220900, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220900
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(181)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41502C.1.pep
US-10-424-599-220900

Query Match 60.6%; Score 43; DB 4; Length 181;
Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
||| ||| ||
Db 24 DDFGQKAYV 33

RESULT 17

US-10-425-114-67090
; Sequence 67090, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67090
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4758-032-F6_FLI.pep
US-10-425-114-67090

Query Match 60.6%; Score 43; DB 4; Length 237;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
||| ||| ||

Db 45 DDFGGQKAYV 54

RESULT 18

US-10-425-114-59316
; Sequence 59316, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59316
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB189-006-G11_FLI.pep
US-10-425-114-59316

Query Match 60.6%; Score 43; DB 4; Length 262;

Best Local Similarity 70.0%; Pred. No. 68;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTTV 10

|||||

Db 45 DDFGGQKAYV 54

RESULT 19

US-10-425-114-67441
; Sequence 67441, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67441
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4756-014-D4_FLI.pep
US-10-425-114-67441

Query Match 60.6%; Score 43; DB 4; Length 262;

Best Local Similarity 70.0%; Pred. No. 68;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTTV 10

|||||

Db 45 DDFGGQKAYV 54

RESULT 20

US-10-425-115-246614

; Sequence 246614, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 246614
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_156496C.1.pep
US-10-425-115-246614

Query Match 60.6%; Score 43; DB 4; Length 269;

Best Local Similarity 70.0%; Pred. No. 70;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTTV 10

|||||

Db 52 DDFGGQKAYV 61

RESULT 21

US-10-369-493-12370
; Sequence 12370, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12370
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(362)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-12370

Query Match 60.6%; Score 43; DB 4; Length 362;

Best Local Similarity 70.0%; Pred. No. 93;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTTV 10

|||||

Db 88 DDYGGMSAYL 97

RESULT 22

US-10-282-122A-76434
; Sequence 76434, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 76434
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Treponema pallidum
US-10-282-122A-76434

Query Match 60.6%; Score 43; DB 4; Length 450;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 YGGQSTYV 10
Db 253 YGGQSTYI 260
|||||:

RESULT 23
US-10-437-963-142503
; Sequence 142503, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142503

; LENGTH: 491
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43503C.1.pep
US-10-437-963-142503

Query Match 60.6%; Score 43; DB 4; Length 491;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYV 10
Db 182 DDYGGKAQYV 191
|||||:

RESULT 24
US-10-767-701-44652
; Sequence 44652, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44652
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7231_2.pep
US-10-767-701-44652

Query Match 59.2%; Score 42; DB 4; Length 216;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYV 10
Db 25 DDFGGQKAYI 34
|||||:

RESULT 25
US-10-437-963-147555
; Sequence 147555, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147555
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48072C.1.pep
US-10-437-963-147555

Query Match 59.2%; Score 42; DB 4; Length 230;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 DDYGGOSTY 9
||| | | | | | | | | |
Db 22 DDYGGASSY 30

RESULT 26
US-10-424-599-221681
; Sequence 221681, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221681
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_42206C.1.pap
US-10-424-599-221681

Query Match 57.7%; Score 41; DB 4; Length 62;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGOSTYVMD 12
| | | | | | | | | | | |
Db 21 DTNCGQSTFKMD 32

RESULT 27
US-10-424-599-160533
; Sequence 160533, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160533
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11597C.1.pap
US-10-424-599-160533

Query Match 57.7%; Score 41; DB 4; Length 72;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGOSTYV 10
: | | | | : | | | |
Db 25 NDYGGKSQYV 34

RESULT 28
US-10-282-122A-57623
; Sequence 57623, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57623
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57623

Query Match 57.7%; Score 41; DB 4; Length 410;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMDA 13
: | | | | : | | | |
Db 97 ENYDGESTIVLDA 109

RESULT 29
US-10-652-870-290
; Sequence 290, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment
; TITLE OF INVENTION: Meningococcal Disease

; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 290
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-290

Query Match 56.3%; Score 40; DB 4; Length 42;
Best Local Similarity 58.3%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYVMD 12
|||: ||: |:
Db 11 DDAGGKLTYYTID 22

RESULT 30
US-10-424-599-268301
; Sequence 268301, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 268301
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(100)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8429C.1.pap
US-10-424-599-268301

Query Match 56.3%; Score 40; DB 4; Length 100;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 DYGGQSTV 10
|||: |||:
Db 48 DYGARSTV 56

RESULT 31
US-10-488-786B-11
; Sequence 11, Application US/10488786B
; Publication No. US2005022385A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SPA
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: HYBRID AND TANDEM EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 002441.00081
; CURRENT APPLICATION NUMBER: US/10/488,786B
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: PCT/IB02/03904
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-488-786B-11

Query Match 56.3%; Score 40; DB 5; Length 225;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYVMD 12
|||: |||: |:
Db 130 DDAGGKLTYYTID 141

RESULT 32
US-10-488-786B-12
; Sequence 12, Application US/10488786B
; Publication No. US2005022385A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SPA
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: HYBRID AND TANDEM EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 002441.00081
; CURRENT APPLICATION NUMBER: US/10/488,786B
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: PCT/IB02/03904
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-488-786B-12

Query Match 56.3%; Score 40; DB 5; Length 225;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYVMD 12
|||: |||: |:
Db 130 DDAGGKLTYYTID 141

RESULT 33
US-10-488-786B-8
; Sequence 8, Application US/10488786B
; Publication No. US2005022385A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SPA
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: HYBRID AND TANDEM EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 002441.00081
; CURRENT APPLICATION NUMBER: US/10/488,786B
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: PCT/IB02/03904
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-488-786B-8

Query Match 56.3%; Score 40; DB 5; Length 228;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DDYGGQSTYVMD 12
|||: |||: |:
Db 133 DDAGGKLTYYTID 144

```
RESULT 34
US-10-488-786B-6
; Sequence 6, Application US/10488786B
; Publication No. US20050222385A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SPA
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: HYBRID AND TANDEM EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 002441.00081
; CURRENT APPLICATION NUMBER: US/10/488,786B
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: PCT/IB02/03904
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-488-786B-6

Query Match          56.3%; Score 40; DB 5; Length 229;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 134 DDAGGKLTITID 145

RESULT 35
US-10-220-480-26
; Sequence 26, Application US/10220480
; Publication No. US20040092711A1
; GENERAL INFORMATION:
; APPLICANT: Chiron SPA
; TITLE OF INVENTION: Hybrid Expression of Neisserial Proteins
; FILE REFERENCE: P02678WO
; CURRENT APPLICATION NUMBER: US/10/220,480
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: GB 0004695.3
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: GB 0027675.8
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 26
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deltaG741
US-10-220-480-26

Query Match          56.3%; Score 40; DB 4; Length 248;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 153 DDAGGKLTITID 164

RESULT 36
US-10-652-870-182
; Sequence 182, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
```

```
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-182

Query Match          56.3%; Score 40; DB 4; Length 249;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTITID 171

RESULT 37
US-10-652-870-186
; Sequence 186, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-186

Query Match          56.3%; Score 40; DB 4; Length 249;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTITID 171

RESULT 38
US-10-652-870-188
; Sequence 188, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
```

; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-188

Query Match 56.3%; Score 40; DB 4; Length 249;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 39
US-10-652-870-192
; Sequence 192, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-192

Query Match 56.3%; Score 40; DB 4; Length 249;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 160 DDAGGKLTYYTID 171

RESULT 40
US-10-652-870-184
; Sequence 184, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026

; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 184
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-184

Query Match 56.3%; Score 40; DB 4; Length 250;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 161 DDAGGKLTYYTID 172

RESULT 41
US-10-652-870-190
; Sequence 190, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-190

Query Match 56.3%; Score 40; DB 4; Length 250;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
Db 161 DDAGGKLTYYTID 172

RESULT 42
US-10-652-870-158
; Sequence 158, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870

; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-158

Query Match 56.3%; Score 40; DB 4; Length 253;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:
Db 158 DDAGGKLTITD 169

RESULT 43
US-10-652-870-162
; Sequence 162, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-162

Query Match 56.3%; Score 40; DB 4; Length 253;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:
Db 158 DDAGGKLTITD 169

RESULT 44
US-10-652-870-74
; Sequence 74, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 74
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-74

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||:|:|:
Db 159 DDAGGKLTITD 170

RESULT 45
US-10-652-870-78
; Sequence 78, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-78

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 159 DDAGGKLTITD 170

RESULT 46
US-10-652-870-80
; Sequence 80, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 10/652,870
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 254
; TYPE: PRT

; ORGANISM: Neisseria meningitidis
US-10-652-870-80

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
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Db 159 DDAGGKLTYYTID 170

RESULT 47

US-10-652-870-84
; Sequence 84, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-84

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
|||:|:|:
Db 159 DDAGGKLTYYTID 170

RESULT 48

US-10-652-870-86
; Sequence 86, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-86

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 159 DDAGGKLTYYTID 170

RESULT 49

US-10-652-870-90
; Sequence 90, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
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; SEQ ID NO 90
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-90

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 159 DDAGGKLTYYTID 170

RESULT 50

US-10-652-870-92
; Sequence 92, Application US/10652870
; Publication No. US20040167068A1
; GENERAL INFORMATION:
; APPLICANT: Zlotnick, Gary
; APPLICANT: Fletcher, Leah
; APPLICANT: John, Farley
; APPLICANT: Bernfield, Liesel
; APPLICANT: Zagursky, Robert
; APPLICANT: Metcalf, Benjamin
; TITLE OF INVENTION: Novel Immunogenic Compositions for the Prevention and Treatment of
; FILE REFERENCE: 38523.000026
; CURRENT APPLICATION NUMBER: US/10/652,870
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-652-870-92

Query Match 56.3%; Score 40; DB 4; Length 254;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 159 DDAGGKLYTID 170

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OM protein - protein search, using sw model

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Title: US-10-808-538-3

Perfect score: 71

Sequence: 1 DDYGGQSTYVMDA 13

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Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:

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- 6: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
- 8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	43	60.6	252 11	US-11-096-568A-15108
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4	40	56.3	248 11	US-11-067-260-25
5	40	56.3	590 11	US-11-067-260-50
6	40	56.3	593 11	US-11-067-260-30
7	40	56.3	612 11	US-11-067-260-56
8	40	56.3	645 11	US-11-067-260-44
9	40	56.3	648 11	US-11-067-260-28
10	40	56.3	672 11	US-11-067-260-36
11	40	56.3	675 11	US-11-067-260-34
12	40	56.3	710 9	US-10-336-263A-14
13	40	56.3	1312 11	US-11-067-260-20
14	40	56.3	1312 11	US-11-067-260-32
15	39	54.9	357 11	US-11-261-135-2
16	38	53.5	346 9	US-10-878-556A-58
17	38	53.5	1351 11	US-11-129-741-2937
18	38	53.5	1351 11	US-11-129-741-2947
19	38	53.5	1385 11	US-11-129-741-3655
20	37	52.1	329 11	US-11-096-568A-23511
21	37	52.1	352 11	US-11-096-568A-23510

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97	33	46.5	117	11	US-11-203-253A-3	Sequence 3, Appli	170	32	45.1	203	11	US-11-087-099-6478	Sequence 6478, Ap
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108	33	46.5	316	9	US-10-510-386-244	Sequence 244, App	181	32	45.1	249	11	US-11-054-515-1335	Sequence 1335, Ap
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110	33	46.5	326	11	US-11-096-568A-28586	Sequence 28586, A	183	32	45.1	252	11	US-11-054-515-1311	Sequence 1311, Ap
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113	33	46.5	345	8	US-10-511-937-2446	Sequence 2446, Ap	186	32	45.1	252	11	US-11-188-298-8440	Sequence 8440, Ap
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117	33	46.5	367	11	US-11-188-298-7697	Sequence 7697, Ap	190	32	45.1	253	11	US-11-054-515-1449	Sequence 1449, Ap
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123	33	46.5	384	11	US-11-000-463-807	Sequence 807, App	196	32	45.1	253	11	US-11-030-300-13	Sequence 13, Appl
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152	32	45.1	70	11	US-11-079-463-7379	Sequence 7379, Ap	225	32	45.1	631	11	US-11-087-099-12446	Sequence 12446, A
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245	32	45.1	1059	9	US-10-336-263A-56	Sequence 56, Appl	318	31	43.7	434	11	US-11-045-004-992	Sequence 992, App
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250	31	43.7	105	11	US-11-096-568A-25159	Sequence 25159, A	323	31	43.7	446	11	US-11-087-099-5485	Sequence 5485, Ap
251	31	43.7	129	9	US-10-993-543-8	Sequence 8, Appli	324	31	43.7	446	11	US-11-087-099-6010	Sequence 6010, Ap
252	31	43.7	129	11	US-11-096-568A-25158	Sequence 25158, A	325	31	43.7	449	9	US-10-878-556A-57	Sequence 57, Appl
253	31	43.7	137	11	US-11-074-373-39	Sequence 39, Appl	326	31	43.7	449	9	US-10-500-941-5	Sequence 5, Appli
254	31	43.7	159	11	US-11-000-463-333	Sequence 333, App	327	31	43.7	452	11	US-11-133-949-19	Sequence 19, Appl
255	31	43.7	160	11	US-11-096-568A-25157	Sequence 25157, A	328	31	43.7	452	11	US-11-087-099-11368	Sequence 11368, A
256	31	43.7	160	11	US-11-072-740-2346	Sequence 2346, Ap	329	31	43.7	452	11	US-11-096-568A-31741	Sequence 31741, A
257	31	43.7	184	11	US-11-179-463-8854	Sequence 8854, Ap	330	31	43.7	457	9	US-10-784-004-323	Sequence 323, App
258	31	43.7	201	11	US-11-096-568A-4676	Sequence 4676, Ap	331	31	43.7	457	9	US-10-784-004-907	Sequence 907, Appl
259	31	43.7	203	11	US-11-221-683-10	Sequence 10, Appl	332	31	43.7	458	11	US-11-122-144-16	Sequence 16, Appl
260	31	43.7	203	11	US-11-221-683-12	Sequence 12, Appl	333	31	43.7	459	10	US-11-302-262-2	Sequence 2, Appli
261	31	43.7	207	9	US-10-467-657-4974	Sequence 4974, Ap	334	31	43.7	461	11	US-11-087-099-1829	Sequence 1829, Ap
262	31	43.7	209	11	US-11-045-004-1819	Sequence 1819, Ap	335	31	43.7	468	10	US-11-251-465-27	Sequence 27, Appl
263	31	43.7	216	11	US-11-096-568A-1038	Sequence 1038, Ap	336	31	43.7	468	11	US-11-122-144-8	Sequence 8, Appli
264	31	43.7	218	11	US-11-096-568A-21440	Sequence 21440, A	337	31	43.7	482	9	US-10-784-004-644	Sequence 644, App
265	31	43.7	219	11	US-11-264-096-349	Sequence 349, App	338	31	43.7	482	9	US-10-784-004-1048	Sequence 1048, Ap
266	31	43.7	226	11	US-11-096-568A-1037	Sequence 1037, Ap	339	31	43.7	483	11	US-11-188-298-7218	Sequence 7218, Ap
267	31	43.7	240	11	US-11-096-568A-4675	Sequence 4675, Ap	340	31	43.7	483	11	US-11-188-298-19654	Sequence 19654, A
268	31	43.7	246	11	US-11-054-515-1314	Sequence 1314, Ap	341	31	43.7	492	11	US-11-199-233-19	Sequence 19, Appl
269	31	43.7	246	11	US-11-096-568A-4674	Sequence 4674, Ap	342	31	43.7	498	11	US-11-096-568A-31740	Sequence 31740, A
270	31	43.7	246	11	US-11-266-444-1314	Sequence 1314, Ap	343	31	43.7	504	11	US-11-096-568A-18211	Sequence 18211, A
271	31	43.7	247	11	US-11-054-515-1652	Sequence 1652, Ap	344	31	43.7	515	11	US-11-199-233-6	Sequence 6, Appli
272	31	43.7	247	11	US-11-096-568A-16681	Sequence 16681, A	345	31	43.7	527	11	US-11-096-568A-28901	Sequence 28901, A
273	31	43.7	247	11	US-11-266-444-1652	Sequence 1652, Ap	346	31	43.7	532	9	US-10-506-454-190	Sequence 190, App
274	31	43.7	249	11	US-11-054-515-1635	Sequence 1635, Ap	347	31	43.7	533	11	US-11-072-512-3224	Sequence 3224, Ap
275	31	43.7	249	11	US-11-096-568A-16680	Sequence 16680, A	348	31	43.7	540	11	US-11-096-568A-18210	Sequence 18210, A
276	31	43.7	249	11	US-11-266-444-1635	Sequence 1635, Ap	349	31	43.7	584	11	US-11-096-568A-31265	Sequence 31265, A
277	31	43.7	251	10	US-11-251-465-11	Sequence 11, App	350	31	43.7	596	11	US-11-096-568A-28900	Sequence 28900, A
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279	31	43.7	252	11	US-11-140-416-32	Sequence 32, Appl	352	31	43.7	610	11	US-11-188-298-19318	Sequence 31264, A
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281	31	43.7	257	11	US-11-140-416-29	Sequence 29, Appl	354	31	43.7	660	11	US-11-143-984A-114	Sequence 114, App
282	31	43.7	260	9	US-10-055-877-166	Sequence 166, App	355	31	43.7	775	9	US-10-131-826A-120	Sequence 120, App
283	31	43.7	270	11	US-11-096-568A-16679	Sequence 16679, A	356	31	43.7	775	9	US-10-973-115B-120	Sequence 120, App
284	31	43.7	273	11	US-11-045-004-229	Sequence 229, App	357	31	43.7	775	9	US-10-137-873A-120	Sequence 120, App
285	31	43.7	274	9	US-10-467-657-2140	Sequence 2140, Ap	358	31	43.7	775	11	US-10-152-370-120	Sequence 120, App
286	31	43.7	285	11	US-11-096-568A-30635	Sequence 30635, A	359	31	43.7	775	11	US-11-290-153-120	Sequence 120, App
287	31	43.7	288	11	US-11-096-568A-31742	Sequence 31742, A	360	31	43.7	842	11	US-11-188-298-2502	Sequence 2502, Ap
288	31	43.7	291	11	US-11-096-568A-13381	Sequence 13381, A	361	31	43.7	842	11	US-11-188-298-6227	Sequence 6227, Ap
289	31	43.7	291	11	US-11-096-568A-13381	Sequence 13381, A	362	31	43.7	902	11	US-11-098-686-11082	Sequence 11082, A
290	31	43.7	306	11	US-11-045-004-2232	Sequence 2232, Ap	363	31	43.7	1006	9	US-10-467-657-8400	Sequence 8400, Ap
291	31	43.7	312	11	US-11-188-298-11513	Sequence 11513, A	364	31	43.7	1023	9	US-10-821-234-1377	Sequence 1377, Ap
292	31	43.7	312	11	US-11-188-298-12287	Sequence 12287, A	365	31	43.7	1069	11	US-11-098-686-10296	Sequence 10296, A
293	31	43.7	319	11	US-11-096-568A-13380	Sequence 13380, A	366	31	43.7	1097	11	US-11-079-463-7169	Sequence 7169, Ap
294	31	43.7	322	11	US-11-096-568A-21980	Sequence 21980, A	367	31	43.7	1144	9	US-10-467-657-1820	Sequence 1820, Ap
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296	31	43.7	344	11	US-11-188-298-15207	Sequence 15207, A	369	31	43.7	1234	9	US-11-079-463-8094	Sequence 8094, Ap
297	31	43.7	346	11	US-11-087-099-12047	Sequence 12047, A	370	31	43.7	1437	11	US-11-091-936-1	Sequence 1, Appli
298	31	43.7	346	11	US-11-188-298-11106	Sequence 11106, A	371	31	43.7	1525	11	US-11-052-554A-280	Sequence 280, App
299	31	43.7	347	11	US-11-096-568A-14984	Sequence 14984, A	372	31	43.7	1588	11	US-11-040-472-8	Sequence 8, Appli
300	31	43.7	354	11	US-11-087-099-6801	Sequence 6801, Ap	373	31	43.7	1881	11	US-11-143-980-47	Sequence 47, Appl
301	31	43.7	355	11	US-11-096-568A-6032	Sequence 6032, Ap	374	30.5	43.0	5712	11	US-11-054-281-84	Sequence 84, Appl
302	31	43.7	359	11	US-11-096-568A-13379	Sequence 13379, A	375	30.5	43.0	277	11	US-11-010-795-28	Sequence 28, Appl
303	31	43.7	367	11	US-11-087-099-2917	Sequence 2917, Ap	376	30.5	43.0	315	11	US-11-079-463-5272	Sequence 5272, Ap
304	31	43.7	368	11	US-11-188-298-3953	Sequence 3953, Ap	377	30	42.3	555	11	US-10-510-229-82	Sequence 82, Appl
305	31	43.7	370	11	US-11-096-568A-6031	Sequence 6031, Ap	378	30	42.3	12	9	US-10-834-397-179	Sequence 179, App
306	31	43.7	370	11	US-11-045-004-1465	Sequence 1465, Ap	379	30	42.3	15	9	US-10-993-543-291	Sequence 291, App
307	31	43.7	387	11	US-11-188-298-16782	Sequence 16782, A	380	30	42.3	15	11	US-11-054-669-105	Sequence 105, App
308	31	43.7	389	11	US-11-079-463-5925	Sequence 5925, Ap	381	30	42.3	15	11	US-11-061-848-29	Sequence 29, Appl
309	31	43.7	393	11	US-11-188-298-8636	Sequence 8636, Ap	382	30	42.3	15	11	US-11-004-590-107	Sequence 107, App
310	31	43.7	393	11	US-11-188-298-21046	Sequence 21046, A	383	30	42.3	17	11	US-11-240-195-9	Sequence 9, Appli
311	31	43.7	414	11	US-11-096-568A-28902	Sequence 28902, A	384	30	42.3	21	9	US-10-939-890-514	Sequence 514, App
312	31	43.7	422	9	US-10-336-263A-12	Sequence 12, Appl	385	30	42.3	21	9	US-10-939-890-526	Sequence 526, App
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387	30	42.3	21	9	US-10-939-890-561	Sequence 561, App	460	30	42.3	115	11	US-11-127-932-2	Sequence 2, Appli
388	30	42.3	25	11	US-11-009-840A-145	Sequence 145, App	461	30	42.3	115	11	US-11-127-932-3	Sequence 3, Appli
389	30	42.3	25	11	US-11-009-873A-145	Sequence 145, App	462	30	42.3	115	11	US-11-127-932-6	Sequence 6, Appli
390	30	42.3	25	11	US-11-009-769A-145	Sequence 145, App	463	30	42.3	115	11	US-11-127-932-7	Sequence 7, Appli
391	30	42.3	26	11	US-11-009-840A-133	Sequence 133, App	464	30	42.3	115	11	US-11-127-932-8	Sequence 8, Appli
392	30	42.3	26	11	US-11-009-873A-133	Sequence 133, App	465	30	42.3	115	11	US-11-127-932-9	Sequence 9, Appli
393	30	42.3	26	11	US-11-009-769A-133	Sequence 133, App	466	30	42.3	115	11	US-11-127-932-10	Sequence 10, Appli
394	30	42.3	27	11	US-11-009-840A-125	Sequence 125, App	467	30	42.3	115	11	US-11-127-903-2	Sequence 2, Appli
395	30	42.3	27	11	US-11-009-873A-125	Sequence 125, App	468	30	42.3	115	11	US-11-127-903-3	Sequence 3, Appli
396	30	42.3	27	11	US-11-009-769A-125	Sequence 125, App	469	30	42.3	115	11	US-11-127-903-6	Sequence 6, Appli
397	30	42.3	28	11	US-11-009-840A-135	Sequence 135, App	470	30	42.3	115	11	US-11-127-903-7	Sequence 7, Appli
398	30	42.3	28	11	US-11-009-873A-135	Sequence 135, App	471	30	42.3	115	11	US-11-127-903-8	Sequence 8, Appli
399	30	42.3	28	11	US-11-009-840A-140	Sequence 140, App	472	30	42.3	115	11	US-11-127-903-9	Sequence 9, Appli
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401	30	42.3	28	11	US-11-009-769A-135	Sequence 135, App	474	30	42.3	115	11	US-11-127-903-2	Sequence 2, Appli
402	30	42.3	28	11	US-11-009-769A-140	Sequence 140, App	475	30	42.3	115	11	US-11-127-903-3	Sequence 3, Appli
403	30	42.3	29	11	US-11-009-840A-117	Sequence 117, App	476	30	42.3	115	11	US-11-127-903-7	Sequence 7, Appli
404	30	42.3	29	11	US-11-009-873A-117	Sequence 117, App	477	30	42.3	115	11	US-11-127-903-8	Sequence 8, Appli
405	30	42.3	29	11	US-11-009-769A-117	Sequence 117, App	478	30	42.3	115	11	US-11-127-903-9	Sequence 9, Appli
406	30	42.3	30	9	US-10-923-112A-40	Sequence 40, Appl	479	30	42.3	115	11	US-11-127-903-27	Sequence 27, Appl
407	30	42.3	31	11	US-11-009-840A-126	Sequence 126, App	480	30	42.3	115	11	US-11-127-903-28	Sequence 28, Appl
408	30	42.3	31	11	US-11-009-873A-126	Sequence 126, App	481	30	42.3	115	11	US-11-127-903-33	Sequence 33, Appl
409	30	42.3	31	11	US-11-009-769A-126	Sequence 126, App	482	30	42.3	115	11	US-11-127-903-35	Sequence 35, Appl
410	30	42.3	34	11	US-11-009-840A-120	Sequence 120, App	483	30	42.3	115	11	US-11-127-903-38	Sequence 38, Appl
411	30	42.3	34	11	US-11-009-873A-132	Sequence 132, App	484	30	42.3	115	11	US-11-127-919-147	Sequence 147, App
412	30	42.3	34	11	US-11-009-840A-132	Sequence 132, App	485	30	42.3	115	11	US-11-098-758-225	Sequence 225, App
413	30	42.3	34	11	US-11-009-873A-120	Sequence 120, App	486	30	42.3	115	11	US-11-098-758-227	Sequence 227, App
414	30	42.3	34	11	US-11-009-873A-132	Sequence 132, App	487	30	42.3	115	11	US-11-098-758-229	Sequence 229, App
415	30	42.3	34	11	US-11-009-769A-120	Sequence 120, App	488	30	42.3	115	11	US-11-098-758-334	Sequence 334, App
416	30	42.3	38	9	US-10-925-366A-339	Sequence 339, App	489	30	42.3	116	9	US-10-925-366A-1	Sequence 1, Appli
417	30	42.3	58	11	US-11-098-758-339	Sequence 339, App	490	30	42.3	116	9	US-10-925-366A-209	Sequence 209, App
418	30	42.3	75	11	US-11-240-195-48	Sequence 48, Appl	491	30	42.3	116	9	US-10-925-366A-213	Sequence 213, App
419	30	42.3	85	9	US-10-925-366A-350	Sequence 350, App	492	30	42.3	116	9	US-10-925-366A-214	Sequence 214, App
420	30	42.3	85	11	US-11-098-758-350	Sequence 350, App	493	30	42.3	116	9	US-10-925-366A-215	Sequence 215, App
421	30	42.3	86	9	US-10-925-366A-345	Sequence 345, App	494	30	42.3	116	9	US-10-925-366A-223	Sequence 223, App
422	30	42.3	86	9	US-10-925-366A-345	Sequence 345, App	495	30	42.3	116	9	US-10-925-366A-224	Sequence 224, App
423	30	42.3	86	11	US-11-098-758-347	Sequence 347, App	496	30	42.3	116	9	US-10-925-366A-226	Sequence 226, App
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426	30	42.3	89	9	US-10-925-366A-362	Sequence 362, App	499	30	42.3	116	9	US-10-925-366A-231	Sequence 231, App
427	30	42.3	89	9	US-10-925-366A-367	Sequence 367, App	500	30	42.3	116	9	US-10-925-366A-282	Sequence 282, App
428	30	42.3	89	11	US-11-098-758-342	Sequence 342, App	501	30	42.3	116	11	US-11-054-669-112	Sequence 112, App
429	30	42.3	89	11	US-11-098-758-362	Sequence 362, App	502	30	42.3	116	11	US-11-093-274-20	Sequence 20, Appl
430	30	42.3	89	11	US-11-098-758-367	Sequence 367, App	503	30	42.3	116	11	US-11-125-837-38	Sequence 38, Appl
431	30	42.3	92	11	US-11-240-195-84	Sequence 84, Appl	504	30	42.3	116	11	US-11-127-677-51	Sequence 51, Appl
432	30	42.3	96	9	US-10-925-366A-222	Sequence 222, App	505	30	42.3	116	11	US-11-102-621-6	Sequence 6, Appli
433	30	42.3	96	11	US-11-098-758-222	Sequence 222, App	506	30	42.3	116	11	US-11-127-932-4	Sequence 4, Appli
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436	30	42.3	112	9	US-10-487-324A-10	Sequence 10, Appl	509	30	42.3	116	11	US-11-102-424-6	Sequence 6, Appli
437	30	42.3	112	9	US-10-487-324A-19	Sequence 19, Appl	510	30	42.3	116	11	US-11-102-424-7	Sequence 7, Appli
438	30	42.3	112	9	US-10-487-324A-20	Sequence 20, Appl	511	30	42.3	116	11	US-11-102-424-8	Sequence 8, Appli
439	30	42.3	112	11	US-11-144-248-12	Sequence 12, Appl	512	30	42.3	116	11	US-11-102-424-9	Sequence 9, Appli
440	30	42.3	112	11	US-11-127-677-3	Sequence 3, Appli	513	30	42.3	116	11	US-11-102-424-10	Sequence 10, Appl
441	30	42.3	112	11	US-11-127-932-1	Sequence 1, Appli	514	30	42.3	116	11	US-11-102-424-11	Sequence 11, Appl
442	30	42.3	112	11	US-11-144-232-12	Sequence 12, Appl	515	30	42.3	116	11	US-11-102-424-12	Sequence 12, Appl
443	30	42.3	112	11	US-11-127-903-1	Sequence 1, Appli	516	30	42.3	116	11	US-11-102-424-13	Sequence 13, Appl
444	30	42.3	112	11	US-11-182-343-12	Sequence 12, Appl	517	30	42.3	116	11	US-11-102-424-14	Sequence 14, Appl
445	30	42.3	112	11	US-11-224-623-8	Sequence 8, Appli	518	30	42.3	116	11	US-11-102-424-15	Sequence 15, Appl
446	30	42.3	112	11	US-11-224-623-10	Sequence 10, Appl	519	30	42.3	116	11	US-11-049-536-318	Sequence 318, App
447	30	42.3	112	11	US-11-240-195-20	Sequence 20, Appl	520	30	42.3	116	11	US-11-199-739-318	Sequence 318, App
448	30	42.3	113	9	US-10-665-658-6	Sequence 6, Appli	521	30	42.3	116	11	US-11-102-512-1	Sequence 1, Appli
449	30	42.3	113	11	US-11-219-121-24	Sequence 24, Appl	522	30	42.3	116	11	US-11-102-512-7	Sequence 7, Appli
450	30	42.3	113	11	US-11-049-536-106	Sequence 106, App	523	30	42.3	116	11	US-11-102-512-8	Sequence 8, Appli
451	30	42.3	113	11	US-11-199-739-106	Sequence 106, App	524	30	42.3	116	11	US-11-102-512-9	Sequence 9, Appli
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453	30	42.3	114	11	US-11-217-919-153	Sequence 153, App	526	30	42.3	116	11	US-11-102-512-13	Sequence 13, Appl
454	30	42.3	114	11	US-11-217-919-165	Sequence 165, App	527	30	42.3	116	11	US-11-102-512-16	Sequence 16, Appl
455	30	42.3	115	8	US-10-546-594-115	Sequence 115, App	528	30	42.3	116	11	US-11-102-512-21	Sequence 21, Appl
456	30	42.3	115	9	US-10-925-366A-225	Sequence 225, App	529	30	42.3	116	11	US-11-102-512-22	Sequence 22, Appl
457	30	42.3	115	9	US-10-925-366A-227	Sequence 227, App	530	30	42.3	116	11	US-11-102-512-25	Sequence 25, Appl
458	30	42.3	115	9	US-10-925-366A-229	Sequence 229, App	531	30	42.3	116	11	US-11-102-512-26	Sequence 26, Appl
459	30	42.3	115	9	US-10-925-366A-334	Sequence 334, App	532	30	42.3	116	11	US-11-102-512-27	Sequence 27, Appl

533	30	42.3	116	11	US-11-102-512-28	Sequence 28, Appl	606	30	42.3	117	11	US-11-049-536-634	Sequence 634, App
534	30	42.3	116	11	US-11-102-512-29	Sequence 29, Appl	607	30	42.3	117	11	US-11-049-536-642	Sequence 642, App
535	30	42.3	116	11	US-11-102-512-30	Sequence 30, Appl	608	30	42.3	117	11	US-11-049-536-690	Sequence 690, App
536	30	42.3	116	11	US-11-102-512-31	Sequence 31, Appl	609	30	42.3	117	11	US-11-250-411-102	Sequence 102, App
537	30	42.3	116	11	US-11-102-512-32	Sequence 32, Appl	610	30	42.3	117	11	US-11-250-411-106	Sequence 106, App
538	30	42.3	116	11	US-11-102-512-33	Sequence 33, Appl	611	30	42.3	117	11	US-11-199-739-178	Sequence 178, App
539	30	42.3	116	11	US-11-102-512-34	Sequence 34, Appl	612	30	42.3	117	11	US-11-199-739-190	Sequence 190, App
540	30	42.3	116	11	US-11-102-512-35	Sequence 35, Appl	613	30	42.3	117	11	US-11-199-739-222	Sequence 222, App
541	30	42.3	116	11	US-11-102-512-44	Sequence 44, Appl	614	30	42.3	117	11	US-11-199-739-226	Sequence 226, App
542	30	42.3	116	11	US-11-102-512-45	Sequence 45, Appl	615	30	42.3	117	11	US-11-199-739-274	Sequence 274, App
543	30	42.3	116	11	US-11-102-512-59	Sequence 59, Appl	616	30	42.3	117	11	US-11-199-739-354	Sequence 354, App
544	30	42.3	116	11	US-11-102-512-60	Sequence 60, Appl	617	30	42.3	117	11	US-11-199-739-414	Sequence 414, App
545	30	42.3	116	11	US-11-102-512-63	Sequence 63, Appl	618	30	42.3	117	11	US-11-199-739-438	Sequence 438, App
546	30	42.3	116	11	US-11-102-512-65	Sequence 64, Appl	619	30	42.3	117	11	US-11-199-739-582	Sequence 582, App
547	30	42.3	116	11	US-11-102-512-66	Sequence 65, Appl	620	30	42.3	117	11	US-11-199-739-602	Sequence 602, App
548	30	42.3	116	11	US-11-102-512-66	Sequence 66, Appl	621	30	42.3	117	11	US-11-199-739-634	Sequence 634, App
549	30	42.3	116	11	US-11-102-512-72	Sequence 72, Appl	622	30	42.3	117	11	US-11-199-739-642	Sequence 642, App
550	30	42.3	116	11	US-11-102-512-73	Sequence 73, Appl	623	30	42.3	117	11	US-11-199-739-690	Sequence 690, App
551	30	42.3	116	11	US-11-102-512-76	Sequence 76, Appl	624	30	42.3	117	11	US-11-102-512-12	Sequence 12, Appl
552	30	42.3	116	11	US-11-102-512-77	Sequence 77, Appl	625	30	42.3	118	8	US-10-981-300-51	Sequence 51, Appl
553	30	42.3	116	11	US-11-102-512-80	Sequence 80, Appl	626	30	42.3	118	9	US-10-925-366A-208	Sequence 208, App
554	30	42.3	116	11	US-11-102-512-81	Sequence 81, Appl	627	30	42.3	118	9	US-10-771-257-8	Sequence 8, Appl
555	30	42.3	116	11	US-11-217-919-87	Sequence 87, Appl	628	30	42.3	118	9	US-10-771-257-15	Sequence 15, Appl
556	30	42.3	116	11	US-11-098-758-1	Sequence 1, Appl	629	30	42.3	118	9	US-10-771-257-17	Sequence 17, Appl
557	30	42.3	116	11	US-11-098-758-1	Sequence 209, App	630	30	42.3	118	9	US-10-850-635-8	Sequence 25, Appl
558	30	42.3	116	11	US-11-098-758-209	Sequence 209, App	631	30	42.3	118	9	US-11-211-917-109	Sequence 109, App
559	30	42.3	116	11	US-11-098-758-213	Sequence 213, App	632	30	42.3	118	10	US-11-105-268-7	Sequence 7, Appl
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561	30	42.3	116	11	US-11-098-758-215	Sequence 215, App	634	30	42.3	118	11	US-11-127-677-15	Sequence 15, Appl
562	30	42.3	116	11	US-11-098-758-223	Sequence 223, App	635	30	42.3	118	11	US-11-127-677-17	Sequence 17, Appl
563	30	42.3	116	11	US-11-098-758-224	Sequence 224, App	636	30	42.3	118	11	US-11-049-536-206	Sequence 206, App
564	30	42.3	116	11	US-11-098-758-226	Sequence 226, App	637	30	42.3	118	11	US-11-049-536-334	Sequence 334, App
565	30	42.3	116	11	US-11-098-758-228	Sequence 228, App	638	30	42.3	118	11	US-11-049-536-338	Sequence 338, App
566	30	42.3	116	11	US-11-098-758-230	Sequence 230, App	639	30	42.3	118	11	US-11-049-536-350	Sequence 350, App
567	30	42.3	116	11	US-11-098-758-231	Sequence 231, App	640	30	42.3	118	11	US-11-049-536-382	Sequence 382, App
568	30	42.3	116	11	US-11-098-758-282	Sequence 282, App	641	30	42.3	118	11	US-11-049-536-546	Sequence 546, App
569	30	42.3	116	11	US-11-166-496-8	Sequence 8, Appl	642	30	42.3	118	11	US-11-049-536-654	Sequence 654, App
570	30	42.3	117	9	US-10-771-257-9	Sequence 9, Appl	643	30	42.3	118	11	US-11-049-536-654	Sequence 654, App
571	30	42.3	117	9	US-10-771-257-18	Sequence 18, Appl	644	30	42.3	118	11	US-11-049-536-654	Sequence 654, App
572	30	42.3	117	9	US-10-771-257-53	Sequence 53, Appl	645	30	42.3	118	11	US-11-049-536-654	Sequence 654, App
573	30	42.3	117	9	US-10-771-257-85	Sequence 85, Appl	646	30	42.3	118	11	US-11-049-536-654	Sequence 654, App
574	30	42.3	117	9	US-10-771-257-91	Sequence 91, Appl	647	30	42.3	118	11	US-11-112-481C-5	Sequence 5, Appl
575	30	42.3	117	9	US-10-771-257-97	Sequence 97, Appl	648	30	42.3	118	11	US-11-112-481C-13	Sequence 13, Appl
576	30	42.3	117	9	US-10-834-397-22	Sequence 22, Appl	649	30	42.3	118	11	US-11-199-739-206	Sequence 206, App
577	30	42.3	117	9	US-10-834-397-24	Sequence 24, Appl	650	30	42.3	118	11	US-11-199-739-334	Sequence 334, App
578	30	42.3	117	9	US-10-981-356A-6	Sequence 6, Appl	651	30	42.3	118	11	US-11-199-739-338	Sequence 338, App
579	30	42.3	117	9	US-10-956-008-18	Sequence 18, Appl	652	30	42.3	118	11	US-11-199-739-350	Sequence 350, App
580	30	42.3	117	9	US-10-956-008-58	Sequence 58, Appl	653	30	42.3	118	11	US-11-199-739-382	Sequence 382, App
581	30	42.3	117	11	US-11-012-353-75	Sequence 75, Appl	654	30	42.3	118	11	US-11-199-739-546	Sequence 546, App
582	30	42.3	117	11	US-11-012-353-79	Sequence 79, Appl	655	30	42.3	118	11	US-11-199-739-606	Sequence 606, App
583	30	42.3	117	11	US-11-012-353-83	Sequence 83, Appl	656	30	42.3	118	11	US-11-199-739-654	Sequence 654, App
584	30	42.3	117	11	US-11-127-677-9	Sequence 9, Appl	657	30	42.3	118	11	US-11-199-739-678	Sequence 678, App
585	30	42.3	117	11	US-11-127-677-18	Sequence 18, Appl	658	30	42.3	118	11	US-11-102-512-14	Sequence 14, Appl
586	30	42.3	117	11	US-11-096-046-6	Sequence 6, Appl	659	30	42.3	118	11	US-11-217-919-156	Sequence 156, App
587	30	42.3	117	11	US-11-127-903-29	Sequence 29, Appl	660	30	42.3	118	11	US-11-217-919-159	Sequence 159, App
588	30	42.3	117	11	US-11-127-903-30	Sequence 30, Appl	661	30	42.3	118	11	US-11-217-919-174	Sequence 174, App
589	30	42.3	117	11	US-11-127-903-32	Sequence 32, Appl	662	30	42.3	118	11	US-11-217-919-180	Sequence 180, App
590	30	42.3	117	11	US-11-127-903-34	Sequence 34, Appl	663	30	42.3	118	11	US-11-217-919-186	Sequence 186, App
591	30	42.3	117	11	US-11-127-903-36	Sequence 36, Appl	664	30	42.3	118	11	US-11-098-758-208	Sequence 208, App
592	30	42.3	117	11	US-11-127-903-37	Sequence 37, Appl	665	30	42.3	119	9	US-10-925-366A-210	Sequence 210, App
593	30	42.3	117	11	US-11-127-903-42	Sequence 42, Appl	666	30	42.3	119	9	US-10-925-366A-336	Sequence 336, App
594	30	42.3	117	11	US-11-165-023-30	Sequence 44, Appl	667	30	42.3	119	9	US-10-925-366A-336	Sequence 336, App
595	30	42.3	117	11	US-11-165-023-30	Sequence 44, Appl	668	30	42.3	119	9	US-10-925-366A-352	Sequence 352, App
596	30	42.3	117	11	US-11-049-536-178	Sequence 178, App	669	30	42.3	119	9	US-10-925-366A-354	Sequence 354, App
597	30	42.3	117	11	US-11-049-536-190	Sequence 190, App	670	30	42.3	119	9	US-10-925-366A-359	Sequence 359, App
598	30	42.3	117	11	US-11-049-536-222	Sequence 222, App	671	30	42.3	119	9	US-10-925-366A-364	Sequence 364, App
599	30	42.3	117	11	US-11-049-536-226	Sequence 226, App	672	30	42.3	119	9	US-10-771-257-10	Sequence 10, Appl
600	30	42.3	117	11	US-11-049-536-274	Sequence 274, App	673	30	42.3	119	9	US-10-771-257-21	Sequence 21, Appl
601	30	42.3	117	11	US-11-049-536-354	Sequence 354, App	674	30	42.3	119	9	US-10-834-397-21	Sequence 21, Appl
602	30	42.3	117	11	US-11-049-536-414	Sequence 414, App	675	30	42.3	119	9	US-10-834-397-26	Sequence 26, Appl
603	30	42.3	117	11	US-11-049-536-438	Sequence 438, App	676	30	42.3	119	9	US-10-834-397-39	Sequence 39, Appl
604	30	42.3	117	11	US-11-049-536-582	Sequence 582, App	677	30	42.3	119	9	US-10-834-397-65	Sequence 65, Appl
605	30	42.3	117	11	US-11-049-536-602	Sequence 602, App	678	30	42.3	119	9	US-10-530-171-7	Sequence 7, Appl
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681	30	42.3	119	10	US-11-254-182-30	Sequence 30, Appl	754	30	42.3	120	9	US-10-834-397-67	Sequence 67, Appl
682	30	42.3	119	10	US-11-300-563-11	Sequence 11, Appl	755	30	42.3	120	9	US-10-982-440-47	Sequence 47, Appl
683	30	42.3	119	11	US-11-120-338-9	Sequence 9, Appli	756	30	42.3	120	9	US-10-982-440-49	Sequence 49, Appl
684	30	42.3	119	11	US-11-127-677-10	Sequence 10, Appl	757	30	42.3	120	10	US-11-183-218-36	Sequence 36, Appl
685	30	42.3	119	11	US-11-127-677-21	Sequence 21, Appl	758	30	42.3	120	10	US-11-221-902-18	Sequence 18, Appl
686	30	42.3	119	11	US-11-127-903-31	Sequence 31, Appl	759	30	42.3	120	10	US-11-221-902-19	Sequence 19, Appl
687	30	42.3	119	11	US-11-127-903-41	Sequence 41, Appl	760	30	42.3	120	10	US-11-221-902-21	Sequence 21, Appl
688	30	42.3	119	11	US-11-106-820-9	Sequence 9, Appli	761	30	42.3	120	11	US-11-077-968-7	Sequence 7, Appli
689	30	42.3	119	11	US-11-154-337-4	Sequence 4, Appli	762	30	42.3	120	11	US-11-054-669-116	Sequence 116, App
690	30	42.3	119	11	US-11-154-337-6	Sequence 6, Appli	763	30	42.3	120	11	US-11-084-554-13	Sequence 13, Appl
691	30	42.3	119	11	US-11-182-908-4	Sequence 4, Appli	764	30	42.3	120	11	US-11-102-201-1	Sequence 1, Appli
692	30	42.3	119	11	US-11-182-908-6	Sequence 6, Appli	765	30	42.3	120	11	US-11-127-677-44	Sequence 44, Appl
693	30	42.3	119	11	US-11-182-908-6	Sequence 6, Appli	766	30	42.3	120	11	US-11-149-943-59	Sequence 59, Appl
694	30	42.3	119	11	US-11-049-536-314	Sequence 314, App	767	30	42.3	120	11	US-11-005-726-4	Sequence 4, Appli
695	30	42.3	119	11	US-11-049-536-362	Sequence 362, App	767	30	42.3	120	11	US-11-136-250-13	Sequence 13, Appl
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697	30	42.3	119	11	US-11-049-536-470	Sequence 470, App	769	30	42.3	120	11	US-11-049-536-518	Sequence 518, App
698	30	42.3	119	11	US-11-049-536-490	Sequence 490, App	770	30	42.3	120	11	US-11-049-536-586	Sequence 586, App
699	30	42.3	119	11	US-11-049-536-502	Sequence 502, App	771	30	42.3	120	11	US-11-049-536-618	Sequence 618, App
700	30	42.3	119	11	US-11-049-536-506	Sequence 506, App	772	30	42.3	120	11	US-11-176-525-6	Sequence 6, Appli
701	30	42.3	119	11	US-11-049-536-524	Sequence 524, App	773	30	42.3	120	11	US-11-183-205-36	Sequence 36, Appl
702	30	42.3	119	11	US-11-049-536-542	Sequence 542, App	774	30	42.3	120	11	US-11-194-989-26	Sequence 26, Appl
703	30	42.3	119	11	US-11-049-536-562	Sequence 562, App	775	30	42.3	120	11	US-11-195-207-26	Sequence 26, Appl
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706	30	42.3	119	11	US-11-190-364-9	Sequence 9, Appli	778	30	42.3	120	11	US-11-199-739-586	Sequence 586, App
707	30	42.3	119	11	US-11-102-120-4	Sequence 4, Appli	779	30	42.3	120	11	US-11-199-739-618	Sequence 618, App
708	30	42.3	119	11	US-11-147-780-9	Sequence 9, Appli	781	30	42.3	120	11	US-11-102-512-17	Sequence 17, Appl
709	30	42.3	119	11	US-11-223-361-4	Sequence 4, Appli	782	30	42.3	120	11	US-11-102-512-23	Sequence 23, Appl
710	30	42.3	119	11	US-11-223-361-6	Sequence 6, Appli	783	30	42.3	120	11	US-11-102-512-47	Sequence 47, Appl
711	30	42.3	119	11	US-11-143-386-9	Sequence 9, Appli	784	30	42.3	120	11	US-11-102-512-62	Sequence 62, Appl
712	30	42.3	119	11	US-11-199-739-314	Sequence 314, App	785	30	42.3	120	11	US-11-217-919-91	Sequence 91, Appl
713	30	42.3	119	11	US-11-199-739-362	Sequence 362, App	786	30	42.3	120	11	US-11-221-281-42	Sequence 42, Appl
714	30	42.3	119	11	US-11-199-739-394	Sequence 394, App	787	30	42.3	120	11	US-11-208-422-6	Sequence 6, Appli
715	30	42.3	119	11	US-11-199-739-470	Sequence 470, App	788	30	42.3	120	11	US-11-098-758-235	Sequence 235, App
716	30	42.3	119	11	US-11-199-739-490	Sequence 490, App	789	30	42.3	120	11	US-11-098-758-286	Sequence 286, App
717	30	42.3	119	11	US-11-199-739-502	Sequence 502, App	790	30	42.3	120	11	US-11-155-843-155	Sequence 155, App
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719	30	42.3	119	11	US-11-199-739-524	Sequence 524, App	792	30	42.3	120	11	US-11-155-843-159	Sequence 159, App
720	30	42.3	119	11	US-11-199-739-542	Sequence 542, App	793	30	42.3	120	11	US-11-155-843-161	Sequence 161, App
721	30	42.3	119	11	US-11-199-739-562	Sequence 562, App	794	30	42.3	120	11	US-11-155-843-163	Sequence 163, App
722	30	42.3	119	11	US-11-199-739-638	Sequence 638, App	795	30	42.3	120	11	US-11-155-843-165	Sequence 165, App
723	30	42.3	119	11	US-11-102-512-20	Sequence 20, Appl	796	30	42.3	120	11	US-11-155-843-167	Sequence 167, App
724	30	42.3	119	11	US-11-187-364-9	Sequence 46, Appl	797	30	42.3	120	11	US-11-155-843-169	Sequence 169, App
725	30	42.3	119	11	US-11-217-919-150	Sequence 9, Appli	798	30	42.3	120	11	US-11-155-843-171	Sequence 171, App
726	30	42.3	119	11	US-11-217-919-162	Sequence 162, App	799	30	42.3	120	11	US-11-155-843-173	Sequence 173, App
727	30	42.3	119	11	US-11-217-919-168	Sequence 168, App	800	30	42.3	120	11	US-11-155-843-175	Sequence 175, App
728	30	42.3	119	11	US-11-217-919-171	Sequence 171, App	801	30	42.3	120	11	US-11-233-256-429	Sequence 429, App
729	30	42.3	119	11	US-11-217-919-177	Sequence 177, App	802	30	42.3	121	9	US-10-789-273-9	Sequence 9, Appli
730	30	42.3	119	11	US-11-217-919-183	Sequence 183, App	803	30	42.3	121	9	US-10-932-334-81	Sequence 81, Appl
731	30	42.3	119	11	US-11-208-422-4	Sequence 4, Appli	804	30	42.3	121	9	US-10-925-366A-212	Sequence 212, App
732	30	42.3	119	11	US-11-098-758-210	Sequence 210, App	805	30	42.3	121	9	US-10-665-658-5	Sequence 5, Appli
733	30	42.3	119	11	US-11-098-758-336	Sequence 336, App	806	30	42.3	121	9	US-10-665-658-24	Sequence 24, Appl
734	30	42.3	119	11	US-11-098-758-347	Sequence 347, App	807	30	42.3	121	9	US-10-771-257-16	Sequence 16, Appl
735	30	42.3	119	11	US-11-098-758-352	Sequence 352, App	808	30	42.3	121	9	US-10-771-257-20	Sequence 20, Appl
736	30	42.3	119	11	US-11-098-758-354	Sequence 354, App	809	30	42.3	121	9	US-10-834-397-37	Sequence 37, Appl
737	30	42.3	119	11	US-11-098-758-359	Sequence 359, App	810	30	42.3	121	9	US-10-834-397-61	Sequence 61, Appl
738	30	42.3	119	11	US-11-098-758-364	Sequence 364, App	811	30	42.3	121	10	US-11-211-917-26	Sequence 26, Appl
739	30	42.3	119	11	US-11-098-758-364	Sequence 4, Appli	812	30	42.3	121	11	US-11-084-554-2	Sequence 2, Appli
740	30	42.3	119	11	US-11-222-587-4	Sequence 4, Appli	813	30	42.3	121	11	US-11-096-074-60	Sequence 60, Appl
741	30	42.3	119	11	US-11-222-587-6	Sequence 6, Appli	814	30	42.3	121	11	US-11-105-268-23	Sequence 23, Appl
742	30	42.3	119	11	US-11-234-586-4	Sequence 4, Appli	815	30	42.3	121	11	US-11-127-677-16	Sequence 16, Appl
743	30	42.3	119	11	US-11-234-586-6	Sequence 6, Appli	816	30	42.3	121	11	US-11-127-677-20	Sequence 20, Appl
744	30	42.3	120	9	US-10-925-366A-235	Sequence 235, App	817	30	42.3	121	11	US-11-107-028-50	Sequence 50, Appl
745	30	42.3	120	9	US-10-925-366A-286	Sequence 286, App	818	30	42.3	121	11	US-11-095-822-60	Sequence 60, Appl
746	30	42.3	120	9	US-10-834-397-45	Sequence 45, Appl	819	30	42.3	121	11	US-11-104-117-2	Sequence 2, Appli
747	30	42.3	120	9	US-10-834-397-38	Sequence 38, Appl	820	30	42.3	121	11	US-11-149-031-2	Sequence 2, Appli
748	30	42.3	120	9	US-10-834-397-36	Sequence 36, Appl	821	30	42.3	121	11	US-11-136-250-2	Sequence 2, Appli
749	30	42.3	120	9	US-10-834-397-40	Sequence 40, Appl	822	30	42.3	121	11	US-11-049-536-98	Sequence 98, Appl
750	30	42.3	120	9	US-10-834-397-40	Sequence 40, Appl	823	30	42.3	121	11	US-11-049-536-202	Sequence 202, App
751	30	42.3	120	9	US-10-834-397-57	Sequence 57, Appl	824	30	42.3	121	11	US-11-049-536-522	Sequence 522, App

825	30	42.3	121	11	US-11-049-536-682	Sequence 682, App	898	30	42.3	123	11	US-11-098-758-217	Sequence 217, App
826	30	42.3	121	11	US-11-233-252-2	Sequence 2, Appli	899	30	42.3	123	11	US-11-098-758-218	Sequence 218, App
827	30	42.3	121	11	US-11-199-739-98	Sequence 98, Appl	900	30	42.3	124	9	US-10-925-366A-211	Sequence 211, App
828	30	42.3	121	11	US-11-199-739-202	Sequence 202, App	901	30	42.3	124	9	US-10-771-257-19	Sequence 19, Appl
829	30	42.3	121	11	US-11-199-739-522	Sequence 522, App	902	30	42.3	124	9	US-10-771-257-22	Sequence 22, Appl
830	30	42.3	121	11	US-11-199-739-682	Sequence 682, App	903	30	42.3	124	9	US-10-981-356A-4	Sequence 4, Appli
831	30	42.3	121	11	US-11-240-195-7	Sequence 7, Appli	904	30	42.3	124	10	US-11-271-008-8	Sequence 8, Appli
832	30	42.3	121	11	US-11-240-195-31	Sequence 31, Appl	905	30	42.3	124	11	US-11-105-268-9	Sequence 9, Appli
833	30	42.3	121	11	US-11-240-195-52	Sequence 52, Appl	906	30	42.3	124	11	US-11-127-677-19	Sequence 19, Appl
834	30	42.3	121	11	US-11-240-195-111	Sequence 111, App	907	30	42.3	124	11	US-11-127-677-22	Sequence 22, Appl
835	30	42.3	121	11	US-11-102-512-19	Sequence 19, Appl	908	30	42.3	124	11	US-11-096-046-4	Sequence 4, Appli
836	30	42.3	121	11	US-11-208-422-14	Sequence 14, Appl	909	30	42.3	124	11	US-11-107-028-10	Sequence 10, Appl
837	30	42.3	121	11	US-11-208-422-54	Sequence 54, Appl	910	30	42.3	124	11	US-11-107-028-11	Sequence 11, Appl
838	30	42.3	121	11	US-11-098-758-212	Sequence 212, App	911	30	42.3	124	11	US-11-107-028-12	Sequence 12, Appl
839	30	42.3	121	11	US-11-245-254-2	Sequence 2, Appli	912	30	42.3	124	11	US-11-102-512-61	Sequence 61, Appl
840	30	42.3	122	9	US-10-771-257-11	Sequence 11, Appl	913	30	42.3	124	11	US-11-102-512-68	Sequence 68, Appl
841	30	42.3	122	9	US-10-515-241-11	Sequence 11, Appl	914	30	42.3	124	11	US-11-102-512-71	Sequence 71, Appl
842	30	42.3	122	10	US-11-211-917-110	Sequence 110, App	915	30	42.3	124	11	US-11-102-512-74	Sequence 74, Appl
843	30	42.3	122	11	US-11-105-268-29	Sequence 29, Appl	916	30	42.3	124	11	US-11-098-758-211	Sequence 211, App
844	30	42.3	122	11	US-11-127-677-11	Sequence 11, Appl	917	30	42.3	125	9	US-10-771-257-6	Sequence 6, Appli
845	30	42.3	122	11	US-11-049-536-186	Sequence 186, App	918	30	42.3	125	11	US-11-096-074-57	Sequence 57, Appl
846	30	42.3	122	11	US-11-049-536-302	Sequence 302, App	919	30	42.3	125	11	US-11-096-074-58	Sequence 58, Appl
847	30	42.3	122	11	US-11-049-536-574	Sequence 574, App	920	30	42.3	125	11	US-11-127-677-6	Sequence 6, Appli
848	30	42.3	122	11	US-11-199-739-186	Sequence 186, App	921	30	42.3	125	11	US-11-064-174-8	Sequence 8, Appli
849	30	42.3	122	11	US-11-199-739-302	Sequence 302, App	922	30	42.3	125	11	US-11-064-174-9	Sequence 9, Appli
850	30	42.3	122	11	US-11-199-739-574	Sequence 574, App	923	30	42.3	125	11	US-11-064-174-20	Sequence 20, Appl
851	30	42.3	122	11	US-11-102-512-48	Sequence 48, Appl	924	30	42.3	125	11	US-11-064-174-21	Sequence 21, Appl
852	30	42.3	122	11	US-11-102-512-75	Sequence 75, Appl	925	30	42.3	125	11	US-11-064-174-22	Sequence 22, Appl
853	30	42.3	123	8	US-10-546-594-64	Sequence 64, Appl	926	30	42.3	125	11	US-11-064-174-23	Sequence 23, Appl
854	30	42.3	123	8	US-10-546-594-66	Sequence 66, Appl	927	30	42.3	125	11	US-11-064-174-24	Sequence 24, Appl
855	30	42.3	123	8	US-10-546-594-68	Sequence 68, Appl	928	30	42.3	125	11	US-11-127-903-21	Sequence 21, Appl
856	30	42.3	123	8	US-10-546-594-70	Sequence 70, Appl	929	30	42.3	125	11	US-11-127-903-43	Sequence 43, Appl
857	30	42.3	123	9	US-10-925-366A-216	Sequence 216, App	930	30	42.3	125	11	US-11-127-903-46	Sequence 46, Appl
858	30	42.3	123	9	US-10-925-366A-217	Sequence 217, App	931	30	42.3	125	11	US-11-095-822-57	Sequence 57, Appl
859	30	42.3	123	9	US-10-925-366A-218	Sequence 218, App	932	30	42.3	125	11	US-11-095-822-58	Sequence 58, Appl
860	30	42.3	123	9	US-10-771-257-59	Sequence 59, Appl	933	30	42.3	125	11	US-11-049-536-174	Sequence 174, App
861	30	42.3	123	9	US-10-834-397-41	Sequence 41, Appl	934	30	42.3	125	11	US-11-049-536-486	Sequence 486, App
862	30	42.3	123	9	US-10-834-397-69	Sequence 69, Appl	935	30	42.3	125	11	US-11-199-739-174	Sequence 174, App
863	30	42.3	123	9	US-10-982-440-3	Sequence 3, Appli	936	30	42.3	125	11	US-11-199-739-486	Sequence 486, App
864	30	42.3	123	9	US-10-982-440-21	Sequence 21, Appl	937	30	42.3	126	8	US-10-546-594-119	Sequence 119, App
865	30	42.3	123	9	US-10-982-440-51	Sequence 51, Appl	938	30	42.3	126	9	US-10-771-257-13	Sequence 13, Appl
866	30	42.3	123	9	US-10-982-440-59	Sequence 59, Appl	939	30	42.3	126	9	US-10-771-257-45	Sequence 45, Appl
867	30	42.3	123	9	US-10-515-241-10	Sequence 10, Appl	940	30	42.3	126	10	US-11-211-917-42	Sequence 42, Appl
868	30	42.3	123	9	US-10-956-008-50	Sequence 50, Appl	941	30	42.3	126	10	US-11-127-677-13	Sequence 13, Appl
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871	30	42.3	123	11	US-11-127-903-39	Sequence 39, Appl	944	30	42.3	126	11	US-11-064-174-149	Sequence 149, App
872	30	42.3	123	11	US-11-127-903-40	Sequence 40, Appl	945	30	42.3	126	11	US-11-127-903-5	Sequence 5, Appli
873	30	42.3	123	11	US-11-127-903-45	Sequence 45, Appl	946	30	42.3	126	11	US-11-049-536-322	Sequence 322, App
874	30	42.3	123	11	US-11-127-903-47	Sequence 47, Appl	947	30	42.3	126	11	US-11-049-536-430	Sequence 430, App
875	30	42.3	123	11	US-11-127-903-48	Sequence 48, Appl	948	30	42.3	126	11	US-11-199-739-322	Sequence 322, App
876	30	42.3	123	11	US-11-095-822-56	Sequence 56, Appl	949	30	42.3	126	11	US-11-199-739-430	Sequence 430, App
877	30	42.3	123	11	US-11-049-536-60	Sequence 60, Appl	950	30	42.3	127	9	US-10-993-543-164	Sequence 164, App
878	30	42.3	123	11	US-11-049-536-238	Sequence 238, App	951	30	42.3	127	11	US-11-105-268-31	Sequence 31, Appl
879	30	42.3	123	11	US-11-049-536-378	Sequence 378, App	952	30	42.3	127	11	US-11-064-174-18	Sequence 18, Appl
880	30	42.3	123	11	US-11-049-536-398	Sequence 398, App	953	30	42.3	127	11	US-11-064-174-19	Sequence 19, Appl
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882	30	42.3	123	11	US-11-199-739-60	Sequence 60, Appl	955	30	42.3	127	11	US-11-199-739-454	Sequence 454, App
883	30	42.3	123	11	US-11-199-739-238	Sequence 238, App	956	30	42.3	128	9	US-10-993-543-108	Sequence 108, App
884	30	42.3	123	11	US-11-199-739-378	Sequence 378, App	957	30	42.3	128	11	US-11-049-536-76	Sequence 76, Appl
885	30	42.3	123	11	US-11-199-739-398	Sequence 398, App	958	30	42.3	128	11	US-11-049-536-102	Sequence 102, App
886	30	42.3	123	11	US-11-240-195-109	Sequence 109, App	959	30	42.3	128	11	US-11-199-739-76	Sequence 76, Appl
887	30	42.3	123	11	US-11-102-512-15	Sequence 15, Appl	960	30	42.3	128	11	US-11-199-739-102	Sequence 102, App
888	30	42.3	123	11	US-11-102-512-18	Sequence 18, Appl	961	30	42.3	128	11	US-11-221-281-44	Sequence 44, Appl
889	30	42.3	123	11	US-11-102-512-56	Sequence 56, Appl	962	30	42.3	129	9	US-10-771-257-61	Sequence 61, Appl
890	30	42.3	123	11	US-11-102-512-57	Sequence 57, Appl	963	30	42.3	129	9	US-10-993-543-28	Sequence 28, Appl
891	30	42.3	123	11	US-11-102-512-58	Sequence 58, Appl	964	30	42.3	129	11	US-11-127-677-59	Sequence 59, Appl
892	30	42.3	123	11	US-11-102-512-69	Sequence 69, Appl	965	30	42.3	129	11	US-11-064-174-143	Sequence 143, App
893	30	42.3	123	11	US-11-102-512-70	Sequence 70, Appl	966	30	42.3	130	9	US-10-993-543-68	Sequence 68, Appl
894	30	42.3	123	11	US-11-102-512-78	Sequence 78, Appl	967	30	42.3	131	9	US-10-993-543-80	Sequence 80, Appl
895	30	42.3	123	11	US-11-102-512-79	Sequence 79, Appl	968	30	42.3	131	9	US-10-993-543-104	Sequence 104, App
896	30	42.3	123	11	US-11-102-512-85	Sequence 85, Appl	969	30	42.3	131	9	US-10-993-543-116	Sequence 116, App
897	30	42.3	123	11	US-11-098-758-216	Sequence 216, App	970	30	42.3	131	9		

971 30 42.3 131 11 US-11-049-536-92 Sequence 92, Appl
972 30 42.3 131 11 US-11-199-739-92 Sequence 92, Appl
973 30 42.3 131 11 US-11-188-298-20067 Sequence 2067, A
974 30 42.3 132 9 US-10-993-543-12 Sequence 12, Appl
975 30 42.3 132 9 US-10-993-543-84 Sequence 84, Appl
976 30 42.3 132 9 US-10-993-543-148 Sequence 148, App
977 30 42.3 132 9 US-10-993-543-152 Sequence 152, App
978 30 42.3 132 11 US-11-049-536-4 Sequence 4, Appl
979 30 42.3 132 11 US-11-049-536-8 Sequence 8, Appl
980 30 42.3 132 11 US-11-049-536-32 Sequence 32, Appl
981 30 42.3 132 11 US-11-199-739-4 Sequence 4, Appl
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983 30 42.3 132 11 US-11-199-739-32 Sequence 32, Appl
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985 30 42.3 133 11 US-11-051-453-51 Sequence 51, Appl
986 30 42.3 134 9 US-10-993-543-172 Sequence 172, App
987 30 42.3 135 9 US-10-993-543-120 Sequence 120, App
988 30 42.3 135 11 US-11-012-353-77 Sequence 77, Appl
989 30 42.3 135 11 US-11-012-353-81 Sequence 81, Appl
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991 30 42.3 136 11 US-11-250-411-91 Sequence 91, Appl
992 30 42.3 136 11 US-11-250-411-95 Sequence 95, Appl
993 30 42.3 137 9 US-10-475-075-914 Sequence 914, App
994 30 42.3 137 11 US-11-049-536-56 Sequence 56, Appl
995 30 42.3 137 11 US-11-049-536-68 Sequence 68, Appl
996 30 42.3 137 11 US-11-049-536-72 Sequence 72, Appl
997 30 42.3 137 11 US-11-049-536-80 Sequence 80, Appl
998 30 42.3 137 11 US-11-049-536-88 Sequence 88, Appl
999 30 42.3 137 11 US-11-199-739-56 Sequence 56, Appl
1000 30 42.3 137 11 US-11-199-739-68 Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-11-096-568A-15109
; Sequence 15109, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15109
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(241)
; OTHER INFORMATION: Ceres Seq. ID no. 12342228
US-11-096-568A-15109

Query Match 60.6%; Score 43; DB 11; Length 241;
Best Local Similarity 70.0%; Pred. No. 5.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
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Db 24 DDFGGQKAYV 33

RESULT 2
US-11-096-568A-15108
; Sequence 15108, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15108
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(252)
; OTHER INFORMATION: Ceres Seq. ID no. 12342227
US-11-096-568A-15108

Query Match 60.6%; Score 43; DB 11; Length 252;
Best Local Similarity 70.0%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYV 10
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Db 35 DDFGGQKAYV 44

RESULT 3
US-11-067-260-26
; Sequence 26, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067.260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: deletion G741
US-11-067-260-26

Query Match 56.3%; Score 40; DB 11; Length 248;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVND 12
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Db 153 DDAGGKLTITID 164

RESULT 4
US-11-067-260-25
; Sequence 25, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067.260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 25
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Protein 741
US-11-067-260-25

Query Match 56.3%; Score 40; DB 11; Length 274;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
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Db 179 DDAGGKLTYYTD 190

RESULT 5

US-11-067-260-50
; Sequence 50, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067,260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 961c-741
US-11-067-260-50

Query Match 56.3%; Score 40; DB 11; Length 590;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||: ||: ||:
Db 487 DDAGGKLTYYTD 498

RESULT 6

US-11-067-260-30
; Sequence 30, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067,260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: deletion G741-961c
US-11-067-260-30

Query Match 56.3%; Score 40; DB 11; Length 593;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||: ||: ||:
Db 154 DDAGGKLTYYTD 165

RESULT 7

US-11-067-260-56
; Sequence 56, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067,260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 961cL-741
US-11-067-260-56

Query Match 56.3%; Score 40; DB 11; Length 612;
Best Local Similarity 58.3%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
|||: ||: ||:
Db 509 DDAGGKLTYYTD 520

RESULT 8

US-11-067-260-44
; Sequence 44, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067,260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 961-741
US-11-067-260-44

Query Match 56.3%; Score 40; DB 11; Length 645;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
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Db 542 DDAGGKLTYYTID 553

RESULT 9

US-11-067-260-28

; Sequence 28, Application US/11067260

; Publication No. US20060051840A1

; GENERAL INFORMATION:

; APPLICANT: Arico, Maria

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS

; FILE REFERENCE: 223002099501

; CURRENT APPLICATION NUMBER: US/11/067,260

; CURRENT FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: 10/220,480

; PRIOR FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: PCT/IB01/00420

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 28

; LENGTH: 648

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: deletion G741-961

US-11-067-260-28

Query Match 56.3%; Score 40; DB 11; Length 648;

Best Local Similarity 58.3%; Pred. No. 43;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12

|||: ||: ||:

Db 154 DDAGGKLTYYTID 165

RESULT 10

US-11-067-260-36

; Sequence 36, Application US/11067260

; Publication No. US20060051840A1

; GENERAL INFORMATION:

; APPLICANT: Arico, Maria

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS

; FILE REFERENCE: 223002099501

; CURRENT APPLICATION NUMBER: US/11/067,260

; CURRENT FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: 10/220,480

; PRIOR FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: PCT/IB01/00420

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 36

; LENGTH: 672

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: ORF46.1-741

US-11-067-260-36

Query Match 56.3%; Score 40; DB 11; Length 672;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12

|||: ||: ||:

Db 569 DDAGGKLTYYTID 580

RESULT 11

US-11-067-260-34

; Sequence 34, Application US/11067260

; Publication No. US20060051840A1

; GENERAL INFORMATION:

; APPLICANT: Arico, Maria

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS

; FILE REFERENCE: 223002099501

; CURRENT APPLICATION NUMBER: US/11/067,260

; CURRENT FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: 10/220,480

; PRIOR FILING DATE: 2002-08-28

; PRIOR APPLICATION NUMBER: PCT/IB01/00420

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34

; LENGTH: 675

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: deletion G741-ORF46.1

US-11-067-260-34

Query Match 56.3%; Score 40; DB 11; Length 675;

Best Local Similarity 58.3%; Pred. No. 45;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12

|||: ||: ||:

Db 154 DDAGGKLTYYTID 165

RESULT 12

US-10-336-263A-14

; Sequence 14, Application US/10336263A

; Publication No. US20050251882A1

; GENERAL INFORMATION:

; APPLICANT: D'Ordine, Robert L

; APPLICANT: Dotson, Stanton B

; APPLICANT: Duff, Stephen M

; APPLICANT: Sisson, Pamela J

; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA

; FILE REFERENCE: 38-21 (52176) A

; CURRENT APPLICATION NUMBER: US/10/336,263A

; CURRENT FILING DATE: 2003-01-03

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 710

; TYPE: PRT

; ORGANISM: Synecococcus sp.

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(710)

; OTHER INFORMATION:

US-10-336-263A-14

Query Match 56.3%; Score 40; DB 9; Length 710;

Best Local Similarity 63.6%; Pred. No. 47;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DYGGQSTYVMD 12

||||: ||: ||:

Db 28 DTGGQTLVLD 38

RESULT 13

US-11-067-260-20

; Sequence 20, Application US/11067260

; Publication No. US20060051840A1

; GENERAL INFORMATION:

; APPLICANT: Arico, Maria

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS

; FILE REFERENCE: 223002099501

; CURRENT APPLICATION NUMBER: US/11/067,260

```
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1312
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: deletion G983-741
US-11-067-260-20

Query Match          56.3%; Score 40; DB 11; Length 1312;
Best Local Similarity 58.3%; Pred. No. 86;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   |||||: |||: ||
Db 1209 DDAGGKLTITD 1220

RESULT 14
US-11-067-260-32
; Sequence 32, Application US/11067260
; Publication No. US20060051840A1
; GENERAL INFORMATION:
; APPLICANT: Arico, Maria
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
; FILE REFERENCE: 223002099501
; CURRENT APPLICATION NUMBER: US/11/067,260
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 10/220,480
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/IB01/00420
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 1312
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: deletion G741-983
US-11-067-260-32

Query Match          56.3%; Score 40; DB 11; Length 1312;
Best Local Similarity 58.3%; Pred. No. 86;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   |||||: |||: ||
Db 154 DDAGGKLTITD 165

RESULT 15
US-11-261-135-2
; Sequence 2, Application US/11261135
; Publication No. US20060041948A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
; FILE REFERENCE: R-365
; CURRENT APPLICATION NUMBER: US/11/261,135
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/09/903,377
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/217,255
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/221,483

; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/262,113
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting vector
US-11-261-135-2

Query Match          54.9%; Score 39; DB 11; Length 357;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 12
   |||||: |||: ||
Db 3 DDYGESTSSME 14

RESULT 16
US-10-878-556A-58
; Sequence 58, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/roh3_human
; DATABASE ENTRY DATE: 1993-07-01
US-10-878-556A-58

Query Match          53.5%; Score 38; DB 9; Length 346;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDYGGQSTY 9
   |||||: |
Db 151 DDYGGYNNY 159

RESULT 17
US-11-129-741-2937
; Sequence 2937, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
```

; SEQ ID NO 2937
; LENGTH: 1351
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2937

Query Match 53.5%; Score 38; DB 11; Length 1351;
Best Local Similarity 46.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
|:||||:|:|
Db 1335 DEYGHNDVFIKA 1347

RESULT 18
US-11-129-741-2947
; Sequence 2947, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2947
; LENGTH: 1351
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2947

Query Match 53.5%; Score 38; DB 11; Length 1351;
Best Local Similarity 46.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
|:||||:|:|
Db 1335 DEYGHNDVFIKA 1347

RESULT 19
US-11-129-741-3655
; Sequence 3655, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3655

; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-3655

Query Match 53.5%; Score 38; DB 11; Length 1385;
Best Local Similarity 46.2%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
|:||||:|:|
Db 1369 DEYGHNDVFIKA 1381

RESULT 20
US-11-096-568A-23511
; Sequence 23511, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23511
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(329)
; OTHER INFORMATION: Ceres Seq. ID no. 12413226
US-11-096-568A-23511

Query Match 52.1%; Score 37; DB 11; Length 329;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
|:||||
Db 315 DDYGGNDY 323

RESULT 21
US-11-096-568A-23510
; Sequence 23510, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23510
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(352)
; OTHER INFORMATION: Ceres Seq. ID no. 12413225
US-11-096-568A-23510

Query Match 52.1%; Score 37; DB 11; Length 352;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
|:||||
|

```
Db      338 DDYGGNDY 346

RESULT 22
US-10-513-639-24
; Sequence 24, Application US/10513639
; Publication No. US20060010511A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yicheng
; APPLICANT: Chen, Yancheng
; APPLICANT: Li, Fengmei
; APPLICANT: Tian, Zhexion
; APPLICANT: Lin, Min
; APPLICANT: Wang, Yiping
; TITLE OF INVENTION: NOVEL GLYPHOSATE-TOLERANT
; TITLE OF INVENTION: 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE AND THE GENE
; TITLE OF INVENTION: ENCODING THE SAME
; FILE REFERENCE: 18495-002U51
; CURRENT APPLICATION NUMBER: US/10/513,639
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: CN 02117991.3
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: CN 02117647.7
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: PCT/CN02/00539
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
US-10-513-639-24

Query Match      52.1%; Score 37; DB 9; Length 444;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GGQSTYVMD 12
Db      115 GGNATYVLD 123

RESULT 23
US-11-225-780-5
; Sequence 5, Application US/11225780
; Publication No. US20060059581A1
; GENERAL INFORMATION:
; APPLICANT: SPENCER, MICHAEL
; APPLICANT: MUMM, RITA
; APPLICANT: GWYN, J. JEFFERSON
; APPLICANT: MCELROY, DAVID
; APPLICANT: STEPHENS, MICHAEL A.
; TITLE OF INVENTION: METHOD FOR PLANT BREEDING
; FILE REFERENCE: DERM:157USC2
; CURRENT APPLICATION NUMBER: US/11/225,780
; CURRENT FILING DATE: 2005-09-13
; PRIOR APPLICATION NUMBER: US/10/869,324
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 09/698,789
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 08/927,368
; PRIOR FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: 08/899,247
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Zea mays
US-11-225-780-5

Query Match      52.1%; Score 37; DB 9; Length 444;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GGQSTYVMD 12
Db      115 GGNATYVLD 123

Query Match      52.1%; Score 37; DB 11; Length 570;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GGQSTYVMD 12
Db      241 GGNATYVLD 249

RESULT 24
US-10-927-641-77
; Sequence 77, Application US/10927641
; Publication No. US20050244968A1
; GENERAL INFORMATION:
; APPLICANT: Perez, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Bagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-927-641-77

Query Match      52.1%; Score 37; DB 9; Length 805;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DYGGQSTYVMD 12
Db      298 DTGGQVYVLD 308

RESULT 25
US-11-087-099-5243
; Sequence 5243, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5243
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Ceratodon purpureus
; FEATURE:
; NAME/KEY: unsure
```

```
; LOCATION: (1)..(1126)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-5243

Query Match          52.1%; Score 37; DB 11; Length 1126;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDYGGQST 8
Db 349 DDFGGQQT 356

RESULT 26
US-10-939-890-551
; Sequence 551, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 551
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-584

Query Match          51.4%; Score 36.5; DB 9; Length 21;
Best Local Similarity 64.3%; Pred. No. 6.1;
Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DDY-GGGSTYYMDA 13
Db 8 DDYFGGIICYIDA 21

RESULT 27
US-10-939-890-584
; Sequence 584, Application US/10939890
```

```
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 584
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-584

Query Match          50.7%; Score 36; DB 9; Length 21;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDYGGQSTY 9
Db 9 DPYGGESCY 17

RESULT 28
US-10-997-201A-6
; Sequence 6, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-997-201A-6

Query Match 50.7%; Score 36; DB 9; Length 102;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTVY 10
||| ||| |||
Db 89 DDYWGQGTIV 98

RESULT 29

US-10-771-257-7
; Sequence 7, Application US/10771257
; Publication No. US2005028864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Maritan, Amos
; APPLICANT: Visintin, Michela
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-7

Query Match 50.7%; Score 36; DB 9; Length 121;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTVY 10
||| ||| |||
Db 108 DDYWGQGTIV 117

RESULT 30

US-11-127-677-7
; Sequence 7, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-7

Query Match 50.7%; Score 36; DB 11; Length 121;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDYGGQSTVY 10
||| ||| |||
Db 108 DDYWGQGTIV 117

RESULT 31

US-11-049-536-52
; Sequence 52, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-049-536-52

Query Match 50.7%; Score 36; DB 11; Length 147;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 DYGGQSTY 9
||| ||| |||
Db 100 DYGGNSAY 107

RESULT 32

US-11-199-739-52
; Sequence 52, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12

```
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-199-739-52

Query Match          50.7%; Score 36; DB 11; Length 147;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 DYGGQSTY 9
Db      100 DYGGNSAY 107

RESULT 33
US-10-506-454-198
; Sequence 198, Application US/10506454
; Publication No. US20060069386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezneva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Koz'yavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-198

Query Match          50.7%; Score 36; DB 9; Length 335;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 DYGGQSTYVMD 12
Db      224 EFGDRSTYQMD 234

RESULT 34
US-11-098-686-11222
; Sequence 11222, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
```

```
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11222
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11222

Query Match          50.7%; Score 36; DB 11; Length 435;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      3 YGGQSTYV 10
Db      256 YGGQSTHL 263

RESULT 35
US-11-074-176-212
; Sequence 212, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAnuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-212

Query Match          50.7%; Score 36; DB 11; Length 450;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DDYGGQSTYVMD 12
Db      324 DEYGGTSGIVTD 335

RESULT 36
US-11-188-298-7836
; Sequence 7836, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7836
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(466)
```

```
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-7836

Query Match          50.7%; Score 36; DB 11; Length 466;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDYGGQSTYVMD 13
DB 165 DDYQAMLYYMA 177

RESULT 37
US-10-336-263A-6
; Sequence 6, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336,263A
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Prochlorococcus marinus
; NAME/KEY: PEPTIDE
; LOCATION: (1)-(471)
; OTHER INFORMATION:
US-10-336-263A-6

Query Match          50.7%; Score 36; DB 9; Length 471;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DYGGQSTYVMD 12
DB 27 DTGGQTVYVLE 37

RESULT 38
US-11-079-463-7504
; Sequence 7504, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRAGILIS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7504
; LENGTH: 624
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-7504

Query Match          50.7%; Score 36; DB 11; Length 624;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 YGGQSTYVMD 12
DB 136 YGNHSTYMQD 145

RESULT 39
US-10-982-440-168
; Sequence 168, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-168

Query Match          49.3%; Score 35; DB 9; Length 14;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQS 7
DB 3 DDYGGNS 9

RESULT 40
US-10-982-440-27
; Sequence 27, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-27

Query Match          49.3%; Score 35; DB 9; Length 123;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDYGGQS 7
DB 101 DDYGGNS 107

RESULT 41
US-11-140-416-26
; Sequence 26, Application US/11140416
; Publication No. US20060029547A1
; GENERAL INFORMATION:
; APPLICANT: D-Gen Limited
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PRION DISEASE
```


; FILE REFERENCE: ICOT/P21952
; CURRENT APPLICATION NUMBER: US/11/140,416
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: GB 9824091.4
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Antilocapra americana
US-11-140-416-26

Query Match 49.3%; Score 35; DB 11; Length 256;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
| | | | | | | | | | | | | | | |
Db 170 DQYNNQNTFVHD 181

RESULT 42

US-11-056-950-8
; Sequence 8, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: elk prion protein
US-11-056-950-8

Query Match 49.3%; Score 35; DB 11; Length 256;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
| | | | | | | | | | | | | | | |
Db 170 DQYNNQNTFVHD 181

RESULT 43

US-11-056-950-9
; Sequence 9, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: fallow deer prion protein
US-11-056-950-9

Query Match 49.3%; Score 35; DB 11; Length 256;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
| | | | | | | | | | | | | | | |
Db 170 DQYNNQNTFVHD 181

RESULT 44

US-11-056-950-10
; Sequence 10, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mule deer prion protein
US-11-056-950-10

Query Match 49.3%; Score 35; DB 11; Length 256;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
| | | | | | | | | | | | | | | |
Db 170 DQYNNQNTFVHD 181

RESULT 45

US-11-056-950-11
; Sequence 11, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509

```

; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,362
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: white tailed deer
US-11-056-950-11

```

Query Match 49.3%; Score 35; DB 11; Length 256;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDYGGQSTYYMD 12
Db 170 DQYNNQNTFVHD 181

```

RESULT 46
US-11-188-298-513
; Sequence 513, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 513
; LENGTH: 316
; TYPE: prt
; ORGANISM: Glycine max
US-11-188-298-513

```

Query Match 49.3%; Score 35; DB 11; Length 316;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMD 12
:|:|:|:|:|:
Db 149 EDYGIOOHYISD 160

```

RESULT 47
US-11-188-298-4638
; Sequence 4638, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/552,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 4638
; LENGTH: 388
; TYPE: prt
; ORGANISM: Pyrenomonas salina
US-11-188-298-4638

```

Query Match 49.3%; Score 35; DB 11; Length 388;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;

	Matches	6;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps
Qy	1	DDYGGG	STYV	10					
			:						
Db	186	DDYKG	GDTPV	195					

```

RESULT 48
US-11-054-281-301
; Sequence 301, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,025
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 301
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: conses
US-11-054-281-301

```

Query Match	49.3%	Score 35;	DB 11;	Length 393;
Best Local Similarity	46.2%;	Pred. No. 1.9e+02;		
Matches	6;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0

Qy 1 DDYGGQSTYVMDA 13
|:|:|:|:|:
Db 338 DELGGEPTWNMEA 350

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RESULT 49
US-11-087-099-5554
; Sequence 5554, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5554
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Corynebacterium efficiens YS-314
US-11-087-099-5554

```

Query Match	49.3%	Score 35;	DB 11;	Length 476;
Best Local Similarity	66.7%;	Pred. No. 2.3e+02;		
Matches	6;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;

Qy 1 DDYGGQSTY 9
|:|:|:|
Db 51 DDWGGQWNY 59

RESULT 50
US-11-188-298-12113
; Sequence 12113, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12113
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-188-298-12113

Query Match 49.3%; Score 35; DB 11; Length 534;
Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDYGGQSTYVMDA 13
|:|:|:|
Db 157 DKFGRTKTFVLDA 169

Search completed: May 11, 2006, 16:50:35
Job time : 20.1967 secs

GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:15:30 ; Search time 101.705 Seconds
(without alignments)
47.521 Million cell updates/sec

Title: US-10-808-538-4

Perfect score: 56

Sequence: 1 RASQDIGNYLRL 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	11	2	Aaw23433
2	56	100.0	108	2	Aaw23439
3	56	100.0	108	2	Aaw23440
4	56	100.0	108	2	Aaw23442
5	56	100.0	108	2	Aaw23436
6	47	83.9	106	5	ABG76532
7	45	80.4	11	3	AAV94220
8	45	80.4	11	6	ABJ18571
9	45	80.4	11	7	ADJ74691
10	45	80.4	11	8	ADP47046
11	45	80.4	11	8	ADU38479
12	45	80.4	11	9	ADW04827
13	45	80.4	95	9	ADZ47744
14	45	80.4	95	9	ADZ47743
15	45	80.4	107	2	AAW49812
16	45	80.4	107	2	AAW49811
17	45	80.4	107	2	AAW66098
18	45	80.4	107	6	ABJ18571
19	45	80.4	107	6	ABJ18574
20	45	80.4	107	6	ABR55867
21	45	80.4	107	6	ABR55866
22	45	80.4	107	6	ABR54919
23	45	80.4	107	6	ABO27199
24	45	80.4	107	6	AAO27194

25	45	80.4	107	6	ABO10814
26	45	80.4	107	7	ADC84579
27	45	80.4	107	8	ADH50840
28	45	80.4	107	8	ADN49723
29	45	80.4	107	8	ADN49724
30	45	80.4	107	8	ADQ09630
31	45	80.4	107	8	ADT02531
32	45	80.4	107	8	ADU74399
33	45	80.4	107	8	ADU74400
34	45	80.4	107	8	ADW75670
35	45	80.4	107	8	ADW75668
36	45	80.4	107	8	ADY85028
37	45	80.4	107	9	ADZ47655
38	45	80.4	107	9	AEA50145
39	45	80.4	107	9	ABE19295
40	45	80.4	108	1	APB1246
41	45	80.4	108	2	AAW54062
42	45	80.4	108	2	AAW04177
43	45	80.4	108	2	AAW00834
44	45	80.4	108	2	AAW16620
45	45	80.4	108	3	AAV94216
46	45	80.4	108	6	ABO10817
47	45	80.4	108	6	ABO10815
48	45	80.4	108	6	ABO10816
49	45	80.4	108	8	ADH50842
50	45	80.4	108	9	ADZ47742
51	45	80.4	108	9	ABE21885
52	45	80.4	108	9	ABE21887
53	45	80.4	109	2	AAW52039
54	45	80.4	109	6	ABO10818
55	45	80.4	109	8	ADG25821
56	45	80.4	109	9	ABE21853
57	45	80.4	109	9	ABE21858
58	45	80.4	109	9	ABE21856
59	45	80.4	109	9	ABE21859
60	45	80.4	110	9	ADZ47745
61	45	80.4	111	1	AAV81870
62	45	80.4	112	4	AAW84296
63	45	80.4	116	9	ADW04825
64	45	80.4	121	9	AEA88810
65	45	80.4	127	2	AAW29010
66	45	80.4	127	2	AAW32121
67	45	80.4	127	2	AAW39265
68	45	80.4	127	2	AAW99003
69	45	80.4	127	2	AAW11817
70	45	80.4	127	2	AAW11815
71	45	80.4	127	2	AAW60033
72	45	80.4	127	2	AAW60035
73	45	80.4	127	2	AAW49809
74	45	80.4	127	9	AEA88780
75	45	80.4	128	2	AAW29579
76	45	80.4	128	2	AAW54064
77	45	80.4	131	2	AAW84553
78	45	80.4	131	8	ADJ26634
79	45	80.4	212	5	ABP51955
80	45	80.4	214	2	AAW30776
81	45	80.4	214	2	AAW43338
82	45	80.4	214	2	AAW00373
83	45	80.4	214	2	AAW34504
84	45	80.4	214	2	AAW34506
85	45	80.4	214	2	AAW49815
86	45	80.4	214	2	AAW95615
87	45	80.4	214	2	AAW30632
88	45	80.4	214	2	AAW08754
89	45	80.4	214	4	AAW66777
90	45	80.4	214	5	ABG31889
91	45	80.4	214	6	ABR55870
92	45	80.4	214	8	ADK18342
93	45	80.4	214	8	ADN49727
94	45	80.4	214	8	ADU74403
95	45	80.4	214	9	ABE27968
96	45	80.4	215	9	ADO19050
97	45	80.4	233	2	AAW30777

Abol0814	Mouse mon
Adc84579	CDR3 heavy
Adh50840	Mouse ant
Adn49723	Variable
Adn49724	Variable
Adq09630	Variable
Adt02531	Anti-CD22
Adu74399	Human imm
Adu74400	Mouse ant
Adw75670	Novel mod
Adw75668	Novel mod
Ady85028	Monoclonal
Adz47655	Mouse ant
Aea50145	Anti-CD22
Aea19295	IgG kappa
Aap81246	Anti-pseu
Aap54062	Anti-canc
Aaw04177	Variant v
Aaw00834	Variable
Aaw16620	Anti-huma
Aay94216	Murine co
Abol0817	Human ger
Abol0815	Mouse mon
Abol0816	Human ger
Adh50842	Human vL#
Adz47742	Mouse ant
Aeb21885	Human DC-
Aeb21887	Human DC-
Aar52039	Light cha
Abol0818	Mouse/hum
Adg25821	Anti-CD30
Aeb21853	Human DC-
Aeb21858	Human DC-
Aeb21856	Human DC-
Aeb21859	Human DC-
Adz47745	CDR-graft
Apb1870	Anti-pseu
Abh84296	Amino aci
Adw04825	PAPP-A im
Aea88810	Murine SA
Aar29010	Pl46-k3 p
Aar32121	Anti-CD4
Aar39265	Mouse C4G
Aar99003	MAB VLI78
Aaw11817	Humanised
Aaw11815	Mouse ant
Aaw60033	Mouse ant
Aaw60035	Human ant
Aaw49809	Variable
Aea88780	Murine SA
Aar29579	CLN-IgG k
Aar54064	Anti-canc
Aar84553	MAB SCH94
Adi26634	Human ant
Abp51955	Humanised
Aar30776	H52L6-158
Aar43338	Complelet
Aaw00373	Anti-CD18
Aaw34504	Light cha
Aaw34506	Light cha
Aaw49815	Amino aci
Aaw95615	Humanized
Aaw30632	Recombinat
Aay08754	Human ant
Aab66777	rhuMab CD
Abg31889	Humanised
Abf55870	Human imm
Adk18342	Amino aci
Adn49727	Human imm
Adu74403	Human imm
Aeb27968	Humanized
Ado19050	Murine an
Aar30777	pH52-9.0

98	45	80.4	233	4	AAB49242	Aab49242	Chimeric	171	43	76.8	638	5	AAU75370	Aau75370	Diphtheri
99	45	80.4	236	3	RAY96297	Aay96297	Human IGF	172	43	76.8	642	5	AAU75382	Aau75382	Diphtheri
100	45	80.4	237	2	AAW95622	Aaw95622	PS1130 ex	173	43	76.8	642	5	AAO29675	Aao29675	Anti-T ce
101	45	80.4	237	2	AAW30634	Aaw30634	Recombina	174	43	76.8	643	5	AAU75390	Aau75390	Diphtheri
102	45	80.4	237	4	AAB66784	Aab66784	Protein e	175	43	76.8	643	6	AAO29670	Aao29670	Anti-T ce
103	45	80.4	237	6	ABP72745	Abp72745	Anti-CD18	176	43	76.8	652	6	AAU75448	Aau75448	Immunotox
104	45	80.4	237	9	ABE27976	Abe27976	E. coli S	177	43	76.8	656	5	AAU75383	Aau75383	Immunotox
105	45	80.4	246	8	ADH50844	Adh50844	SGI11 RFB	178	43	76.8	657	5	AAU75389	Aau75389	Diphtheri
106	45	80.4	246	8	ADH50847	Adh50847	SGV RFB4	179	43	76.8	895	5	AAU75369	Aau75369	Diphtheri
107	45	80.4	246	8	ADH50843	Adh50843	RFB4 spec	180	43	76.8	895	5	AAU75368	Aau75368	Diphtheri
108	45	80.4	246	8	ADH50845	Adh50845	SGI11 var	181	43	76.8	895	5	AAU75374	Aau75374	Diphtheri
109	45	80.4	246	8	ADH50846	Adh50846	SGIV RFB4	182	43	76.8	895	6	AAO29673	Aao29673	Anti-T ce
110	45	80.4	262	8	ADT05253	Adt05253	Anti-CD22	183	43	76.8	896	5	AAU75367	Aau75367	Diphtheri
111	45	80.4	268	2	AAW44226	Aar44226	Chimeric	184	43	76.8	896	5	AAU75366	Aau75366	Diphtheri
112	45	80.4	273	2	AAW52865	Aar52865	Anti-infl	185	43	76.8	896	5	AAU75373	Aau75373	Diphtheri
113	45	80.4	537	3	AAB03664	Aab03664	Anti-CD18	186	43	76.8	896	6	AAO29672	Aao29672	Anti-T ce
114	45	80.4	555	4	AAB19871	Aab19871	Activatin	187	43	76.8	896	6	AAO29671	Aao29671	Anti-T ce
115	45	80.4	565	4	AAB19873	Aab19873	Activatin	188	43	76.8	896	6	AAO29676	Aao29676	Anti-T ce
116	45	80.4	577	4	AAB19872	Aab19872	Activatin	189	43	76.8	896	9	ADX01023	Adx01023	Amino aci
117	45	80.4	704	4	AAB19888	Aab19888	MLV envel	190	43	76.8	899	5	AAU75375	Aau75375	Diphtheri
118	45	80.4	731	9	AEC08431	Aec08431	SCFV-2-IG	191	43	76.8	899	6	AAO29674	Aao29674	Anti-T ce
119	44	78.6	11	9	ADV21335	Adv21335	Human ant	192	42	75.0	11	3	AAU78319	Aay78319	Anti-zeta
120	44	78.6	78	4	AAU33247	Aau33247	Novel hum	193	42	75.0	11	7	ADJ74701	Adj74701	Human ant
121	44	78.6	107	9	ADV21333	Adv21333	Human ant	194	42	75.0	11	8	ADE85730	Ade85730	Human Eph
122	44	78.6	108	3	AAW52210	Aab52210	Human ant	195	42	75.0	11	8	ADL23068	Adl23068	Human Eph
123	44	78.6	139	7	ADF90904	Adf90904	Human hep	196	42	75.0	11	9	ADY32303	Ady32303	Human Eph
124	44	78.6	236	2	AAW42065	Aar42065	Human ant	197	42	75.0	11	9	AEA45031	Aea45031	Apolipop
125	44	78.6	242	9	ADV21476	Adv21476	Mature fo	198	42	75.0	11	9	AEA45020	Aea45020	Apolipop
126	44	78.6	490	9	ADV21539	Adv21539	Mature fo	199	42	75.0	11	9	AEA34925	Aea34925	Human ant
127	44	78.6	491	9	ADV21543	Adv21543	Mature fo	200	42	75.0	11	9	AEB17166	Aeb17166	EphA2-ep
128	44	78.6	495	9	ADV21517	Adv21517	Mature fo	201	42	75.0	11	9	AEA42966	Aea42966	EphA2 ant
129	44	78.6	495	9	ADV21527	Adv21527	Mature fo	202	42	75.0	107	3	AAU78326	Aay78326	Anti-zeta
130	44	78.6	497	9	ADV21497	Adv21497	Mature fo	203	42	75.0	107	3	RAY90824	Aay90824	52OC9 hyb
131	44	78.6	497	9	ADV21507	Adv21507	Mature fo	204	42	75.0	107	8	ADE85729	Ade85729	Human Eph
132	43	76.8	11	7	ADJ74697	Adj74697	Human ant	205	42	75.0	107	8	ADL23067	Adl23067	Human Eph
133	43	76.8	11	9	ADW04851	Adw04851	PAPP-A im	206	42	75.0	107	9	ADY32226	Ady32226	Human Eph
134	43	76.8	11	9	AEA45034	Aea45034	Apolipop	207	42	75.0	107	9	AEA34924	Aea34924	Human ant
135	43	76.8	11	9	AEA46107	Aea46107	Apolipop	208	42	75.0	107	9	AEB17165	Aeb17165	EphA2-ep
136	43	76.8	11	9	ABE70913	Abe70913	Toll-like	209	42	75.0	107	9	AEA2965	Aea2965	EphA2 ant
137	43	76.8	11	9	ABE72797	Abe72797	Anti-lfai	210	42	75.0	108	9	AEA45096	Aea45096	Apoe-CTD
138	43	76.8	104	2	AAW54322	Aaw54322	Anti-HIV	211	42	75.0	108	9	AEA45107	Aea45107	Apolipop
139	43	76.8	104	2	AAW01291	Aaw01291	VL region	212	42	75.0	109	2	RAY06388	Aay06388	Humanised
140	43	76.8	104	3	RAY98252	Aay98252	Anti-gp12	213	42	75.0	112	5	AAW50879	Aam50879	Anti-bovi
141	43	76.8	104	3	RAY95143	Aay95143	Anti-gp12	214	42	75.0	127	2	AAW50946	Aay50946	HNK-20 va
142	43	76.8	107	2	AAW30768	Aar30768	Murine an	215	42	75.0	243	2	AAW02280	Aaw02280	52OC9 ant
143	43	76.8	107	2	AAW30769	Aar30769	huxCD3v9,	216	42	75.0	243	2	AAW53170	Aaw53170	52OC9 ant
144	43	76.8	107	9	ABE72785	Abe72785	Anti-lfai	217	42	75.0	243	2	AAW80424	Aaw80424	52OC9 sFv
145	43	76.8	108	9	ABW45110	Aeb45110	Apolipop	218	42	75.0	243	7	ABW00716	Abw00716	52OC9 sFv
146	43	76.8	108	9	ABW70912	Aeb70912	Toll-like	219	42	75.0	243	9	ADY60808	Ady60808	52OC9 sFv
147	43	76.8	113	7	ADW28280	Adw28280	Human het	220	42	75.0	246	2	AAW39569	Aar39569	Sequence
148	43	76.8	116	9	ADW04849	Adw04849	PAPP-A im	221	42	75.0	267	4	AAU04944	Aau04944	Humanised
149	43	76.8	209	2	AAW64204	Aaw64204	Monoclon	222	42	75.0	355	2	AAW35125	Aaw35125	R. pipten
150	43	76.8	247	6	AAO27255	Aao27255	Antibody	223	42	75.0	355	2	AAW35129	Aaw35129	R. pipten
151	43	76.8	247	6	AAO27252	Aao27252	Antibody	224	42	75.0	358	2	AAW35127	Aaw35127	R. pipten
152	43	76.8	247	6	AAO27256	Aao27256	Antibody	225	42	75.0	358	2	AAW35130	Aaw35130	R. pipten
153	43	76.8	247	6	AAO27254	Aao27254	Antibody	226	42	75.0	360	2	AAW35128	Aaw35128	R. pipten
154	43	76.8	247	6	AAO27253	Aao27253	Antibody	227	42	75.0	379	2	AAW35126	Aaw35126	R. pipten
155	43	76.8	247	8	ADK42705	Adk42705	Mutant M1	228	42	75.0	409	4	AAU04945	Aau04945	Humanised
156	43	76.8	247	8	ADK42703	Adk42703	M18 scFv	229	42	75.0	532	3	AAU78328	Aay78328	Bispecifi
157	43	76.8	247	8	ADK42701	Adk42701	14B7 scFv	230	42	75.0	534	2	AAW39571	Aar39571	Sequence
158	43	76.8	247	9	ADZ79632	Adz79632	Anti-Baci	231	42	75.0	667	6	ABP97414	Abp97414	Anti-huma
159	43	76.8	247	9	ADZ79630	Adz79630	Anti-Baci	232	41	73.2	11	4	AAW52525	Aar52525	36-71 lig
160	43	76.8	247	9	ADZ79628	Adz79628	Anti-Baci	233	41	73.2	11	4	AAW63614	Aar63614	Complem
161	43	76.8	302	2	AAW60206	Aaw60206	Bispecifi	234	41	73.2	11	8	ADP47264	Adp47264	Human pho
162	43	76.8	504	7	ADD25787	Ad25787	Binding d	235	41	73.2	11	9	ADX98291	Adx98291	Human ant
163	43	76.8	504	9	ADY21738	Ady21738	Anti-CD3	236	41	73.2	74	3	AAW91020	Aay91020	Mouse OBM
164	43	76.8	555	7	ADW86039	Adw86039	Chimaeric	237	41	73.2	75	2	AAW62802	Aaw62802	Amino aci
165	43	76.8	555	8	ADW00036	Adw00036	Antibody	238	41	73.2	75	2	AAW62818	Aaw62818	Amino aci
166	43	76.8	555	9	ADY22069	Ady22069	Antibody	239	41	73.2	76	2	AAW80980	Aaw80980	Variable
167	43	76.8	601	3	ADY22137	Ady22137	Antibody	240	41	73.2	76	6	ABO04825	Abo04825	Human epi
168	43	76.8	601	6	ABW07461	Aab07461	An immuno	241	41	73.2	76	9	AEAl7737	Aeal7737	Hybridoma
169	43	76.8	601	6	ABG72265	Abg72265	Recombina	242	41	73.2	90	4	ABB19441	Abb19441	Protein #
170	43	76.8	637	5	AAU75365	Aau75365	Diphtheri	243	41	73.2					

244	41	73.2	90	4	AAW67153	AAm67153 Human bon	317	41	73.2	234	8	ADL78728	AdL78728 Albumin f
245	41	73.2	90	4	AAW54766	AAm54766 Human bra	318	41	73.2	238	2	AAW21880	AaY21880 Amino aci
246	41	73.2	90	4	ABG48819	ABg48819 Human liv	319	41	73.2	238	9	ABE45883	AeB45883 Human mon
247	41	73.2	90	4	AAW02744	AAm02744 Peptide #	320	41	73.2	240	4	AAW63665	AaY63665 Amino aci
248	41	73.2	90	5	ABG36817	ABg36817 Human pep	321	41	73.2	241	2	AAW21882	AaY21882 Amino aci
249	41	73.2	95	6	ABO27123	ABo27123 Human ger	322	41	73.2	243	8	ADN36307	ADn36307 Hamster a
250	41	73.2	95	6	ABO27124	ABo27124 Human ger	323	41	73.2	272	8	ADN19054	ADn19054 Human ant
251	41	73.2	95	6	ADN99830	ADn99830 Germline	324	41	73.2	286	8	ADN06991	ADn06991 Human BFG
252	41	73.2	95	7	ADN05434	ADn05434 Anti-MUC1	325	41	73.2	299	4	AAW63631	AaY63631 Amino aci
253	41	73.2	95	7	ADP10073	ADp10073 VEGF anti	326	41	73.2	299	4	AAW63636	AaY63636 Amino aci
254	41	73.2	95	7	ADP09968	ADp09968 Antibody	327	41	73.2	316	2	AAW83017	AaW83017 Osteoclas
255	41	73.2	95	7	ADP10176	ADp10176 Antibody	328	41	73.2	316	2	AAW83194	AaW83194 Human ost
256	41	73.2	95	7	ADP10074	ADp10074 VEGF anti	329	41	73.2	316	2	AAW59654	AaW59654 Amino aci
257	41	73.2	95	7	ADP09969	ADp09969 Antibody	330	41	73.2	316	2	AAW17874	AaY17874 Murine TR
258	41	73.2	95	7	ADP10175	ADp10175 Antibody	331	41	73.2	316	3	AAW91024	AaY91024 Mouse OM
259	41	73.2	95	7	ADP09872	ADp09872 Anti-MUC1	332	41	73.2	316	3	AAW84418	AaY84418 Amino aci
260	41	73.2	95	7	ADJ80244	ADj80244 V kappa ge	333	41	73.2	316	3	AAW84419	AaY84419 Amino aci
261	41	73.2	95	7	ADJ80243	ADj80243 V kappa ge	334	41	73.2	316	3	AAW78289	AaU78289 Mouse TRA
262	41	73.2	95	8	ADN007313	ADn007313 Human ant	335	41	73.2	316	5	ADR29338	ADr29338 Mouse RAN
263	41	73.2	95	8	ADN007312	ADn007312 Human ant	336	41	73.2	316	6	ABR42071	ABr42071 Human RAN
264	41	73.2	95	8	ADU86533	ADu86533 Immunoglo	337	41	73.2	316	6	ABU99477	ABu99477 Amino aci
265	41	73.2	95	8	ADU86534	ADu86534 Immunoglo	338	41	73.2	316	6	ABU08463	ABu08463 Amino aci
266	41	73.2	95	9	ADY75418	ADy75418 Human ger	339	41	73.2	316	6	ABR55560	ABr55560 Amino aci
267	41	73.2	95	9	ADY75417	ADy75417 Human ger	340	41	73.2	316	8	ADT08153	ADt08153 Murine RA
268	41	73.2	95	9	ABE13628	ABe13628 Human var	341	41	73.2	316	9	ADY74715	ADy74715 Murine re
269	41	73.2	95	9	ABE13576	ABe13576 Human var	342	41	73.2	316	9	ADZ12652	ADz12652 Murine ca
270	41	73.2	95	9	ABE13575	ABe13575 Human var	343	41	73.2	316	9	ADY97757	ADy97757 Mouse RAN
271	41	73.2	95	9	ABE13629	ABe13629 Human var	344	41	73.2	479	6	ADN09530	ADn09530 Hamster a
272	41	73.2	98	9	ADY31694	ADy31694 Anti-huma	345	41	73.2	502	8	ADN97515	ADn97515 Artificia
273	41	73.2	104	2	AAW62822	AAw62822 Amino aci	346	41	73.2	551	6	ABU09531	ABu09531 Hamster a
274	41	73.2	104	2	AAW62821	AAw62821 Amino aci	347	40	71.4	11	2	AAW70614	AAw70614 Anti-VEGF
275	41	73.2	104	2	AAW62821	AAw62821 Amino aci	348	40	71.4	11	4	AAW81982	AAw81982 Ganglios
276	41	73.2	104	2	AAW62804	AAw62804 Amino aci	349	40	71.4	11	5	AAE28888	AAe28888 Human KDR
277	41	73.2	105	2	AAW52231	AAw52231 Antibody	350	40	71.4	11	5	AAO17647	AAo17647 Human FAP
278	41	73.2	105	2	AAW80978	AAw80978 Kappa lig	351	40	71.4	11	5	AAO17639	AAo17639 Human FAP
279	41	73.2	105	2	AAW80964	AAw80964 Kappa lig	352	40	71.4	11	5	ABP61183	ABp61183 Humanised
280	41	73.2	105	2	AAW80968	AAw80968 Kappa lig	353	40	71.4	11	6	ABU11007	ABu11007 Modified
281	41	73.2	105	2	AAW80974	AAw80974 Kappa lig	354	40	71.4	11	6	ABJ26781	ABj26781 VEGF bind
282	41	73.2	105	6	ABO04838	ABo04838 Human epi	355	40	71.4	11	7	ADD24450	ADd24450 Human lig
283	41	73.2	105	6	ABO04842	ABo04842 Human epi	356	40	71.4	11	7	ADD80827	ADd80827 Human var
284	41	73.2	105	6	ABO04831	ABo04831 Human epi	357	40	71.4	11	8	ADK18303	ADk18303 KDR bindi
285	41	73.2	105	9	AEA17741	AeA17741 Hybridoma	358	40	71.4	11	8	ADQ17118	ADq17118 Murine an
286	41	73.2	105	9	AEA17755	AeA17755 Hybridoma	359	40	71.4	11	8	ADS52420	ADs52420 Fab targe
287	41	73.2	105	9	AEA17751	AeA17751 Hybridoma	360	40	71.4	11	9	ADZ57813	ADz57813 Ganglios
288	41	73.2	105	9	AEA17745	AeA17745 Hybridoma	361	40	71.4	11	9	AEA53832	AeA53832 Novel hum
289	41	73.2	106	8	ADP22224	ADp22224 Human ant	362	40	71.4	11	9	AEA53526	AeA53526 Novel hum
290	41	73.2	107	6	ABP59985	ABp59985 Antibody	363	40	71.4	11	9	AEA45353	AeA45353 Apolipop
291	41	73.2	107	7	ADC99797	ADc99797 Anti-huma	364	40	71.4	11	9	ABE28745	ABe28745 Human CDR
292	41	73.2	107	7	ADD05401	ADd05401 Anti-MUC1	365	40	71.4	51	2	AAW58480	AAw58480 Humanised
293	41	73.2	107	7	ADP69648	ADp69648 Humanised	366	40	71.4	51	2	AAW58481	AAw58481 Humanised
294	41	73.2	107	7	ADP09839	ADp09839 Human ant	367	40	71.4	51	2	AAW58481	AAw58481 Murine hu
295	41	73.2	107	8	ADN49402	ADn49402 Murine an	368	40	71.4	51	8	ADI01214	ADi01214 Murine hu
296	41	73.2	107	8	ADP22412	ADp22412 Human ant	369	40	71.4	51	8	ADI01215	ADi01215 Murine hu
297	41	73.2	107	9	ABE03867	ABe03867 B-CLL pha	370	40	71.4	84	8	ADU72219	ADu72219 Signal pe
298	41	73.2	107	9	ABE45976	ABe45976 Human mon	371	40	71.4	84	9	ADZ73210	ADz73210 Human inc
299	41	73.2	108	4	AAU02534	AaU02534 Anti-adip	372	40	71.4	103	7	ADP09995	ADp09995 Antibody
300	41	73.2	108	7	ADL91347	ADl91347 VL chain	373	40	71.4	103	7	ADP10099	ADp10099 VEGF anti
301	41	73.2	108	8	ADQ36374	ADq36374 Intracell	374	40	71.4	106	9	AEA48163	AeA48163 Rat anti-
302	41	73.2	108	8	ADQ75247	ADq75247 Immunoglo	375	40	71.4	106	9	ABE13715	ABe13715 Human L3
303	41	73.2	108	9	ADP86671	ADp86671 Anti-FLJ3	376	40	71.4	106	9	ABE13713	ABe13713 Human vfk
304	41	73.2	108	9	AEA45097	AeA45097 ApoB-CTD	377	40	71.4	107	2	AAW38614	AAw38614 Low-risk
305	41	73.2	109	2	AAW52040	AAw52040 Light cha	378	40	71.4	107	2	AAW41283	AAw41283 Moderate-
306	41	73.2	111	4	AAW63627	AAw63627 Amino aci	379	40	71.4	107	2	AAW54259	AAw54259 Anti-Hiv
307	41	73.2	112	7	ADD28273	ADd28273 Human het	380	40	71.4	107	2	AAW01282	AAw01282 VL region
308	41	73.2	113	7	ADD28271	ADd28271 Human het	381	40	71.4	107	2	AAW58478	AAw58478 Humanised
309	41	73.2	115	8	ADU86518	ADu86518 Immunoglo	382	40	71.4	107	2	AAW58515	AAw58515 Protein S
310	41	73.2	120	4	ABG11908	ABg11908 Novel hum	383	40	71.4	107	2	AAW86804	AAw86804 Variable
311	41	73.2	129	9	ADX98258	ADx98258 Human ant	384	40	71.4	107	2	AAW86805	AAw86805 Variable
312	41	73.2	164	7	ADP28243	ADp28243 Human het	385	40	71.4	107	2	AAW70623	AAw70623 Humanised
313	41	73.2	164	9	ADW86830	ADw86830 Bacillus	386	40	71.4	107	2	AAW70625	AAw70625 Humanised
314	41	73.2	214	8	ADK52358	ADk52358 Human ant	387	40	71.4	107	3	AAW98243	AAw98243 Anti-gp12
315	41	73.2	234	4	AAW90612	AAw90612 Human eec	388	40	71.4	107	3	AAW95134	AAw95134 Anti-gp12
316	41	73.2	234	5	ABG65461	ABg65461 Human alb	389	40	71.4	107	5	AAE28876	AAe28876 Human KDR

390	40	71.4	107	5	ABP61192	Abp61192 Humanised	463	40	71.4	119	9	AEA53306	Aea53306 Novel hum
391	40	71.4	107	5	ABP61194	Abp61194 Humanised	464	40	71.4	119	9	AEA53936	Aea53936 Novel hum
392	40	71.4	107	6	ABJ26769	Abj26769 VEGF bind	465	40	71.4	126	2	AAR29015	Aar29015 pUC-RV1-P
393	40	71.4	107	7	ADD24430	Add24430 Human lig	466	40	71.4	126	2	AAR29013	Aar29013 pUC-RVh-P
394	40	71.4	107	7	ADD80807	Add80807 Human KDR	467	40	71.4	127	2	AAR28670	Aar28670 pDM-k3 pr
395	40	71.4	107	8	AD101168	Adi01168 Murine mo	468	40	71.4	128	2	AAR33257	Aar33257 Rat immu
396	40	71.4	107	8	AD101228	Adi01228 Murine mo	469	40	71.4	128	2	AAR53340	Aar53340 KM641 H C
397	40	71.4	107	8	ADK18283	Adk18283 KDR bindi	470	40	71.4	128	2	AAY283368	Aay283368 pKM641 LA
398	40	71.4	107	8	ADL93584	Adl93584 Human CD4	471	40	71.4	128	3	AAB01628	Ab01628 Murine im
399	40	71.4	107	9	AEA40449	Aea40449 Anti-VEGF	472	40	71.4	128	4	AAB81994	Ab81994 Gangliosi
400	40	71.4	107	9	AEA40445	Aea40445 Anti-VEGF	473	40	71.4	128	4	AAB81995	Ab81995 Gangliosi
401	40	71.4	107	9	AEA40440	Aea40440 Anti-VEGF	474	40	71.4	128	4	AAB81997	Ab81997 Gangliosi
402	40	71.4	107	9	AEA40443	Aea40443 Anti-VEGF	475	40	71.4	128	4	AAB81978	Ab81978 Gangliosi
403	40	71.4	107	9	AEA40450	Aea40450 Anti-VEGF	476	40	71.4	128	4	AAB81996	Ab81996 Gangliosi
404	40	71.4	107	9	AEA40452	Aea40452 Anti-VEGF	477	40	71.4	128	4	AAB81999	Ab81999 Gangliosi
405	40	71.4	107	9	AEA40447	Aea40447 Anti-VEGF	478	40	71.4	128	4	AAB81993	Ab81993 Gangliosi
406	40	71.4	107	9	AEA40446	Aea40446 Anti-VEGF	479	40	71.4	128	4	AAB81992	Ab81992 Gangliosi
407	40	71.4	107	9	AEA40439	Aea40439 Anti-VEGF	480	40	71.4	128	4	AAB81998	Ab81998 Gangliosi
408	40	71.4	107	9	AEA40444	Aea40444 Anti-VEGF	481	40	71.4	128	6	ABU11003	Abu11003 Modified
409	40	71.4	107	9	AEA40442	Aea40442 Anti-VEGF	482	40	71.4	214	7	ADC26154	Adc26154 Parent an
410	40	71.4	107	9	AEA40451	Aea40451 Anti-VEGF	483	40	71.4	233	8	ADL93655	Adl93655 Human CD4
411	40	71.4	107	9	AEA40448	Aea40448 Anti-VEGF	484	40	71.4	237	2	AAW70703	Aaw70703 Protein e
412	40	71.4	107	9	AEA40722	Aea40722 Anti-VEGF	485	40	71.4	237	5	ABB81107	Abb81107 Anti-VEGF
413	40	71.4	107	9	AEA40441	Aea40441 Anti-VEGF	486	40	71.4	237	5	ABP51952	Abp51952 Plasmid p
414	40	71.4	108	2	AAW70620	Aaw70620 Anti-VEGF	487	40	71.4	237	8	ADO14128	Ado14128 Plasmid p
415	40	71.4	108	2	AAW70618	Aaw70618 Anti-VEGF	488	40	71.4	237	8	ADO14131	Ado14131 Plasmid p
416	40	71.4	108	2	AAW70696	Aaw70696 Anti-VEGF	489	40	71.4	237	8	ADQ90703	Adq90703 Anti-VEGF
417	40	71.4	108	4	AAB81988	Aab81988 Gangliosi	490	40	71.4	237	8	ADQ90701	Adq90701 Anti-VEGF
418	40	71.4	108	4	AAB81986	Aab81986 Gangliosi	491	40	71.4	237	8	ADQ90705	Adq90705 Anti-VEGF
419	40	71.4	108	4	AAB81990	Aab81990 Gangliosi	492	40	71.4	237	8	ADQ90723	Adq90723 Anti-VEGF
420	40	71.4	108	5	ABP61189	Abp61189 Murine an	493	40	71.4	237	8	ADQ90721	Adq90721 Anti-VEGF
421	40	71.4	108	5	ABP61265	Abp61265 Humanised	494	40	71.4	237	8	ADQ90707	Adq90707 Anti-VEGF
422	40	71.4	108	5	ABP61187	Abp61187 Humanised	495	40	71.4	237	8	ADQ90700	Adq90700 Anti-gp54
423	40	71.4	108	6	ABU11011	Abu11011 Modified	496	40	71.4	245	2	AAW26800	Aaw26800 Anti-FAPA
424	40	71.4	108	6	ABU11013	Abu11013 Modified	497	40	71.4	253	5	AAOI4057	Aaoi4057 Anti-FAPA
425	40	71.4	108	7	ADL91348	Adl91348 VL chain	498	40	71.4	255	5	AAOI4054	Aaoi4054 Anti-FAPA
426	40	71.4	108	7	ADL91349	Adl91349 VL chain	499	40	71.4	256	3	AAI55072	Aay55072 Single ch
427	40	71.4	108	8	ADG31770	Adg31770 V(L) doma	500	40	71.4	260	3	AAI55075	Aay55075 Single ch
428	40	71.4	108	8	ADG31782	Adg31782 V(L) doma	501	40	71.4	260	3	AAI55078	Aay55078 Single ch
429	40	71.4	108	8	ADG31768	Adg31768 V(L) doma	502	40	71.4	260	5	AAOI4055	Aaoi4055 Anti-FAPA
430	40	71.4	108	8	ADG31893	Adg31893 V(L) prot	503	40	71.4	272	5	AAOI4058	Aaoi4058 Anti-FAPA
431	40	71.4	108	8	ADO36375	Ado36375 Intracell	504	40	71.4	287	2	AAW96342	Aaw96342 sfVMHC-1
432	40	71.4	108	8	ADO36376	Ado36376 Intracell	505	40	71.4	367	3	AAI55079	Aay55079 Single ch
433	40	71.4	108	8	ADQ75249	Adq75249 Immunoglo	506	40	71.4	381	3	AAI55078	Aay55078 Single ch
434	40	71.4	108	8	ADQ75248	Adq75248 Immunoglo	507	40	71.4	519	3	AAI55080	Aay55080 Single ch
435	40	71.4	108	9	ADX80647	Adx80647 Humanised	508	40	71.4	546	3	AAI55074	Aay55074 Single ch
436	40	71.4	108	9	ADZ57819	Adz57819 Gangliosi	509	40	71.4	626	3	AAI55081	Aay55081 Single ch
437	40	71.4	108	9	ADZ57822	Adz57822 Gangliosi	510	40	71.4	640	3	AAI55082	Aay55082 Single ch
438	40	71.4	108	9	ADZ57823	Adz57823 Gangliosi	511	40	71.4	650	5	ABP61241	Abp61241 Phage-dis
439	40	71.4	108	9	ADZ57817	Adz57817 Gangliosi	512	39	69.6	11	2	AAW24543	Aaw24543 CDR #1 of
440	40	71.4	108	9	ADZ57820	Adz57820 Gangliosi	513	39	69.6	11	2	AAW13942	Aaw13942 CDR-1 fra
441	40	71.4	109	2	AAK13658	Aar13658 Murine OK	514	39	69.6	11	2	AAI05011	Aay05011 Tumour an
442	40	71.4	109	2	AAW26797	Aaw26797 Anti-gp54	515	39	69.6	11	2	AAI05009	Aay05009 Tumour an
443	40	71.4	109	2	AAW62050	Aaw62050 Mouse mon	516	39	69.6	11	2	AAU08346	Aau08346 Antibody
444	40	71.4	109	6	ABP72768	Abp72768 Anti-full	517	39	69.6	11	4	AAW63644	Aaw63644 Complemen
445	40	71.4	109	6	ABE21855	Aeb21855 Human DC-	518	39	69.6	11	4	AAW63641	Aaw63641 Complemen
446	40	71.4	110	2	AAW70673	Aaw70673 Anti-VEGF	519	39	69.6	11	6	ABJ38599	Abj38599 Hepatitis
447	40	71.4	110	2	AAW70677	Aaw70677 Anti-VEGF	520	39	69.6	11	6	ABJ38602	Abj38602 Hepatitis
448	40	71.4	110	2	AAW70687	Aaw70687 Anti-VEGF	521	39	69.6	11	7	ADC82740	Adc82740 CDR regio
449	40	71.4	110	2	AAW70675	Aaw70675 Anti-VEGF	522	39	69.6	11	7	ADC82736	Adc82736 CDR regio
450	40	71.4	110	3	AAW05897	Aaw05897 Humanised	523	39	69.6	11	7	ADJ74703	Adj74703 Human ant
451	40	71.4	110	3	ABJ13380	Abj13380 Anti-VEGF	524	39	69.6	11	7	ADJ74705	Adj74705 Human ant
452	40	71.4	110	3	ABJ13376	Abj13376 F(ab)-12	525	39	69.6	11	7	ADJ74705	Adj74705 Human ant
453	40	71.4	110	5	ABP61242	Abp61242 Humanised	526	39	69.6	11	9	ADZ23001	Adz23001 Human CX
454	40	71.4	110	5	ABP61256	Abp61256 Humanised	527	39	69.6	11	9	AEA53696	Aea53696 Novel hum
455	40	71.4	110	5	ABP61244	Abp61244 Humanised	528	39	69.6	11	9	AEA46059	Aea46059 Apolipop
456	40	71.4	110	5	ABP61246	Abp61246 Humanised	529	39	69.6	11	9	AEA28691	Aea28691 Human CDR
457	40	71.4	110	9	ADY96989	Ady96989 Human imm	530	39	69.6	86	2	AAW62806	Aaw62806 Amino aci
458	40	71.4	110	9	ADY96967	Ady96967 Human imm	531	39	69.6	88	3	AAW56659	Aaw56659 Partial p
459	40	71.4	111	8	ADP47307	Adp47307 Human pho	532	39	69.6	88	2	ADU04212	Adu04212 Human imm
460	40	71.4	111	8	ADP47105	Adp47105 Human pho	533	39	69.6	101	2	AAR22577	Aar22577 Light cha
461	40	71.4	118	5	AAOI4050	Aaoi4050 Human ant	534	39	69.6	103	6	ABJ18569	Abj18569 Gangliosi
462	40	71.4	118	5	AAOI4053	Aaoi4053 Humanised	535	39	69.6	105	6	ABO04827	Ab004827 Human epi

536	39	69.6	106	8	ADT55238	Amino aci	Adt55238	609	39	69.6	132	5	AAU10775	Aau10775	Light cha
537	39	69.6	107	2	AAK30770	Consensus	Aar30770	610	39	69.6	133	5	ABP62217	Abp62217	Human imm
538	39	69.6	107	2	AAK54262	Anti-HIV	Aar54262	611	39	69.6	133	6	ABG71752	Abg71752	Antibody
539	39	69.6	107	2	AAW01286	VL region	Aaw01286	612	39	69.6	166	9	ADV86831	Adv86831	Human het
540	39	69.6	107	3	AAW98247	Anti-gp12	Aay98247	613	39	69.6	166	9	ADV86831	Adv86831	Bacillus
541	39	69.6	107	3	AAW95138	Anti-gp12	Aay95138	614	39	69.6	215	4	AAU08379	Aau08379	Anti-OPGb
542	39	69.6	107	3	AAW62087	Human V1	Aab62087	615	39	69.6	240	6	ABJ38592	Abj38592	Hepatit
543	39	69.6	107	4	AAW60400	Consensus	Aab60400	616	39	69.6	241	6	ABJ38592	Abj38592	Hepatit
544	39	69.6	107	4	AAW93661	Human ant	Aag93661	617	39	69.6	241	6	ABJ38592	Abj38592	Hepatit
545	39	69.6	107	4	AAW93667	Human ant	Aag93667	618	39	69.6	248	5	ABP45349	Abp45349	Human Bly
546	39	69.6	107	4	AAW93667	Human ant	Aag93667	619	39	69.6	248	5	ABP45349	Abp45349	Human Bly
547	39	69.6	107	6	AAW61585	Human var	Aab61585	620	39	69.6	248	8	ADH34569	Adh34569	scFv SC02
548	39	69.6	107	6	ABO27474	Anti-Rh(D	Abo27474	621	39	69.6	259	4	AAW23532	Aaw23532	Human EST
549	39	69.6	107	7	ABO27468	Anti-Rh(D	Abo27468	621	39	69.6	260	5	ABP41164	Abp41164	Human ova
550	39	69.6	107	7	ADW051596	Consensus	Adw051596	622	39	69.6	299	4	AAW63657	Aaw63657	Amino aci
551	39	69.6	107	8	ADW11454	Human TAG	Adw11454	623	39	69.6	300	4	AAW63658	Aaw63658	Amino aci
552	39	69.6	107	8	ADG34381	Humanised	Adg34381	624	39	69.6	349	2	AAW12128	Aaw12128	1B1 IGG a
553	39	69.6	107	8	ADG34381	Humanised	Adg34381	625	39	69.6	401	2	AAW12129	Aaw12129	1B1 IGG a
554	39	69.6	107	8	ADJ88008	Human var	Adj88008	626	39	69.6	414	2	AAW13111	Aaw13111	1B1 IGG a
555	39	69.6	107	8	ADN12054	Variable	Adn12054	627	39	69.6	414	2	AAW13018	Aaw13018	1B1 IGG a
556	39	69.6	107	8	ADP43328	Human mon	Adp43328	628	39	69.6	444	6	ABW68088	Abw68088	Photorhab
557	39	69.6	107	9	ADW21305	Human kap	Adw21305	629	39	69.6	634	6	ABW68088	Abw68088	Photorhab
558	39	69.6	107	9	ADY34078	Anti-Tie	Ady34078	630	38	67.9	11	2	AAW99018	Aaw99018	Anti-thyr
559	39	69.6	107	9	ADY34039	Anti-Tie	Ady34039	631	38	67.9	11	3	AAW30598	Aaw30598	Human ant
560	39	69.6	107	9	ADY22999	Human CXC	Ady22999	632	38	67.9	11	7	ADJ74696	Adj74696	Human ant
561	39	69.6	108	2	AAW54258	Anti-HIV	Aaw54258	633	38	67.9	11	8	ADP47051	Adp47051	Murine 11
562	39	69.6	108	2	AAW01281	VL region	Aaw01281	634	38	67.9	11	8	ADW24438	Adw24438	HCWV-Fab
563	39	69.6	108	2	AAW70622	Human con	Aaw70622	635	38	67.9	11	9	ADV21303	Adv21303	Human ant
564	39	69.6	108	3	AAW82345	Human con	Aay82345	636	38	67.9	11	9	ADV21319	Adv21319	Human ant
565	39	69.6	108	3	AAW98242	Anti-gp12	Aay98242	637	38	67.9	11	9	ADV21351	Adv21351	Human ant
566	39	69.6	108	3	AAW95133	Anti-gp12	Aay95133	638	38	67.9	11	9	ADW04835	Adw04835	PAPP-A Im
567	39	69.6	108	5	ABP61191	Human ant	Abp61191	639	38	67.9	11	9	AEA53695	Aea53695	Novel hum
568	39	69.6	108	8	ADG38991	Human con	Adg38991	640	38	67.9	11	9	AEA5595	Aea5595	Apoliopor
569	39	69.6	108	8	ADP47107	Human pho	Adp47107	641	38	67.9	11	9	AEA45515	Aea45515	Apoliopor
570	39	69.6	108	8	ADP3366	Human sub	Adi03366	642	38	67.9	11	9	AEA46054	Aea46054	Apoliopor
571	39	69.6	108	8	ADP79572	Human kap	Adp79572	643	38	67.9	11	9	AEA46057	Aea46057	Apoliopor
572	39	69.6	109	2	AAW30764	Consensus	Aar30764	644	38	67.9	11	9	AEA45024	Aea45024	Apoliopor
573	39	69.6	109	2	AAW47041	Sequence	Aar47041	645	38	67.9	16	4	AAW66408	Aaw66408	Human Fab
574	39	69.6	109	5	AAU74544	Human sub	Aau74544	646	38	67.9	88	3	AAW56652	Aaw56652	Partial p
575	39	69.6	109	6	ADA89232	Human ant	Aad89232	647	38	67.9	95	6	ABO27125	AbO27125	Human ger
576	39	69.6	109	6	ADA89228	Human ant	Aad89228	648	38	67.9	95	6	ABO27128	AbO27128	Human ger
577	39	69.6	109	7	ADW05385	Anti-MUC1	Adw05385	649	38	67.9	95	7	ADC99834	Adc99834	Germline
578	39	69.6	109	7	ADW05385	Anti-MUC1	Adw05385	650	38	67.9	95	7	ADW05438	Adw05438	Anti-MUC1
579	39	69.6	109	7	ADP09823	Human ant	Adp09823	651	38	67.9	95	7	ADP10174	Adp10174	Antibody
580	39	69.6	109	9	ADY96965	Human imm	Ady96965	652	38	67.9	95	7	ADP09967	Adp09967	Antibody
581	39	69.6	109	9	ADY96960	Human imm	Ady96960	653	38	67.9	95	7	ADF10072	Adf10072	VEGF anti
582	39	69.6	109	9	AEA38745	Human VL	Aea38745	654	38	67.9	95	7	ADF10068	Adf10068	VEGF anti
583	39	69.6	110	5	AAE28149	Human con	Aae28149	655	38	67.9	95	7	ADP10170	Adp10170	Antibody
584	39	69.6	111	4	AAW63653	Amino aci	Aag63653	656	38	67.9	95	7	ADP09963	Adp09963	Antibody
585	39	69.6	111	6	ABJ38612	Hepatit	Abj38612	657	38	67.9	95	7	ADP09876	Adp09876	Anti-MUC1
586	39	69.6	112	4	AAW63654	Amino aci	Aag63654	658	38	67.9	95	7	ADP09876	Adp09876	Anti-MUC1
587	39	69.6	112	6	ABJ38613	Hepatit	Abj38613	659	38	67.9	95	7	ADK18909	Adk18909	Anti-huma
588	39	69.6	113	2	ADW28277	Human het	Adw28277	660	38	67.9	95	7	ADK18921	Adk18921	Anti-huma
589	39	69.6	114	2	AAW13928	Light cha	Aaw13928	661	38	67.9	95	7	ADK18911	Adk18911	Anti-huma
590	39	69.6	115	7	ADW28272	Human het	Adw28272	662	38	67.9	95	7	ADJ80248	Adj80248	Vkappa ge
591	39	69.6	120	9	AEA53330	Novel hum	Aea53330	663	38	67.9	95	7	ADJ80245	Adj80245	Vkappa ge
592	39	69.6	120	9	AEA53360	Novel hum	Aea53360	664	38	67.9	95	8	ADW07317	Adw07317	Human ant
593	39	69.6	122	2	AAW24538	Immunoglo	Aaw24538	665	38	67.9	95	8	ADO07314	Ado07314	Human ant
594	39	69.6	125	6	ABG71755	Variable	Abg71755	666	38	67.9	95	8	ADY75419	Ady75419	Human ger
595	39	69.6	125	9	ADY58503	Consensus	Ady58503	667	38	67.9	95	9	ADY75422	Ady75422	Human ger
596	39	69.6	126	2	AAW17492	Consensus	Aay17492	668	38	67.9	95	9	ABE13574	Aeb13574	Human var
597	39	69.6	126	2	AAW08704	Human lig	Aay08704	669	38	67.9	95	9	ABE13627	Aeb13627	Human var
598	39	69.6	126	2	AAW08703	Human lig	Aay08703	670	38	67.9	95	9	ABE13623	Aeb13623	Human var
599	39	69.6	126	2	AAW08701	Human con	Aay08701	671	38	67.9	95	9	ABE13570	Aeb13570	Human var
600	39	69.6	126	3	AAW83645	Conserved	Aay83645	672	38	67.9	96	7	ADK18905	Adk18905	Anti-huma
601	39	69.6	126	5	ABW04943	Human CD2	Abw04943	673	38	67.9	96	7	ADK18903	Adk18903	Anti-huma
602	39	69.6	126	5	ABW04943	Human CD2	Abw04943	674	38	67.9	96	8	ADQ17217	Adq17217	Human bof
603	39	69.6	126	6	ABG71656	Consensus	Abg71656	675	38	67.9	96	9	AEA53958	Aea53958	Novel hum
604	39	69.6	126	6	ABG71769	Variable	Abg71769	676	38	67.9	102	3	AAW71446	Aay71446	Humanised
605	39	69.6	126	7	ADW00054	Human con	Adw00054	677	38	67.9	102	3	AAW71454	Aay71454	Humanised
606	39	69.6	128	5	ABW04947	Human ant	Abw04947	678	38	67.9	102	3	ABW07183	Abw07183	CB2187 ka
607	39	69.6	129	3	AAW56724	Amino aci	Aay56724	679	38	67.9	102	6	AAE38330	Aae38330	Human ant
608	39	69.6	130	5	AAU10776	Light cha	Aau10776	680	38	67.9	102	8	ADJ26682	Adj26682	Human ant
	39	69.6	131	6	ABG71753	Antibody	Abg71753	681	38	67.9	105	2	AAW54310	Aaw54310	Anti-HIV

682	38	67.9	105	2	AAW01268	AAw01268 VL region	755	38	67.9	125	6	ABR55900	ABr55900 Human mAb
683	38	67.9	105	3	AAy71455	AAy71455 Humanised	756	38	67.9	127	6	AAE37202	AAe37202 Human AB-
684	38	67.9	105	3	AAy98229	AAy98229 Anti-gp12	757	38	67.9	127	6	AAE16219	AAe16219 Anti-huma
685	38	67.9	105	3	AAy95120	AAy95120 Anti-gp12	758	38	67.9	128	3	AAy56717	AAy56717 Amino aci
686	38	67.9	105	3	AAAB30583	AAAB30583 A variabl	759	38	67.9	136	6	ABR55901	ABr55901 Human mAb
687	38	67.9	105	8	ADW24445	ADW24445 HCMV-Fab-	760	38	67.9	211	3	AAAB30592	AAAB30592 Variable
688	38	67.9	105	2	AAAR54304	AAAR54304 Anti-HIV	761	38	67.9	213	8	ADP88495	ADp88495 Humanised
689	38	67.9	106	2	AAAR54306	AAAR54306 Anti-HIV	762	38	67.9	214	9	ADX02220	ADx02220 SARS coro
690	38	67.9	106	2	AAW01262	AAW01262 VL region	763	38	67.9	232	9	ADX39141	ADx39141 Humanized
691	38	67.9	106	3	AAy98223	AAy98223 Anti-gp12	764	38	67.9	234	9	ADX39101	ADx39101 Mouse mon
692	38	67.9	106	3	AAy98225	AAy98225 Anti-gp12	765	38	67.9	234	9	ADX39138	ADx39138 Mouse mon
693	38	67.9	106	3	AAy95116	AAy95116 Anti-gp12	766	38	67.9	235	3	AAAB30684	AAAB30684 Immunoglo
694	38	67.9	106	3	AAy95114	AAy95114 Anti-gp12	767	38	67.9	235	7	ADB72849	ADb72849 Human AAA
695	38	67.9	107	2	AAAR54303	AAAR54303 Anti-HIV	768	38	67.9	236	7	ADC64780	ADc64780 Hu-A8-1 c
696	38	67.9	107	2	AAAR54305	AAAR54305 Anti-HIV	769	38	67.9	238	9	ABEA45863	ABeA45863 Human mon
697	38	67.9	107	2	AAW01264	AAW01264 VL region	770	38	67.9	239	5	AAU90905	AAu90905 Insulin/i
698	38	67.9	107	2	AAW01261	AAW01261 VL region	771	38	67.9	239	7	ADG30447	ADg30447 Human GMB
699	38	67.9	107	2	AAW01263	AAW01263 VL region	772	38	67.9	241	5	ABP45566	ABp45566 Human Bly
700	38	67.9	107	3	AAy98222	AAy98222 Anti-gp12	773	38	67.9	241	7	ADG96393	ADg96393 Single ch
701	38	67.9	107	3	AAy98224	AAy98224 Anti-gp12	774	38	67.9	241	9	AEA22109	AEa22109 Campyloba
702	38	67.9	107	3	AAy95113	AAy95113 Anti-gp12	775	38	67.9	242	5	ABP45904	ABp45904 Human Bly
703	38	67.9	107	3	AAy95115	AAy95115 Anti-gp12	776	38	67.9	242	5	AAU90902	AAu90902 Insulin/i
704	38	67.9	107	4	AAAG93657	AAAG93657 Human ant	777	38	67.9	242	5	AAU90904	AAu90904 Insulin/i
705	38	67.9	107	6	ABO27464	ABO27464 Anti-Rh(D	778	38	67.9	242	7	ADG96731	ADg96731 Single ch
706	38	67.9	107	7	ADK18800	ADK18800 Anti-huma	779	38	67.9	243	8	ADI58047	ADi58047 Reg IV-sp
707	38	67.9	107	7	ADK18910	ADK18910 Anti-huma	780	38	67.9	244	9	ADV21474	ADv21474 Mature fo
708	38	67.9	107	7	ADK18799	ADK18799 Anti-huma	781	38	67.9	244	9	ADX39104	ADx39104 Humanized
709	38	67.9	107	7	ADK18833	ADK18833 Anti-huma	782	38	67.9	245	5	AAU90901	AAu90901 Insulin/i
710	38	67.9	107	7	ADK18608	ADK18608 Anti-huma	783	38	67.9	245	5	AAU90947	AAu90947 Insulin/i
711	38	67.9	107	7	ADK18610	ADK18610 Anti-huma	784	38	67.9	247	7	ADG98056	ADg98056 TNF proli
712	38	67.9	107	7	ADK18834	ADK18834 Anti-huma	785	38	67.9	247	8	ADE83873	ADe83873 Chemokine
713	38	67.9	107	7	ADP03946	ADP03946 Murine-ex	786	38	67.9	247	9	ADV21472	ADv21472 Mature fo
714	38	67.9	107	8	ADL22134	ADL22134 Anti-plat	787	38	67.9	248	5	ABP45435	ABp45435 Human Bly
715	38	67.9	107	8	ADL25438	ADL25438 Human mAb	788	38	67.9	248	7	ADG96262	ADg96262 Single ch
716	38	67.9	107	8	ADL25434	ADL25434 Human mAb	789	38	67.9	248	8	ADE83868	ADe83868 Chemokine
717	38	67.9	107	8	ADP22358	ADP22358 Human ant	790	38	67.9	249	5	AAU75150	AAu75150 Mature fo
718	38	67.9	107	8	ADP22400	ADP22400 Human ant	791	38	67.9	249	5	ABP45910	ABp45910 Human Bly
719	38	67.9	107	8	ADU86569	ADU86569 Immunoglo	792	38	67.9	251	5	ADG96737	ADg96737 Single ch
720	38	67.9	107	9	ADV21349	ADV21349 Human ant	793	38	67.9	251	7	ADG96737	ADg96737 Single ch
721	38	67.9	107	9	ADV21301	ADV21301 Human ant	794	38	67.9	251	8	ADI58043	ADi58043 Reg IV-sp
722	38	67.9	107	9	ADV21317	ADV21317 Human ant	795	38	67.9	251	8	ADI58059	ADi58059 Reg IV-sp
723	38	67.9	107	9	ADX39145	ADX39145 Humanized	796	38	67.9	251	9	ADW90307	ADw90307 Phage scf
724	38	67.9	108	2	AAAR54320	AAAR54320 Anti-HIV	797	38	67.9	251	9	ADX01799	ADx01799 SARS coro
725	38	67.9	108	2	AAW01288	AAW01288 VL region	798	38	67.9	318	4	AAAB82092	AAAB82092 Rat osteo
726	38	67.9	108	2	AAW15524	AAW15524 Anti-TGF	799	38	67.9	318	9	ADY74716	ADy74716 Rat recep
727	38	67.9	108	3	AAy71450	AAy71450 Humanised	800	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
728	38	67.9	108	3	AAy71445	AAy71445 Murine mo	801	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
729	38	67.9	108	3	AAy98249	AAy98249 Anti-gp12	802	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
730	38	67.9	108	3	AAy95140	AAy95140 Anti-gp12	803	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
731	38	67.9	108	3	AAy56678	AAy56678 Anti-inte	804	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
732	38	67.9	108	3	AAy56704	AAy56704 Murine an	805	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
733	38	67.9	108	7	ADK18904	ADK18904 Anti-huma	806	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
734	38	67.9	108	8	ADP46983	ADP46983 Murine li	807	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
735	38	67.9	108	8	ADP46980	ADP46980 Murine li	808	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
736	38	67.9	108	8	ADP46982	ADP46982 Murine li	809	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
737	38	67.9	108	8	ADP46984	ADP46984 Murine li	810	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
738	38	67.9	108	9	ADX01787	ADX01787 SARS coro	811	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
739	38	67.9	108	9	AEA45100	AEA45100 Apolipop	812	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
740	38	67.9	108	9	ABE21884	ABE21884 Human DC-	813	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
741	38	67.9	109	2	AAAR40956	AAAR40956 Human ger	814	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
742	38	67.9	109	4	AAAB66406	AAAB66406 Human Fab	815	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
743	38	67.9	109	9	ADY96958	ADY96958 Human imm	816	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
744	38	67.9	109	9	ADY96957	ADY96957 Human imm	817	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
745	38	67.9	109	9	ADY96992	ADY96992 Human imm	818	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
746	38	67.9	110	6	ABR40155	ABR40155 Humanised	819	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
747	38	67.9	110	6	ABR40153	ABR40153 Humanised	820	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
748	38	67.9	110	8	ADG64756	ADG64756 Humanised	821	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
749	38	67.9	110	8	ADG64754	ADG64754 Humanised	822	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
750	38	67.9	112	4	AAE06697	AAE06697 Human imm	823	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
751	38	67.9	113	7	ADD28279	ADD28279 Human het	824	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
752	38	67.9	116	9	ADW04833	ADW04833 PAPP-A im	825	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
753	38	67.9	119	9	AEA53957	AEA53957 Novel hum	826	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL
754	38	67.9	119	9	AEA53326	AEA53326 Novel hum	827	38	67.9	318	9	ADY97758	ADy97758 Rat RANKL

755	38	67.9	125	6	ABR55900	ABr55900 Human mAb	755	38	67.9	125	6	ABR55900	ABr55900 Human mAb
756	38	67.9	127	6	AAE37202	AAe37202 Human AB-	756	38	67.9	127	6	AAE37202	AAe37202 Human AB-
757	38	67.9	127	6	AAE16219	AAe16219 Anti-huma	757	38	67.9	127	6	AAE16219	AAe16219 Anti-huma
758	38	67.9	128	3	AAy56717	AAy56717 Amino aci	758	38	67.9	128	3	AAy56717	AAy56717 Amino aci
759	38	67.9	136	6	ABR55901	ABr55901 Human mAb	759	38	67.9	136	6	ABR55901	ABr55901 Human mAb
760	38	67.9	211	3	AAAB30592	AAAB30592 Variable	760	38	67.9	211	3	AAAB30592	AAAB30592 Variable
761	38	67.9	213	8	ADP88495	ADp88495 Humanised	761	38	67.9	213	8	ADP88495	ADp88495 Humanised
762	38	67.9	214	9	ADX02220	ADx02220 SARS coro	762	38	67.9	214	9	ADX02220	ADx02220 SARS coro
763	38	67.9	232	9	ADX39141	ADx39141 Humanized	763	38	67.9	232	9	ADX39141	ADx39141 Humanized
764	38	67.9	234	9	ADX39101	ADx39101 Mouse mon	764	38	67.9	234	9	ADX39101	ADx39101 Mouse mon
765	38	67.9	234	9	ADX39138	ADx39138 Mouse mon	765	38	67.9	234	9	ADX39138	ADx39138 Mouse mon
766	38	67.9	235	3	AAAB30684	AAAB30684 Immunoglo	766	38	67.9	235	3	AAAB30684	AAAB30684 Immunoglo
767	38	67.9	235	7	ADB72849	ADb72849 Human AAA	767	38	67.9	235	7	ADB72849	ADb72849 Human AAA
768	38	67.9	236	7	ADC64780	ADc64780 Hu-A8-1 c	768	38	67.9	236	7	ADC64780	ADc64780 Hu-A8-1 c
769	38	67.9	238	9	ABEA45863	ABeA45863 Human mon	769	38	67.9	238	9	ABEA45863	ABeA45863 Human mon
770	38	67.9	239	5	AAU90905	AAu90905 Insulin/i	770	38	67.9	239	5	AAU90905	AAu90905 Insulin/i
771	38	67.9	239	7	ADG30447	ADg30447 Human GMB	771	38	67.9	239	7	ADG30447	ADg30447 Human GMB
772	38	67.9	241	5	ABP45566	ABp45566 Human Bly	772	38	67.9	241	5	ABP45566	ABp45566 Human Bly
773	38	67.9											

828	37	66.1	95	7	ADFI0206	Adfi0206	Antibody	901	37	66.1	236	2	AAR14700	Aar14700	Vh-lab-Vl
829	37	66.1	95	7	ADJ80280	Adj80280	Vkappa ge	902	37	66.1	236	2	AAR14701	Aar14701	Vh-lab-Vl
830	37	66.1	95	8	ADQ07349	Adq07349	Human ant	903	37	66.1	236	2	AAR15690	Aar15690	Vl-lab-Vh
831	37	66.1	95	9	ADY75454	Ady75454	Human ger	904	37	66.1	236	7	ADD93785	Ad93785	Monoclonal
832	37	66.1	95	9	AEb13658	Aeb13658	Human var	905	37	66.1	236	9	ADW95680	Adw95680	Mouse ant
833	37	66.1	100	5	AAE23393	Aae23393	Human MOG	906	37	66.1	236	9	ADX15685	Adx15685	Mouse ant
834	37	66.1	102	4	AAW77337	Aaw77337	Human bon	907	37	66.1	237	2	AAR15691	Aar15691	Vl-lab-Vh
835	37	66.1	104	2	AAW77914	Aaw77914	Human Igb	908	37	66.1	237	3	AAy44595	Aay44595	EsCFV#125
836	37	66.1	106	9	AAW65052	Aaw65052	Human L c	909	37	66.1	237	7	ADW57549	Adw57549	Human Pro
837	37	66.1	106	9	AEA48152	Aea48152	Rat anti-l	910	37	66.1	237	7	ADD47098	Add47098	Human Pro
838	37	66.1	106	9	AEb00155	Aeb00155	Novel den	911	37	66.1	237	7	ADD48668	Add48668	Human Pro
839	37	66.1	106	9	AEb13711	Aeb13711	Human ant	912	37	66.1	238	2	AAR15692	Aar15692	Vl-lab-Vh
840	37	66.1	107	2	AAW78972	Aaw78972	Light cha	913	37	66.1	239	2	AAR15693	Aar15693	Vl-lab-Vh
841	37	66.1	107	2	AAW79247	Aaw79247	Light cha	914	37	66.1	240	6	ABJ38595	Abj38595	Hepatitib
842	37	66.1	107	2	AAW79250	Aaw79250	Light cha	915	37	66.1	243	2	AAAR14698	Aaar14698	Vl-lab-Vh
843	37	66.1	107	2	AAW27121	Aaw27121	Murine an	916	37	66.1	243	3	AAy44596	Aay44596	EsCFV#125
844	37	66.1	107	2	AAW58505	Aaw58505	H65 prote	917	37	66.1	246	4	AAAB86037	Aaab86037	Murine an
845	37	66.1	107	7	ADP03929	Adp03929	Murine-ex	918	37	66.1	252	5	AAU72863	Aau72863	P4-14 ein
846	37	66.1	107	7	ADP03926	Adp03926	Murine-ex	919	37	66.1	257	5	AAU72869	Aau72869	P5-11 ein
847	37	66.1	107	8	ADl01167	Adl01167	Murine mo	920	37	66.1	299	4	AAAG63660	Aag63660	Amino aci
848	37	66.1	107	8	ADQ06814	Adq06814	Virucidal	921	37	66.1	428	4	ABG08766	Abg08766	Novel hum
849	37	66.1	107	8	ADR73589	Adr73589	Anti-AR a	922	37	66.1	470	8	ADN24068	Adn24068	Bacterial
850	37	66.1	107	8	ADR73600	Adr73600	Humanised	923	37	66.1	499	2	AAAR07068	Aar07068	Phenol ox
851	37	66.1	107	9	AEA50163	Aea50163	Anti-CD22	924	37	66.1	499	2	AAAR07069	Aar07069	Phenol ox
852	37	66.1	107	9	AEA40458	Aea40458	Anti-VBGF	925	37	66.1	499	2	AAAR05279	Aar05279	Amino aci
853	37	66.1	107	9	AEA40460	Aea40460	Anti-VBGF	926	37	66.1	1832	5	AAU72872	Aau72872	3B10xP4-1
854	37	66.1	108	2	AAAR21310	Aaar21310	Light cha	927	37	66.1	2188	4	AAAB66467	Aaab66467	Protein e
855	37	66.1	108	3	AAy44587	Aay44587	Mouse ant	928	37	66.1	2188	4	AAAB66467	Aaab66467	Protein e
856	37	66.1	108	4	AAy44587	Aay44587	Human HIV	929	36	64.3	11	2	AAAR52526	Aar52526	3D6 light
857	37	66.1	108	8	ADl26702	Adl26702	Mouse ant	930	36	64.3	11	2	AAAR99015	Aar99015	Anti-thyr
858	37	66.1	108	8	ADQ07309	Adq07309	Human pro	931	36	64.3	11	2	AAAW27566	Aaw27566	Anti-TNF-
859	37	66.1	108	9	AEb00107	Aeb00107	Novel den	932	36	64.3	11	8	ADJ57620	Adj57620	TNFalpha
860	37	66.1	108	9	AEb00123	Aeb00123	Novel den	933	36	64.3	11	8	ADJ58751	Adj58751	Human D2E
861	37	66.1	108	9	AEC20811	Aec20811	Human var	934	36	64.3	11	8	ADO60477	Ado60477	Mouse ant
862	37	66.1	109	2	AAW18271	Aaw18271	Prp 37 li	935	36	64.3	11	9	AEA46173	Aea46173	Apolipop
863	37	66.1	109	2	AAW85910	Aaw85910	Prp 37 li	936	36	64.3	11	9	AEA45030	Aea45030	Apolipop
864	37	66.1	109	4	AAAG65862	Aag65862	Anti-Prp	937	36	64.3	11	9	AEA45190	Aea45190	Apolipop
865	37	66.1	109	5	ABP51796	Abp51796	Anti-prio	938	36	64.3	11	9	AEA40603	Aea40603	Anti-VBGF
866	37	66.1	109	6	ABU58877	Abu58877	Anti-prio	939	36	64.3	11	9	ABE24629	Abe24629	Humanized
867	37	66.1	109	8	ADJ10235	Adj10235	Murine an	940	36	64.3	106	8	ADU86527	Adu86527	Immunoglo
868	37	66.1	109	8	ABE92150	Abe92150	Human pr	941	36	64.3	17	8	ADP71369	Adp71369	CDR seque
869	37	66.1	111	4	AAAG63656	Aag63656	Amino aci	942	36	64.3	56	2	AAy02525	Aay02525	Clone bel
870	37	66.1	111	6	ABU38615	Abu38615	Hepatitib	943	36	64.3	88	3	AAy56671	Aay56671	Partial p
871	37	66.1	113	7	ADD28267	Add28267	Human het	944	36	64.3	101	2	AAy34316	Aay34316	IGG antib
872	37	66.1	113	7	ADD28266	Add28266	Human het	945	36	64.3	104	8	ADU86527	Adu86527	Immunoglo
873	37	66.1	113	7	ADD28266	Add28266	Human het	946	36	64.3	106	8	ADT89014	Adt89014	Murine pl
874	37	66.1	113	9	ADY50130	Ady50130	Endotheli	947	36	64.3	107	2	AAAR38601	Aar38601	HYH light
875	37	66.1	127	8	ADR73597	Adr73597	Anti-AR a	948	36	64.3	107	2	AAAR54319	Aar54319	Anti-HIV
876	37	66.1	127	8	ADR73605	Adr73605	HuPAR34 s	949	36	64.3	107	2	AAAR92082	Aar92082	Murine l3
877	37	66.1	128	2	AAAR09426	Aar09426	ME4 Light	950	36	64.3	107	2	AAAR92083	Aar92083	Murine l3
878	37	66.1	128	2	AAW06215	Aaw06215	MAB ME4 1	951	36	64.3	107	2	AAW01287	Aaw01287	VL region
879	37	66.1	128	2	AAW85062	Aaw85062	Mouse MB4	952	36	64.3	107	2	AAW27568	Aaw27568	Anti-TNF-
880	37	66.1	128	6	ABU58896	Abu58896	Mouse ant	953	36	64.3	107	2	AAW58482	Aaw58482	Murine HY
881	37	66.1	129	2	AAAR30880	Aar30880	pxOW2. 3/	954	36	64.3	107	2	AAW23953	Aaw23953	Chimeric
882	37	66.1	130	8	ADl26651	Adl26651	Human ant	955	36	64.3	107	2	AAW23956	Aaw23956	Mus muscu
883	37	66.1	130	8	ADQ05580	Adq05580	C. jacchu	956	36	64.3	107	3	AAy98248	Aay98248	Anti-gp12
884	37	66.1	135	3	AAy44599	Aay44599	Mouse lig	957	36	64.3	107	3	AAy95139	Aay95139	Anti-gp12
885	37	66.1	142	2	AAAR81311	Aar81311	Rat monoc	958	36	64.3	107	3	AAy90825	Aay90825	650S2 hyb
886	37	66.1	144	8	ADJ57086	Adj57086	3G4 antib	959	36	64.3	107	5	ABG31429	Abg31429	Humanised
887	37	66.1	153	8	ADJ57089	Adj57089	3G4-2BVz-	960	36	64.3	107	5	ABG31430	Abg31430	Amino aci
888	37	66.1	156	2	AAAR53807	Aar53807	F19.9 v-m	961	36	64.3	107	6	AAAO16459	Aao16459	Human ant
889	37	66.1	214	9	ADY50072	Ady50072	Endotheli	962	36	64.3	107	6	AAO23067	Aao23067	Murine K8
890	37	66.1	215	2	AAAR53803	Aar53803	FAB light	963	36	64.3	107	7	ADDC99801	Adc99801	Anti-huma
891	37	66.1	215	8	ADQ019052	Adq019052	Murine an	964	36	64.3	107	7	ADDO5405	Add05405	Anti-MUC1
892	37	66.1	228	2	AAAR14704	Aar14704	Vl-lab-Vh	965	36	64.3	107	7	ADFO9843	Adf09843	Human ant
893	37	66.1	228	2	AAAR14789	Aar14789	Vl-lab-Vh	966	36	64.3	107	8	ADl01144	Adl01144	Murine HY
894	37	66.1	235	2	AAAR14695	Aar14695	Vl-lab-Vh	967	36	64.3	107	8	ADJ57622	Adj57622	TNFalpha
895	37	66.1	235	2	AAAR14696	Aar14696	Vl-lab-Vh	968	36	64.3	107	8	ADJ57614	Adj57614	TNFalpha
896	37	66.1	235	2	AAAR14697	Aar14697	Vl-lab-Vh	969	36	64.3	107	8	ADJ58745	Adj58745	Human D2E
897	37	66.1	235	2	AAAR14694	Aar14694	Vl-lab-Vh	970	36	64.3	107	8	ADJ58753	Adj58753	Human 2SD
898	37	66.1	236	2	AAAR14702	Aar14702	Vh-lab-Vl	971	36	64.3	107	9	AEA40462	Aea40462	Anti-VBGF
899	37	66.1	236	2	AAAR14703	Aar14703	Vh-lab-Vl	972	36	64.3	107	9	AEA40457	Aea40457	Anti-VBGF
900	37	66.1	236	2	AAAR14699	Aar14699	Vh-lab-Vl	973	36	64.3	107	9	AEA40461	Aea40461	Anti-VBGF

974 36 64.3 108 8 ADO01441 Human mut
 975 36 64.3 108 8 ADO60445 Humanised
 976 36 64.3 108 8 ADO60443 Mouse ant
 977 36 64.3 108 8 ADU8526 Immunoglo
 978 36 64.3 108 8 ADU8525 Immunoglo
 979 36 64.3 108 8 ADU8524 Immunoglo
 980 36 64.3 108 9 ADY34145 Anti-lyso
 981 36 64.3 108 9 ADZ70845 Human Ig
 982 36 64.3 108 9 AEA45202 Apolipoppr
 983 36 64.3 108 9 AEA45106 ApoE-CTD
 984 36 64.3 108 9 AEB24597 Humanized
 985 36 64.3 108 9 AEB24595 Murine MA
 986 36 64.3 108 9 AEB24642 Humanized
 987 36 64.3 108 9 AEB28917 Human ant
 988 36 64.3 109 2 AAR52033 Light cha
 989 36 64.3 109 2 AAY06382 Humanised
 990 36 64.3 109 9 ADY96959 Human imm
 991 36 64.3 113 7 ADD28274 Human het
 992 36 64.3 127 6 AAE37204 Human AB-
 993 36 64.3 127 6 AAO23066 Murine K8
 994 36 64.3 127 7 ABR62342 Anti-HLA-
 995 36 64.3 127 9 AEA16223 Anti-huma
 996 36 64.3 128 3 AAY56736 Amino aci
 997 36 64.3 129 2 AAR57482 Humanised
 998 36 64.3 129 2 AAR92085 Humanised
 999 36 64.3 129 2 AAW09815 PeIB-VL34
 1000 36 64.3 129 5 ABG31444 Amino aci

ALIGNMENTS

RESULT 1
 AAW23433
 ID AAW23433 standard; peptide; 11 AA.

XX AC AAW23433;
 XX DT 23-APR-1998 (first entry)
 XX DE CDR-1 of rW12 light chain.
 XX KW Antibody; complementarity determining region; CDR; light chain; rat; CEA;
 XX KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 XX KW therapy; idiotype region.
 XX OS Rattus sp.
 XX PN WO9734636-A1.
 XX PD 25-SEP-1997.
 XX PF 19-MAR-1997; 97WO-US004696.
 XX PR 20-MAR-1996; 96US-0013708P.
 XX PA (IMMU-) IMMUNOMEDICS INC.
 XX PI Leung S, Loeman MJ, Hansen H;
 XX DR WPI; 1997-479997/44.
 XX PT Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 XX PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 XX PT stimulate immune response against cancer.

PS Claim 4; Page 30; 46pp; English.

XX This sequence represents the complementarity determining region-1 (CDR-1)
 CC of the rW12 light chain. This sequence is used in an antibody of the
 CC invention. The antibody of the invention is a chimeric or humanised anti-
 CC idiotype antibodies (cab and hab, respectively) or a fragment which
 CC specifically binds to the idiotype region of an anti-carcinoembryonic

CC antigen (CEA), where: (i) cab comprises the rW12 light (L) and heavy (H)
 CC chain variable regions, or silent mutations; and (ii) hab comprises rW12
 CC complementarity determining regions (CDR) and humanised framework (FR)
 CC regions. The hab is used as a vaccine to stimulate an immune response in
 CC a patient against cancers expressing CEA. The hab, can be used to clear
 CC non-targeted antibody in a method of diagnosis or treatment of a patient
 CC where a CEA antibody is used as a (pre-)targeting or therapy agent. The
 CC cab is used to detect the presence of an antibody that specifically binds
 CC to CEA in a sample
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 56; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00086;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYLRL 11
 Db 1 RASQDIGNYLRL 11

RESULT 2
 AAW23439
 ID AAW23439 standard; protein; 108 AA.

XX AC AAW23439;
 XX DT 23-APR-1998 (first entry)

XX Modified light chain variable region REIW12VKRS.

XX KW Antibody; complementarity determining region; heavy chain; rat; CEA;
 XX KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 XX KW therapy; idiotype region; mutein; variable region.

XX OS Synthetic.
 OS Rattus sp.

XX Key Location/Qualifiers
 FT Misc-difference 4 /note= "L to M mutation"
 FT Misc-difference 9 /note= "A to S mutation"
 FT Misc-difference 12 /note= "P to S mutation"
 FT Misc-difference 15 /note= "L to V mutation"
 FT Region 24. .34
 FT Misc-difference 39 /note= "complementarity determining region-1"
 FT Misc-difference 43 /note= "K to T mutation"
 FT Misc-difference 45 /note= "S to A mutation"
 FT Misc-difference 50. .56 /note= "R to K mutation"
 FT Region 50. .56 /note= "complementarity determining region-2"
 FT Misc-difference 72 /note= "S to T mutation"
 FT Misc-difference 73 /note= "L to F mutation"
 FT Misc-difference 76 /note= "N to S mutation"
 FT Misc-difference 79 /note= "E to Q mutation"
 FT Misc-difference 80 /note= "S to P mutation"
 FT Misc-difference 83 /note= "M to I mutation"
 FT Misc-difference 85 /note= "I to T mutation"
 FT Region 89. .97 /note= "complementarity determining region-3"

FT	Misc-difference 105	/note= "E to Q mutation"	FT	Misc-difference 12	/note= "P to S mutation"
FT	Misc-difference 106	/note= "R to I mutation"	FT	Misc-difference 15	/note= "L to V mutation"
FT			FT	Region	24. .34
XX	W09734636-A1.		FT		/note= "complementarity determining region-1"
XX	25-SEP-1997.		FT	Misc-difference 39	/note= "K to T mutation"
XX	19-MAR-1997; 97WO-US004696.		FT	Misc-difference 43	/note= "S to A mutation"
XX	20-MAR-1996; 96US-0013708P.		FT	Misc-difference 45	/note= "R to K mutation"
XX	(IMMU-) IMMUNOMEDICS INC.		FT	Region	50. .56
PA	Leung S, Loeman MJ, Hansen H;		FT	Misc-difference 66	/note= "complementarity determining region-2"
XX	WPI; 1997-479997/44.		FT	Misc-difference 69	/note= "R to G mutation"
XX			FT	Misc-difference 72	/note= "S to T mutation"
XX	Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer.		FT	Misc-difference 73	/note= "S to T mutation"
XX	Claim 8; Fig 2; 46pp; English.		FT	Misc-difference 76	/note= "L to F mutation"
XX	This sequence represents a modified version of the rat rW12 light chain variable region, designated REIW12VKRS. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotypic antibodies (cab and hab, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcinoembryonic antigen (CEA), where: (i) cab comprises the rW12 light (L) and heavy (H) chain variable regions, or silent mutations; and (ii) hab comprises rW12 complementarity determining regions (CDR) and humanised framework (FR) regions. The hab is used as a vaccine to stimulate an immune response in a patient against cancers expressing CEA. The hab, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CEA antibody is used as a (pre-)targeting or therapy agent. The cab is used to detect the presence of an antibody that specifically binds to CEA in a sample		FT	Misc-difference 79	/note= "N to S mutation"
XX	Sequence 108 AA;		FT	Misc-difference 80	/note= "E to Q mutation"
XX	Query Match 100.0%; Score 56; DB 2; Length 108;		FT	Misc-difference 83	/note= "S to P mutation"
XX	Best Local Similarity 100.0%; Pred. No. 0.01;		FT	Misc-difference 85	/note= "I to T mutation"
XX	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		FT	Region	89. .97
Qy	1 RASQDIGNYL 11		FT	Misc-difference 105	/note= "complementarity determining region-3"
Db	24 RASQDIGNYL 34		FT	Misc-difference 106	/note= "E to Q mutation"
XX			XX	Misc-difference 106	/note= "R to I mutation"
XX			XX	W09734636-A1.	
XX			XX	25-SEP-1997.	
XX			XX	19-MAR-1997; 97WO-US004696.	
XX			XX	20-MAR-1996; 96US-0013708P.	
XX			XX	(IMMU-) IMMUNOMEDICS INC.	
XX			XX	Leung S, Loeman MJ, Hansen H;	
XX			XX	WPI; 1997-479997/44.	
XX			XX	Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer.	
XX			XX	Claim 8; Fig 2; 46pp; English.	
XX			XX	This sequence represents a modified version of the rat rW12 light chain variable region, designated REIW12VKRS. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotypic antibodies (cab and hab, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcinoembryonic antigen (CEA), where: (i) cab comprises the rW12 light (L) and heavy (H) chain variable regions, or silent mutations; and (ii) hab comprises rW12 complementarity determining regions (CDR) and humanised framework (FR) regions. The hab is used as a vaccine to stimulate an immune response in a patient against cancers expressing CEA. The hab, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CEA antibody is used as a (pre-)targeting or therapy agent. The cab is used to detect the presence of an antibody that specifically binds to CEA in a sample	
XX			XX	Sequence 108 AA;	
XX			XX	Query Match 100.0%; Score 56; DB 2; Length 108;	
XX			XX	Best Local Similarity 100.0%; Pred. No. 0.01;	
XX			XX	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 RASQDIGNYL 11		XX	Misc-difference 12	/note= "P to S mutation"
Db	24 RASQDIGNYL 34		XX	Misc-difference 15	/note= "L to V mutation"
XX			XX	Region	24. .34
XX			XX		/note= "complementarity determining region-1"
XX			XX	Misc-difference 39	/note= "K to T mutation"
XX			XX	Misc-difference 43	/note= "S to A mutation"
XX			XX	Misc-difference 45	/note= "R to K mutation"
XX			XX	Region	50. .56
XX			XX	Misc-difference 66	/note= "complementarity determining region-2"
XX			XX	Misc-difference 69	/note= "R to G mutation"
XX			XX	Misc-difference 72	/note= "S to T mutation"
XX			XX	Misc-difference 73	/note= "S to T mutation"
XX			XX	Misc-difference 76	/note= "L to F mutation"
XX			XX	Misc-difference 79	/note= "N to S mutation"
XX			XX	Misc-difference 80	/note= "E to Q mutation"
XX			XX	Misc-difference 83	/note= "S to P mutation"
XX			XX	Misc-difference 85	/note= "I to T mutation"
XX			XX	Region	89. .97
XX			XX	Misc-difference 105	/note= "complementarity determining region-3"
XX			XX	Misc-difference 106	/note= "E to Q mutation"
XX			XX	Misc-difference 106	/note= "R to I mutation"
XX			XX	W09734636-A1.	
XX			XX	25-SEP-1997.	
XX			XX	19-MAR-1997; 97WO-US004696.	
XX			XX	20-MAR-1996; 96US-0013708P.	
XX			XX	(IMMU-) IMMUNOMEDICS INC.	
XX			XX	Leung S, Loeman MJ, Hansen H;	
XX			XX	WPI; 1997-479997/44.	
XX			XX	Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer.	
XX			XX	Claim 8; Fig 2; 46pp; English.	
XX			XX	This sequence represents a modified version of the rat rW12 light chain variable region, designated REIW12VK. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotypic antibodies (cab and hab, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcino	

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 56; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASQDIGNYLR 11
 |||||
 Db 24 RASQDIGNYLR 34

RESULT 4
 AAW23442
 ID AAW23442 standard; protein; 108 AA.
 XX
 AC AAW23442;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE hW12 light chain.
 XX
 KW Antibody; complementarity determining region; light chain; human; CEA;
 KW hW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 89..97
 FT /note= "complementarity determining region-3"
 FT
 FN WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 PD
 XX
 PF 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX
 XX WPI; 1997-479997/44.
 XX
 XX N-PSDB; AAT86304.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX Disclosure; Fig 4; 46pp; English.
 XX
 XX This sequence represents the human hW12 light chain. This sequence is
 CC used in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotype antibodies (cAb and hAb,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb
 CC comprises the hW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises hW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cAb is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample
 XX
 XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASQDIGNYLR 11
 |||||
 Db 24 RASQDIGNYLR 34

RESULT 5
 AAW23436
 ID AAW23436 standard; protein; 108 AA.
 XX
 AC AAW23436;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE rW12 light chain.
 XX
 KW Antibody; complementarity determining region; light chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 88..97
 FT /note= "complementarity determining region-3"
 FT
 FN WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 PD
 XX
 PF 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX
 XX WPI; 1997-479997/44.
 XX
 XX N-PSDB; AAT86287.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.
 XX
 XX Claim 6; Fig 7; 46pp; English.
 XX
 XX This sequence represents the rat rW12 light chain. This sequence is used
 CC in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotype antibodies (cAb and hAb,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb
 CC comprises the rW12 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hAb comprises rW12 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hAb is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hAb, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cAb is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample
 XX
 XX Sequence 108 AA;

Query Match 100.0%; Score 56; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11
 DB 24 RASQDIGNYL 34

RESULT 6
 ABG76532
 ID ABG76532 standard; protein; 106 AA.
 XX AC ABG76532;
 DT 05-NOV-2002 (first entry)
 XX HCV E1 antigen monoclonal antibody #20.
 DE Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 KW Homo sapiens.
 OS WO200260954-A1.
 XX PN 08-AUG-2002.
 XX PD 14-JAN-2002; 2002WO-SE000044.
 XX PF 12-JAN-2001; 2001US-0260889P.
 XX PR (KARO-) KAROLINSKA INNOVATIONS AB.
 PA Drakenberg K, Persson MAA;
 XX WPI; 2002-608502/65.
 DR Vaccine comprising a human monoclonal antibody against hepatitis C virus
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 XX Disclosure; Page 32; 64pp; English.
 CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX Sequence 106 AA;
 SQ

Query Match 83.9%; Score 47; DB 5; Length 106;
 Best Local Similarity 90.0%; Pred. No. 0.56;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 23 RASQDIGNYL 32

RESULT 7
 AAY94220
 ID AAY94220 standard; peptide; 11 AA.
 XX AC AAY94220;
 XX DT 08-AUG-2000 (first entry)
 XX DE Murine 16E10 light chain complementarily determining region 1.
 KW Antibody; RHAMM; receptor for hyaluronic acid mediated motility;
 KW ras-dependent proliferation; leukaemia; cancer; lymphoma;

KW inflammatory disease; proliferative disease; psoriasis;
 KW inflammatory bowel disease; rheumatoid arthritis;
 KW proliferative cardiovascular disease; restenosis;
 KW proliferative ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; tumour formation; light chain;
 KW variable region; 16E10; CDR1; complementarily determining region 1.
 XX Mus musculus.
 OS WO200029447-A1.
 XX PN 25-MAY-2000.
 XX PD 19-NOV-1999; 99WO-US027565.
 PF 19-NOV-1998; 98US-0109041P.
 PR 14-JUL-1999; 99US-0143692P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Abrahamsen JA, Holmes SD, Jackson JR;
 PI WPI; 2000-387752/33.
 XX DR Antibodies against receptor for hyaluronic acid mediated motility, useful
 PT for treating or preventing proliferative diseases, e.g. cancer or
 PT cardiovascular disease.
 XX Claim 23; Page 35; 39pp; English.
 PS The present sequence is the amino acid sequence for the murine 16E10
 CC light chain complementarily determining region 1. This forms part of the
 CC monoclonal antibody 16E10, which can be used against the receptor for
 CC hyaluronic acid mediated motility (RHAMM). RHAMM is required for ras-
 CC transformation of cells, which leads to tumour formation, and so the
 CC antibody can be used to treat proliferative disorders such as leukaemias,
 CC solid tumour cancers and metastases including lymphomas, soft tissue,
 CC brain, oesophageal, stomach, pancreatic, liver, lung, bladder, bone,
 CC prostate, ovarian, cervical, uterine, skin, breast, testicular, kidney,
 CC head and neck and colon cancers, chronic inflammatory diseases such as
 CC psoriasis, inflammatory bowel disease and rheumatoid arthritis,
 CC proliferative cardiovascular diseases such as restenosis, proliferative
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas
 XX Sequence 11 AA;
 SQ

Query Match 80.4%; Score 45; DB 3; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 1 RASQDIGNYL 10

RESULT 8
 ABJ18553
 ID ABJ18553 standard; peptide; 11 AA.
 XX AC ABJ18553;
 XX DT 18-FEB-2003 (first entry)
 XX DE Ganglioside-associated recombinant antibody peptide region #18.
 KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
 KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
 KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
 KW sarcoma; neuroectodermal.
 XX Homo sapiens.
 OS

XX WO200281496-A2.
 XX 17-OCT-2002.
 PD
 XX
 XX 08-APR-2002; 2002WO-CU0000003.
 XX
 XX 06-APR-2001; 2001CU-00000084.
 XX
 XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 XX (DRIO/) MATEO DE ACOSTA DEL RIO C M.
 PA (VALL/) LOMBARDEO VALLADARES J.
 PA (NAVA/) ROQUE NAVARRO L T.
 PA (REQU/) LOPEZ REQUENA A.
 XX
 XX Mateo De Acosta Del Rio CM, Lombardero Valladares J;
 PI Roque Navarro LT, Lopez Requena A;
 XX
 XX WPI; 2003-046857/04.
 DR
 XX New chimeric antibodies, useful for treatment, prevention and diagnosis
 PT of tumors that express gangliosides, are derived from monoclonal
 PT antibodies P3 or 1E10.
 XX
 XX Claim 9; Page 22; 31pp; Spanish.
 PS
 XX The invention relates to a chimeric antibody, derived from a monoclonal
 CC antibody, which recognises N-glycosylated gangliosides and is produced by
 CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
 CC derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used
 CC for treatment, localisation and in vivo identification of breast cancer
 CC and melanoma, their metastases and relapses, tumours of lung, digestive
 CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
 CC This sequence represents a peptide region of an antibody of the invention
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 80.4%; Score 45; DB 6; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RASQDIGNYL 10
 DB 1 RASQDISNYL 10
 |||||
 |||||
 RESULT 9
 ADJ74691
 ID ADJ74691 standard; peptide; 11 AA.
 XX
 XX ADJ74691;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Human antibody mutant #2 generated by nucleic acid altering method.
 DE
 XX cleavage-directing oligonucleotide; antibody; MUC1; mutant; mutein.
 KW
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX WO2003035842-A2.
 PN
 XX 01-MAY-2003.
 PD
 XX
 XX 24-OCT-2002; 2002WO-US034249.
 PF
 XX
 XX 24-OCT-2001; 2001US-0343954P.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 XX Hoogenboom HRJM, Somers V;
 PI

DR WPI; 2003-482047/45.
 XX
 XX Altering a nucleic acid strand by extending or ligating an annealed
 PT oligonucleotide of the subset to form an altered nucleic acid strand.
 PT
 XX Disclosure; SEQ ID NO 47; 180pp; English.
 PS
 XX The invention relates to a method of altering a nucleic acid (NA) strand
 CC comprising: (i) providing template NA strand and diverse NA; (ii)
 CC annealing a cleavage-directing oligonucleotide (ON) to each of the
 CC diverse NA; (iii) cleaving each diverse NA to form diversity ON; (iv)
 CC combining the diversity ON and the template NA strand; (v) annealing the
 CC diversity ON to the template NA strand; and (vi) extending and/or
 CC ligating an annealed ON to form an altered NA strand. The method is
 CC useful for altering a nucleic acid strand. In an example of the
 CC invention, the method is used to generate mutants and variations in the
 CC amino acid sequence of the CDR's from human antibodies. This sequence
 CC corresponds to one such mutant.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 80.4%; Score 45; DB 7; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RASQDIGNYL 10
 DB 1 RASQDISNYL 10
 |||||
 |||||
 RESULT 10
 ADP47046
 ID ADP47046 standard; peptide; 11 AA.
 XX
 XX ADP47046;
 AC
 XX 09-SEP-2004 (first entry)
 DT
 XX Murine light chain variable anti-amphetamine CDR1 peptide SeqID 102.
 DE
 XX murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine;
 KW PCP; drug addiction; antiaddictive; antibody therapy.
 XX
 XX Mus musculus.
 OS
 XX WO2004050032-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX 02-DEC-2003; 2003WO-US038384.
 XX
 XX 02-DEC-2002; 2002US-0430717P.
 PR
 XX (ABGE-) ABGENIX INC.
 XX
 XX Owens SM, Carroll FI, Abraham P, Gunnell MG, Haak-Frendscho M;
 PI Peng X;
 PI
 XX WPI; 2004-460981/43.
 DR
 XX New isolated antibody or its binding fragment that binds specifically to
 PT a drug of abuse, useful for treating a patient suffering from addiction
 PT to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 PT
 XX Example 1; SEQ ID NO 102; 88pp; English.
 PS
 XX This invention relates to novel antibodies, or binding fragments thereof,
 CC that bind directly to various drugs of abuse. Specifically, it refers to
 CC human or chimeric monoclonal antibodies that are capable of binding to
 CC amphetamine, methamphetamine or phencyclidine (PCP). The present
 CC invention describes generating hybridoma cell lines that produce such
 CC antibodies and transforming a cell with a gene encoding the antibody,
 CC which when conjugated to a therapeutic agent, toxin or radioisotope can

CC be used to treat a patient suffering from a drug addiction. Accordingly,
 CC these compositions exhibit antiaddictive activities and can be used for
 CC antibody therapy to treat patients suffering from a drug addiction. This
 CC peptide sequence is the CDR1 peptide of a murine light chain variable
 CC anti-amphetamine antibody of the invention.

XX SQ Sequence 11 AA;

Query Match 80.4%; Score 45; DB 8; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 DB 1 RASQDISNYL 10

RESULT 11

ID ADU38479
 ADU38479 standard; peptide; 11 AA.

XX AC

XX ADU38479;
 27-JAN-2005 (first entry)

XX DE Mouse antibody 14F7-derived single chain antibody #2 CDR1.

XX KW cytostatic; angiogenesis inhibitor; antibody engineering; antibody;
 KW hybridoma; complementarity determining region; ganglioside; angiogenesis;
 KW melanoma; neoplasm.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO2004094477-A1.

XX PD 04-NOV-2004.

XX PF 22-APR-2004; 2004WO-CU0000006.

XX PR 23-APR-2003; 2003CU-00000092.

XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.

XX PI Roque Navarro LT, Mateo De Acosta Del Rio CM, Rodriguez Gonzalez M;
 PI Rojas Dorantes G, Talavera Perez A, Moreno Frias E;

XX DR WPI; 2004-775911/76.

XX PT New recombinant antibody derived from murine antibody 14F7, useful for
 PT treatment and detection of malignant tumors, is specific for the
 PT ganglioside N-glycolyl-GM3, has reduced immunogenicity.

PS Claim 12; Page 25; 54pp; Spanish.

CC The invention relates to a recombinant antibody (rAb), derived from the
 CC murine monoclonal antibody 14F7 (produced by hybridoma ECACC 98101901),
 CC in which the complementarity determining regions (CDR) have the following
 CC sequences: heavy chain: CDR1, Ser-Tyr-Trp-Ile-His; CDR2, Tyr-Ile-Asp-Pro-
 CC Ala-Thr-Ala-Tyr-Thr-Glu-Ser-Asn-Gln-Lys-Phe-Lys-Asp; CDR3, Glu-Ser-Pro-
 CC Arg-Leu-Arg-Arg-Gly-Ile(Tyr) 3 Ala-Met-Asp-Tyr; light chain: CDR1, Arg-
 CC Ala-Ser-Gln-Ser-Ile-Ser-Asn-Gln-Lys-His; CDR2, Tyr-Ala-Ser-Gln-Ser-Ile-
 CC Ser; CDR3, Gln-Gln-Ser-Asn-Arg-Tyr-Pro-Leu-Thr. The rAb and its
 CC derivatives recognize specifically the ganglioside N-glycolyl-GM3, so
 CC inhibit angiogenesis. The rAb, and derived single-chain Fv fragments, are
 CC used, when labelled with a radioisotope, for treatment of malignant
 CC tumors (especially of the breast, or melanomas), including metastases and
 CC relapses; also when appropriately labelled, they are useful for in vivo
 CC localization and detection of tumors. The rAb and its derivatives are
 CC less immunogenic in humans than 14F7 itself. This sequence corresponds to
 CC the mutated complementarity determining region 1 derived from the mouse
 CC antibody 14F7 and used to generate the antibody of the invention.

XX

SQ Sequence 11 AA;

Query Match 80.4%; Score 45; DB 8; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 DB 1 RASQDISNYL 10

RESULT 12

ID ADW04827
 ADW04827 standard; peptide; 11 AA.

XX AC

XX ADW04827;

XX DT 07-APR-2005 (first entry)

XX DE PAPP-A immunoglobulin variable domain AB b05 light chain CDR1 SEQ ID 152.

XX KW Cytostatic; Vasotropic; Light chain variable domain;
 KW proliferative disorder; restenosis; glioblastoma; osteosarcoma.

XX OS Unidentified.

XX FN US2005009136-A1.

XX PD 13-JAN-2005.

XX PF 19-FEB-2004; 2004US-00783311.

XX PR 19-FEB-2003; 2003US-0448515P.

XX PA (DYAX-) DYAX CORP.

XX PI Nixon A, Hogan S;

XX DR WPI; 2005-080519/09.

XX PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.

XX Example; SEQ ID NO 152; 168pp; English.

CC The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.

SQ Sequence 11 AA;

Query Match 80.4%; Score 45; DB 9; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 DB 1 RASQDISNYL 10

RESULT 13

ID ADZ47744
 ADZ47744 standard; protein; 95 AA.

XX

ADZ47744;
 30-JUN-2005 (first entry)
 Human germline kappa light chain variable region VK-1 O18/O8.
 Drug screening; antibody identification; cell signaling; inflammation;
 antiinflammatory; antibody engineering; humanized antibody;
 light chain variable region.
 Homo sapiens.
 US2005084493-A1.
 21-APR-2005.
 09-NOV-2004; 2004US-00985299.
 27-OCT-2000; 2000US-0244118P.
 29-OCT-2001; 2001US-00011931.
 (AMGE-) AMGEN INC.
 Witte A, Varnum BC, Qian X, Vezina C;
 WPI; 2005-313939/32.
 Screening antibodies and other selective interleukin-1 IL-1 binding
 agents that bind to IL-1 receptor, by detecting binding of IL-lalpa/IL-
 lbeta to IL-1R1 in presence of test agent and selecting agent that
 decreases IL-1 activity.
 Example 2; Fig 6A; 55pp; English.
 The invention relates to methods of screening for antibodies or other
 agents which selectively bind to the pro-inflammatory cytokine
 interleukin-1 (IL-1) to form an antagonist complex which can still bind
 to IL-1 receptor type I (IL-1R1) but which cannot activate it. The agents
 identified using the methods act by blocking the recruitment of the IL-1
 receptor accessory protein (IL-IRACP) by the IL-1/IL-1R1 complex,
 preventing IL-1 signaling and thereby reducing inflammatory responses.
 One screening method of the invention involves detecting the binding of
 IL-lalpa or IL-lbета to IL-1R1 in the presence of a test agent,
 detecting IL-1R1 activity in cells comprising IL-1R1 and IL-lalpa or IL-
 lbeta, and selecting the test agent which allows IL-lalpa or IL-lbета to
 bind to IL-1R1 but which decreases IL-1 activity. A second method
 involves detecting the binding of IL-IRACP to IL-1R1 in the presence of
 IL-lalpa or IL-lbета and a test agent, and selecting the test agent
 whose presence correlates with decreased binding to IL-IRACP to IL-1R1.
 The methods are useful for screening for antibodies and other selective
 IL-1 binding agents which can be used in the treatment of a variety of
 acute and chronic IL-1-mediated diseases (including rheumatoid arthritis,
 Alzheimer's disease, acute pancreatitis, diabetes, graft-versus-host
 disease, osteoporosis, Parkinson's disease, psoriasis, septic shock, and
 uveitis), or an inflammatory condition resulting from trauma, cartilage
 damage, surgery or infection. An example of the invention describes the
 construction of DNA encoding the kappa light chain variable region (VL)
 of a humanized (CDR-grafted) version of the murine anti-IL-lbета
 monoclonal antibody, MAB201, which is capable of blocking the formation
 of the IL-lbета/IL-1 receptor/IL-IRACP complex. The constructed DNA
 encodes a VL (ADZ47745) comprising the Kabat-defined CDRs
 (complementarity-determining regions) of the murine MAB201 VL (ADZ47655,
 ADZ47742), framework regions derived from the human germline kappa light
 chain variable regions VK-1 A20 (ADZ47743) and VK-1 O18/O8 (ADZ47744) and
 the human light chain joining region JK1 (ADZ47746). The present sequence
 represents the human germline kappa VL VK-1 O18/O8 used in the design of
 the humanized MAB201 VL.
 Sequence 95 AA;
 Query Match 80.4%; Score 45; DB 9; Length 95;
 Best Local Similarity 90.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASODIGNYL 10
 DB ||||| ||||
 24 RASODISNYL 33
 RESULT 14
 ADZ47743
 ID ADZ47743 standard; protein; 95 AA.
 XX AC ADZ47743;
 XX XX 30-JUN-2005 (first entry)
 XX DE Human germline kappa light chain variable region VK-1 A20.
 XX XX Drug screening; antibody identification; cell signaling; inflammation;
 KW antiinflammatory; antibody engineering; humanized antibody;
 KW light chain variable region.
 XX OS Homo sapiens.
 XX XX US2005084493-A1.
 XX XX 21-APR-2005.
 XX XX 09-NOV-2004; 2004US-00985299.
 XX XX 27-OCT-2000; 2000US-0244118P.
 PR 29-OCT-2001; 2001US-00011931.
 XX XX (AMGE-) AMGEN INC.
 XX XX Witte A, Varnum BC, Qian X, Vezina C;
 XX WPI; 2005-313939/32.
 XX Screening antibodies and other selective interleukin-1 IL-1 binding
 PT agents that bind to IL-1 receptor, by detecting binding of IL-lalpa/IL-
 PT lbeta to IL-1R1 in presence of test agent and selecting agent that
 XX decreases IL-1 activity.
 PS Example 2; Fig 6A; 55pp; English.
 XX The invention relates to methods of screening for antibodies or other
 CC agents which selectively bind to the pro-inflammatory cytokine
 CC interleukin-1 (IL-1) to form an antagonist complex which can still bind
 CC to IL-1 receptor type I (IL-1R1) but which cannot activate it. The agents
 CC identified using the methods act by blocking the recruitment of the IL-1
 CC receptor accessory protein (IL-IRACP) by the IL-1/IL-1R1 complex,
 CC preventing IL-1 signaling and thereby reducing inflammatory responses.
 CC One screening method of the invention involves detecting the binding of
 CC IL-lalpa or IL-lbета to IL-1R1 in the presence of a test agent,
 CC detecting IL-1R1 activity in cells comprising IL-1R1 and IL-lalpa or IL-
 CC lbeta, and selecting the test agent which allows IL-lalpa or IL-lbета to
 CC bind to IL-1R1 but which decreases IL-1 activity. A second method
 CC involves detecting the binding of IL-IRACP to IL-1R1 in the presence of
 CC IL-lalpa or IL-lbета and a test agent, and selecting the test agent
 CC whose presence correlates with decreased binding to IL-IRACP to IL-1R1.
 CC The methods are useful for screening for antibodies and other selective
 CC IL-1 binding agents which can be used in the treatment of a variety of
 CC acute and chronic IL-1-mediated diseases (including rheumatoid arthritis,
 CC Alzheimer's disease, acute pancreatitis, diabetes, graft-versus-host
 CC disease, osteoporosis, Parkinson's disease, psoriasis, septic shock, and
 CC uveitis), or an inflammatory condition resulting from trauma, cartilage
 CC damage, surgery or infection. An example of the invention describes the
 CC construction of DNA encoding the kappa light chain variable region (VL)
 CC of a humanized (CDR-grafted) version of the murine anti-IL-lbета
 CC monoclonal antibody, MAB201, which is capable of blocking the formation
 CC of the IL-lbета/IL-1 receptor/IL-IRACP complex. The constructed DNA
 CC encodes a VL (ADZ47745) comprising the Kabat-defined CDRs
 CC (complementarity-determining regions) of the murine MAB201 VL (ADZ47655,
 CC ADZ47742), framework regions derived from the human germline kappa light
 CC chain variable regions VK-1 A20 (ADZ47743) and VK-1 O18/O8 (ADZ47744) and
 CC the human light chain joining region JK1 (ADZ47746). The present sequence
 CC represents the human germline kappa VL VK-1 O18/O8 used in the design of
 CC the humanized MAB201 VL.

CC chain variable regions VK-1 A20 (ADZ47743) and VK-1 O18/O8 (ADZ47744) and
 CC the human light chain joining region JK1 (ADZ47746). The present sequence
 CC represents the human germline kappa VL VK-1 A20 used in the design of the
 CC humanized MAB201 VL.

SQ Sequence 95 AA;

Query Match 80.4%; Score 45; DB 9; Length 95;
 Best Local Similarity 90.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33

RESULT 15
 AAW49812
 ID AAW49812 standard; protein; 107 AA.

XX AAW49812;
 AC
 DT 25-MAR-2003 (revised)
 DT 24-SEP-1998 (first entry)
 XX

DE Amino acid sequence of the mouse antibody C4G1 mature light chain.

XX Light chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
 KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
 KW cancer; acute myocardial infarction; unstable angina; stroke;
 KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
 KW extracorporeal cardiopulmonary circulation.

XX Mus sp.

XX Key Location/Qualifiers
 FT Domain 24. .34
 FT /note= "complementarity determining region"
 FT Domain 50. .56
 FT /note= "complementarity determining region"
 FT Domain 89. .97
 FT /note= "complementarity determining region"

XX US5777085-A.

XX 07-JUL-1998.

XX 17-MAY-1995; 95US-00458516.

XX 20-DEC-1991; 91US-00812111.
 PR 09-JUN-1992; 92US-00895952.
 PR 11-SEP-1992; 92US-00944159.
 PR 03-MAY-1993; 93US-00059159.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX Tso JY, Co MS;

XX WPI; 1998-398136/34.

XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
 FT C4G1 antibody, used for inhibiting platelet aggregation for treating
 PT cardiovascular and thromboembolic disorders.

XX Claim 1; Fig 5A; 35pp; English.

XX This is the amino acid sequence of the humanised antibody C4G1 light
 CC chain, used in the method of the invention involving the creation of a
 CC humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody. The
 CC humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
 CC aggregation and also the releasing reaction of platelets. The Ig can be
 CC used for treating cardiovascular diseases and thromboembolic disorders,

CC e.g. acute myocardial infarction, unstable angina, stroke, transient
 CC ischemic episodes, deep vein thrombosis and pulmonary embolism,
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
 CC diagnosing the presence and location of a thrombus, or certain types of
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
 CC detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
 CC 25-MAR-2003 to correct PA field.)

SQ Sequence 107 AA;

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDINNYL 33

RESULT 16
 AAW49811
 ID AAW49811 standard; protein; 107 AA.

XX AAW49811;
 AC
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 24-SEP-1998 (first entry)
 XX

DE Amino acid sequence of the humanised antibody C4G1 mature light chain.
 XX Humanised antibody C4G1; light chain; humanised; immunoglobulin; Ig;
 KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.

XX Mus sp.

XX Homo sapiens.

XX Chimeric.

XX Key Location/Qualifiers
 FT Domain 24. .34
 FT /note= "complementarity determining region"
 FT Domain 50. .56
 FT /note= "complementarity determining region"
 FT Domain 89. .97
 FT /note= "complementarity determining region"

XX US5777085-A.

XX 07-JUL-1998.

XX 17-MAY-1995; 95US-00458516.

XX 20-DEC-1991; 91US-00812111.
 PR 09-JUN-1992; 92US-00895952.
 PR 11-SEP-1992; 92US-00944159.
 PR 03-MAY-1993; 93US-00059159.

XX (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX Tso JY, Co MS;

XX WPI; 1998-398136/34.

XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
 FT C4G1 antibody, used for inhibiting platelet aggregation for treating
 PT cardiovascular and thromboembolic disorders.

XX Claim 2; Fig 5A; 35pp; English.

CC This is the amino acid sequence of the humanised antibody C4G1 light
 CC chain, used in the method of the invention involving the creation of a
 CC humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody. The
 CC humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
 CC aggregation and also the releasing reaction of platelets. The Ig can be
 CC used for treating cardiovascular diseases and thromboembolic disorders,
 CC e.g. acute myocardial infarction, unstable angina, stroke, transient
 CC ischemic episodes, deep vein thrombosis and pulmonary embolism.
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
 CC diagnosing the presence and location of a thrombus, or certain types of
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
 CC detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 17-OCT-2003 to standardise
 CC OS field)

XX SQ Sequence 107 AA;

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| |||
 Db 24 RASQDINNYL 33

RESULT 17

AAW66098
 ID AAW66098 standard; protein; 107 AA.

XX AC AAW66098;

DT 10-DEC-1998 (first entry)

XX anti-CD22 monoclonal antibody light chain variable region.

XX anti-CD22 monoclonal antibody light chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; Immunodiagnosis; RFB4 IgG.

XX OS Mammalia.

XX PN WO9841641-A1.

XX FD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US005453.

XX PR 20-MAR-1997; 97US-0041437P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX FI Fitzgerald D, Pastan I, Mansfield E, Kreitman R;

XX WPI; 1998-521227/44.

XX N-PSDB; RAV07641.

XX Recombinant anti-CD22 antibodies and immuno-conjugates - of antibodies
 PT linked to a therapeutic agent, e.g. Pseudomonas exotoxin or a label; for
 PT inhibiting malignant B-cells.

XX Claim 6; Fig 1; 71pp; English.

XX The invention claims for a recombinant immunoconjugate comprising of a
 CC therapeutic agent (e.g Pseudomonas exotoxin) or a detectable label
 CC peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG) having a
 CC variable heavy (VH; AAW66099) chain with a cysteine residue at amino acid
 CC 44 and the present variable light (VL) chain with a cysteine residue at
 CC amino acid 100. The immunoconjugate is claimed to inhibit the growth of
 CC malignant B-cells in vivo, such as rodent, canine or primate B-cells. The
 CC anti-CD22 antibody is claimed useful for detecting CD22 protein in a
 CC sample or in vivo in a mammal, and can be used in diagnostic kits

SQ Sequence 107 AA;

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| |||
 Db 24 RASQDISNYL 33

RESULT 18

ABJ18571
 ID ABJ18571 standard; protein; 107 AA.

XX AC ABJ18571;

XX 18-FEB-2003 (first entry)

XX Ganglioside-associated recombinant antibody related VklE10 protein.

XX Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
 KW N-glycosylated ganglioside; anti-idiotypic monoclonal IE10; metastatic;
 KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
 KW sarcoma; neuroectodermal.

XX OS Unidentified.

XX PN WO200281496-A2.

XX PD 17-OCT-2002.

XX PF 08-APR-2002; 2002WO-CU0000003.

XX PR 06-APR-2001; 2001CU-00000084.

XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
 PA (VALL/) LOMBARDERO VALLADARES J.
 PA (NAVA/) ROQUE NAVARRO L T.
 PA (REQU/) LOPEZ REQUENA A.

XX Mateo De Acosta Del Rio CM, Lombardero Valladares J;
 PI Roque Navarro LT, Lopez Requena A;

XX WPI; 2003-0468857/04.
 DR N-PSDB; ABT14041.

XX New chimeric antibodies, useful for treatment, prevention and diagnosis
 PT of tumors that express gangliosides, are derived from monoclonal
 PT antibodies P3 or IE10.

XX Example 6; Fig 7; 3lpp; Spanish.

XX The invention relates to a chimeric antibody, derived from a monoclonal
 CC antibody, which recognises N-glycosylated gangliosides and is produced by
 CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
 CC derived from the anti-idiotypic monoclonal IE10 (recognising P3) are used
 CC for treatment, localisation and in vivo identification of breast cancer
 CC and melanoma, their metastases and relapses, tumours of lung, digestive
 CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
 CC This sequence represents a protein relating to the chimeric antibody of
 CC the invention

XX SQ Sequence 107 AA;

Query Match 80.4%; Score 45; DB 6; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| |||
 Db 24 RASQDISNYL 33

RESULT 19
ABJ18574
ID ABJ18574 standard; protein; 107 AA.
XX AC ABJ18574;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related VKI1E10 protein #2.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
KW N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
KW breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
KW sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
PA (VALL/) LOMBARDEO VALLADARES J.
PA (NAVA/) ROQUE NAVARRO L T.
PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
PI Roque Navarro LT, Lopez Requena A;
XX DR WPI; 2003-046857/04.
XX PT New chimeric antibodies, useful for treatment, prevention and diagnosis
PT of tumors that express gangliosides, are derived from monoclonal
PT antibodies P3 or 1E10.
XX PS Example 6; Fig 9; 3lpp; Spanish.
XX CC The invention relates to a chimeric antibody, derived from a monoclonal
CC antibody, which recognises N-glycosylated gangliosides and is produced by
CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
CC derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used
CC for treatment, localisation and in vivo identification of breast cancer
CC and melanoma, their metastases and relapses, tumours of lung, digestive
CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
CC This sequence represents a protein relating to the chimeric antibody of
CC the invention
XX SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 6; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASQDIGNYL 10
DB 24 RASQDISNYL 33
RESULT 20
ABR55867
ID ABR55867 standard; protein; 107 AA.
XX AC ABR55867;
XX DT 02-SEP-2003 (first entry)
XX

DE Anti-glycoprotein Iib/Iiia MAb mature light chain variable region.
XX Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW glycoprotein Iib/Iiia; monoclonal antibody; human; antibody.
XX OS Mus musculus.
XX PN WO2003031464-A2.
XX PD 17-APR-2003.
XX PF 09-OCT-2002; 2002WO-US032263.
XX PR 10-OCT-2001; 2001US-0328523P.
PR 19-OCT-2001; 2001US-0344692P.
PR 28-NOV-2001; 2001US-0334233P.
PR 28-NOV-2001; 2001US-0334301P.
PR 07-JUN-2002; 2002US-0387292P.
PR 25-JUN-2002; 2002US-0391777P.
PR 17-JUL-2002; 2002US-0396594P.
PR 16-AUG-2002; 2002US-040429P.
PR 28-AUG-2002; 2002US-0407527P.
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI De Fress S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX WPI; 2003-449162/42.
XX DR Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT form truncated glycan, and adding or deleting glycosyl groups to a
PT peptide and/or adding modifying group of a peptide to remodel the
PT peptide.
XX PS Example; Fig 76; 900pp; English.
XX CC The invention relates to a cell-free, in vitro method of remodeling a
CC peptide. The method involves removing a saccharyl subunit from the
CC peptide, thus forming a truncated glycan, and contacting the truncated
CC glycan with at least one glycosyltransferase and at least one glycosyl
CC donor under conditions suitable to transfer at least one glycosyl donor
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC glycoprotein Iib/Iiia monoclonal antibody peptide, chimeric anti HBR2
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNP alpha peptide,
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC hormone (HGH) peptide, and a modifying group, where the modifying group
CC is covalently attached to the peptide through an intact glycosyl linking
CC group. The method is useful for a cell-free, in vitro method of
CC remodeling the above mentioned peptides. The present sequence represents
CC an anti-glycoprotein Iib/Iiia monoclonal antibody mature light chain
CC variable region
XX SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 6; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RASQDIGNYL 10
DB 24 RASQDINNYL 33
RESULT 21

```

ABR55866
ID  ABR55866 standard; protein; 107 AA.
AC  ABR55866;
XX
XX
XX  02-SEP-2003 (first entry)
DE  Human immunoglobulin G (IgG) light chain variable region.
XX
XX  Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW  immunoglobulin G; IgG.
XX
XX  Homo sapiens.
XX
XX  WO2003031464-A2.
XX
XX  17-APR-2003.
XX
XX  09-OCT-2002; 2002WO-US032263.
XX
XX  10-OCT-2001; 2001US-0328523P.
XX
XX  19-OCT-2001; 2001US-0344692P.
XX
XX  28-NOV-2001; 2001US-0334233P.
XX
XX  28-NOV-2001; 2001US-0334301P.
XX
XX  07-JUN-2002; 2002US-0387292P.
XX
XX  25-JUN-2002; 2002US-0391777P.
XX
XX  17-JUL-2002; 2002US-0386594P.
XX
XX  16-AUG-2002; 2002US-0404294P.
XX
XX  28-AUG-2002; 2002US-0407527P.
XX
XX  (NEOS-) NEOSE TECHNOLOGIES INC.
XX
XX  De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
XX  WPI; 2003-449162/42.
XX
XX  Remodeling a peptide, by removing a saccharyl subunit from the peptide to
XX  form truncated glycan, and adding or deleting glycosyl groups to a
XX  peptide and/or adding modifying group of a peptide to remodel the
XX  peptide.
XX
XX  Example; Fig 78; 900pp; English.
XX
XX  The invention relates to a cell-free, in vitro method of remodeling a
XX  peptide. The method involves removing a saccharyl subunit from the
XX  peptide, thus forming a truncated glycan, and contacting the truncated
XX  glycan with at least one glycosyltransferase and at least one glycosyl
XX  donor under conditions suitable to transfer at least one glycosyl donor
XX  to the truncated glycan, thus remodeling the peptide. Conjugates can be
XX  formed between a granulocyte colony stimulating factor (G-CSF) peptide,
XX  interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
XX  Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
XX  (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
XX  peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
XX  peptide, beta-glucosidase peptide, tissue plasminogen activator (tPA)
XX  peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
XX  receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
XX  glycoprotein iib/IIia monoclonal antibody peptide, chimeric anti HER2
XX  antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
XX  CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
XX  insulin peptide, hepatitis B surface antigen (HbsAg), human growth
XX  hormone (hGH) peptide, and a modifying group, where the modifying group
XX  is covalently attached to the peptide through an intact glycosyl linking
XX  group. The method is useful for a cell-free, in vitro method of
XX  remodeling the above mentioned peptides. The present sequence represents
XX  a human immunoglobulin G (IgG) light chain variable region
XX
XX  Sequence 107 AA;
XX
XX  Query Match 80.4%; Score 45; DB 6; Length 107;
XX  Best Local Similarity 90.0%; Pred. No. 1.4;
XX  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ABR54919
ID  ABR54919 standard; protein; 107 AA.
AC  ABR54919;
XX
XX  30-JUN-2003 (first entry)
DE  Light chain clone HBPAXK11 3G8 SEQ ID NO:145.
XX
XX  Engineered template; single primer amplification; antibody library;
KW  nucleic acid amplification.
XX
XX  Homo sapiens.
XX
XX  Synthetic.
XX
XX  WO2003025202-A2.
XX
XX  27-MAR-2003.
XX
XX  19-SEP-2002; 2002WO-US029889.
XX
XX  19-SEP-2001; 2001US-0323455P.
XX
XX  (ALEX-) ALEXION PHARM INC.
XX
XX  Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
XX  WPI; 2003-313359/30.
XX
XX  Amplifying nucleic acid by contacting engineered nucleic acid strand
XX  having predetermined sequence at one end and sequence complementary to
XX  predetermined sequence at other end, with primer having predetermined
XX  sequence.
XX
XX  Example 3; Fig 8b-c; 68pp; English.
XX
XX  The present invention describes a method (M1) for amplifying a nucleic
XX  acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX  having a predetermined sequence at one end and a sequence complementary
XX  to the predetermined sequence at the other, and contacting (S) with a
XX  primer having the predetermined sequence in the presence of a polymers
XX  and nucleotides under conditions suitable for polymerisation of the
XX  nucleotides. Also described is an engineered nucleic acid strand (I)
XX  having a predetermined sequence at one end and a sequence complementary
XX  to the predetermined sequence at the other end. M1 is useful for
XX  amplifying a nucleic acid. M1 can be used for producing an antibody
XX  library. M1 is useful for preparing amplified products that can be
XX  ligated into a suitable expression vector, where the vector can be used
XX  to transform an appropriate host organism to produce the polypeptide or
XX  protein encoded by the target sequence. M1 is useful to amplify a family
XX  of related sequences to build a complex library such as, for example an
XX  antibody library. M1 is useful not only for producing large amounts of
XX  one target nucleic acid sequence, but also for amplifying simultaneously
XX  more than one different target nucleic acid sequence located on the same
XX  or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX  ABR54998 represent sequence used in the exemplification of the present
XX  invention
XX
XX  Sequence 107 AA;
XX
XX  Query Match 80.4%; Score 45; DB 6; Length 107;
XX  Best Local Similarity 90.0%; Pred. No. 1.4;
XX  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 RASQDIGNYL 10
||||| |||
24 RASQDINNVL 33

RESULT 22
ABR54919
ID  ABR54919 standard; protein; 107 AA.
AC  ABR54919;
XX
XX  30-JUN-2003 (first entry)
DE  Light chain clone HBPAXK11 3G8 SEQ ID NO:145.
XX
XX  Engineered template; single primer amplification; antibody library;
KW  nucleic acid amplification.
XX
XX  Homo sapiens.
XX
XX  Synthetic.
XX
XX  WO2003025202-A2.
XX
XX  27-MAR-2003.
XX
XX  19-SEP-2002; 2002WO-US029889.
XX
XX  19-SEP-2001; 2001US-0323455P.
XX
XX  (ALEX-) ALEXION PHARM INC.
XX
XX  Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
XX  WPI; 2003-313359/30.
XX
XX  Amplifying nucleic acid by contacting engineered nucleic acid strand
XX  having predetermined sequence at one end and sequence complementary to
XX  predetermined sequence at other end, with primer having predetermined
XX  sequence.
XX
XX  Example 3; Fig 8b-c; 68pp; English.
XX
XX  The present invention describes a method (M1) for amplifying a nucleic
XX  acid strand. M1 comprises providing an engineered nucleic acid strand (S)
XX  having a predetermined sequence at one end and a sequence complementary
XX  to the predetermined sequence at the other, and contacting (S) with a
XX  primer having the predetermined sequence in the presence of a polymers
XX  and nucleotides under conditions suitable for polymerisation of the
XX  nucleotides. Also described is an engineered nucleic acid strand (I)
XX  having a predetermined sequence at one end and a sequence complementary
XX  to the predetermined sequence at the other end. M1 is useful for
XX  amplifying a nucleic acid. M1 can be used for producing an antibody
XX  library. M1 is useful for preparing amplified products that can be
XX  ligated into a suitable expression vector, where the vector can be used
XX  to transform an appropriate host organism to produce the polypeptide or
XX  protein encoded by the target sequence. M1 is useful to amplify a family
XX  of related sequences to build a complex library such as, for example an
XX  antibody library. M1 is useful not only for producing large amounts of
XX  one target nucleic acid sequence, but also for amplifying simultaneously
XX  more than one different target nucleic acid sequence located on the same
XX  or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
XX  ABR54998 represent sequence used in the exemplification of the present
XX  invention
XX
XX  Sequence 107 AA;
XX
XX  Query Match 80.4%; Score 45; DB 6; Length 107;
XX  Best Local Similarity 90.0%; Pred. No. 1.4;
XX  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 RASQDIGNYL 10
||||| |||
24 RASQDINNVL 33

```

RESULT 23
 AAO271199
 ID AAO271199 standard; protein; 107 AA.
 AC AAO271199;
 DT 17-SEP-2003 (first entry)
 XX Murine anti-CD22 antibody, RFB4, VL protein.
 DE Framework-patching; complementarity determining region; CDR; mouse;
 KW murine; cytosstatic activity; cancer; Non-Hodgkin's lymphoma;
 KW gene therapy; rheumatoid arthritis; FR-patching; RFB4 VL; CD22; antibody.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 24..34
 FT /note= "Complementarity determining region (CDR) 1"
 FT Domain 50..56
 FT /note= "Complementarity determining region (CDR) 2"
 FT Domain 89..97
 FT /note= "Complementarity determining region (CDR) 3"
 XX
 PN WO2003002607-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 10-JUN-2002; 2002WO-US018512.
 XX
 PR 27-JUN-2001; 2001US-00892613.
 XX
 PA (LEUN/) LEUNG S S.
 XX
 PI Leung SS;
 DR WPI; 2003-210245/20.
 XX
 PT New re-engineered or framework-patched immunoglobulin, useful for
 PT preparing a composition for treating cancer, preferably Non-Hodgkin's
 PT lymphoma or rheumatoid arthritis.
 XX
 PS Example 1; Fig 1b; 66pp; English.
 CC The invention relates to a novel re-engineered or framework (FR)-patched
 CC immunoglobulin, containing the heavy and/or light chain variable region
 CC (VH/VL) sequences from a parent antibody. Within these chains, at least
 CC one of the compartmentalised framework sequences, defined as FR1, FR2,
 CC FR3 and FR4 are replaced, or patched, by the corresponding framework
 CC sequences from the heavy and light chain immunoglobulin region of a
 CC different species. The FR-patched immunoglobulin binds specifically to an
 CC antigen with affinity comparable to, or within 3-fold of, that of the
 CC parent immunoglobulin. The invention discloses the process of FR-patching
 CC which is used to generate re-engineered immunoglobulin chains having one
 CC or more complementarity determining regions (CDR's) from a donor
 CC immunoglobulin and portions of framework sequences from one or more human
 CC or primate immunoglobulins. The molecules obtained demonstrate cytostatic
 CC activity as well as reduced or eliminated immunogenicity, whilst
 CC maintaining the specificity and affinity of the parent antibody. The FR-
 CC patched immunoglobulin is useful during the preparation of a composition
 CC for treating cancer, preferably Non-Hodgkin's lymphoma and also during
 CC the treatment of rheumatoid arthritis. Furthermore, the molecules of the
 CC invention may also prove useful in gene therapy. The current sequence is
 CC that of the murine anti-CD22 antibody, RFB4, VL protein of the invention
 XX Sequence 107 AA;
 SQ
 Query Match 80.4%; Score 45; DB 6; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33
 RESULT 24
 AAO27194
 ID AAO27194 standard; protein; 107 AA.
 XX
 AC AAO27194;
 DT 17-SEP-2003 (first entry)
 XX Chimeric framework-patched hPRFB4 VL protein.
 DE Framework-patching; complementarity determining region; CDR; human;
 KW mouse; murine; cytosstatic activity; cancer; Non-Hodgkin's lymphoma;
 KW chimeric; gene therapy; rheumatoid arthritis; FR-patching; hPRFB4 VL.
 XX
 OS Homo sapiens.
 FT Domain 24..34
 FT /note= "Complementarity determining region (CDR) 1"
 FT Domain 50..56
 FT /note= "Complementarity determining region (CDR) 2"
 FT Domain 89..97
 FT /note= "Complementarity determining region (CDR) 3"
 XX
 PN WO2003002607-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 10-JUN-2002; 2002WO-US018512.
 XX
 PR 27-JUN-2001; 2001US-00892613.
 XX
 PA (LEUN/) LEUNG S S.
 XX
 PI Leung SS;
 DR WPI; 2003-210245/20.
 DR N-PSDB; AAL55638, AAL55639, AAL55642.
 XX
 PT New re-engineered or framework-patched immunoglobulin, useful for
 PT preparing a composition for treating cancer, preferably Non-Hodgkin's
 PT lymphoma or rheumatoid arthritis.
 XX
 PS Example 1; Fig 3b; 66pp; English.
 CC The invention relates to a novel re-engineered or framework (FR)-patched
 CC immunoglobulin, containing the heavy and/or light chain variable region
 CC (VH/VL) sequences from a parent antibody. Within these chains, at least
 CC one of the compartmentalised framework sequences, defined as FR1, FR2,
 CC FR3 and FR4 are replaced, or patched, by the corresponding framework
 CC sequences from the heavy and light chain immunoglobulin region of a
 CC different species. The FR-patched immunoglobulin binds specifically to an
 CC antigen with affinity comparable to, or within 3-fold of, that of the
 CC parent immunoglobulin. The invention discloses the process of FR-patching
 CC which is used to generate re-engineered immunoglobulin chains having one
 CC or more complementarity determining regions (CDR's) from a donor
 CC immunoglobulin and portions of framework sequences from one or more human
 CC or primate immunoglobulins. The molecules obtained demonstrate cytostatic
 CC activity as well as reduced or eliminated immunogenicity, whilst
 CC maintaining the specificity and affinity of the parent antibody. The FR-
 CC patched immunoglobulin is useful during the preparation of a composition
 CC for treating cancer, preferably Non-Hodgkin's lymphoma and also during
 CC the treatment of rheumatoid arthritis. Furthermore, the molecules of the
 CC invention may also prove useful in gene therapy. The current sequence is
 CC that of the chimeric FR-patched hPRFB4 VL protein of the invention which

is encoded by the chimeric FR-patched hPRFB4 VL DNA

CC
XX
SQ
Sequence 107 AA;
Query Match 80.4%; Score 45; DB 6; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33
RESULT 25
ABO10814
ID ABO10814 standard; protein; 107 AA.
XX
AC ABO10814;
XX
XX
DT 21-AUG-2003 (first entry)
XX
DE Mouse monoclonal antibody kappa chain V region.
XX
XX
KW Mouse; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;
KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;
KW asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
KW chronic fatigue syndrome; coronary condition; congestive heart failure;
KW cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
KW graft versus host disease; haemorrhagic shock; inflammatory condition;
KW inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
KW ischaemia; stroke; lung disease; adult respiratory distress syndrome;
KW multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
KW reperfusion injury; sleep disturbance; uveitis; infection; antibody;
KW MAB201.
XX
OS Mus sp.
XX
XX
XX US2003026806-A1.
XX
XX
PD 06-FEB-2003.
XX
XX
XX 29-OCT-2001; 2001US-00011931.
XX
XX
XX 27-OCT-2000; 2000US-0244118P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Witte A, Varnum BC, Qian X, Vezina C;
XX WPI; 2003-479525/45.
XX
XX Treating interleukin-1 mediated disease, by administering an IL-1
XX selective binding agent that binds to IL-1alpha or IL-1beta, such that
XX the complex binds to IL-1 receptor without activating the receptor.
XX
XX Example 2; Page 19; 39pp; English.
XX
XX The invention relates to treating interleukin-1 (IL-1)-mediated disease,
XX or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
XX involving administering an IL-1 selective binding agent (e.g. a humanised
XX mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
XX 1beta, where the selective binding agent-IL-1 complex is capable of
XX binding to IL-1 receptor without activating the receptor. The activities
XX of mouse, chimeric and humanised monoclonal antibody (MAB)201 in
XX blocking formation of IL-1beta/IL-1 receptor/IL-1RacP complex were
XX studied. The results showed that anti-IL-1beta antibody MAB201 is the
XX most effective inhibitor of IL-1beta signalling. The method is useful for
XX treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
XX lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
XX pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
XX fatigue syndrome, Clostridium associated illness, coronary conditions
XX (e.g. congestive heart failure, coronary restenosis, myocardial
XX infarction, myocardial dysfunction and coronary artery bypass graft),

CC cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
CC glomerulonephritis, graft versus host disease; haemorrhagic shock,
CC inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
CC psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
CC ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
CC learning impairment, lung diseases (adult respiratory distress syndrome
CC (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
CC pain, Parkinson's disease, periodontal disease, preterm labour,
CC psoriasis, reperfusion injury, septic shock, side effects from radiation
CC therapy, temporal mandibular joint disease, sleep disturbance, uveitis
CC and inflammatory conditions resulting from strain, sprain, cartilage
CC damage, trauma, orthopaedic surgery and infection. The present sequence
CC is a heavy, light or kappa chain of the mouse anti-IL-1 monoclonal
CC antibody MAB201 which was humanised or made into a chimeric molecule
CC with human CDR (complementarity determining region) sequences
XX
SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 6; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33
RESULT 26
ADC84579
ID ADC84579 standard; protein; 107 AA.
XX
AC ADC84579;
XX
XX 01-JAN-2004 (first entry)
XX
XX CDR3 heavy chain RFB3.
XX
XX anti-CD22 antibody; RFB4; Cytostatic; Gene therapy; CD22-Antagonist;
XX cancer.
XX Pseudomonas sp.
XX OS
XX WO2003027135-A2.
XX
XX 03-APR-2003.
XX
XX 25-SEP-2002; 2002WO-US030316.
XX
XX 26-SEP-2001; 2001US-0325360P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan IH, Salvatore G, Beers R, Kreitman RJ;
XX WPI; 2003-402972/38.
XX
XX New anti-CD22 antibody, useful for the manufacture of a medicament for
XX detecting or inhibiting growth of CD22+ cancer cell, comprising variable
XX heavy and light chains of RFB4 antibody.
XX
XX Example 1; SEQ ID NO 37; 59pp; English.
XX
XX The present invention relates to a new anti-CD22 antibody has variable
XX light (VL) and variable heavy (VH) chains of the antibody RFB4. The anti-
XX CD22 antibody is useful for the manufacture of a medicament for detecting
XX or inhibiting growth of CD22+ cancer cell. The present sequence
XX represents an RFB4 heavy chain of the invention.
XX
SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 7; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33

RESULT 27

ADH50840
 ID ADH50840 standard; protein; 107 AA.

AC ADH50840;
 XX 25-MAR-2004 (first entry)

DT Mouse anti-human CD22 antibody RFB4 VL.
 DE Humanized antibody; antibody; mouse; CD22; RFB4.

XX Mus sp.
 XX Key Location/Qualifiers

FT Region 24..34
 FT /label= CDR1

FT Region 50..56
 FT /label= CDR2

FT Region 89..97
 FT /label= CDR3

XX WO2003105782-A2.
 XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019333.
 XX 17-JUN-2002; 2002US-0390033P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYRE-) UNIV READING.

XX Rybak S, Krauss J, Arndt M, Martin ACR;
 XX WPI; 2004-082055/08.

XX N-PSDB; ADH50851.
 XX New heavy or light chain variable useful for specificity grafting, or for

XX generating humanized antibody which in turn is useful for treating
 XX lymphocytic leukemia.

XX Disclosure; SEQ ID NO 17; 74pp; English.
 XX The present sequence is the protein sequence of the light chain variable

XX region (VL) of murine anti-human CD22 antibody RFB4. A claimed humanised
 XX antibody comprises a VL region and a heavy chain variable region (VH) in

XX which the complementarity determining regions (CDRs) are from a donor
 XX antibody and in which the VH and VL regions are selected from a set of

XX human frameworks ADH50824-ADH50838. The donor CDRs are preferably from
 XX RFB4, and RFB4 humanised scFv antibodies have been constructed. Claimed

XX immunoconjugates comprise a humanised antibody linked to a detectable or
 XX therapeutic (especially cytotoxic) moiety. The invention also provides a

XX new method of identifying framework acceptor regions in framework
 XX sequences for back-mutation to graft a donor sequence to the human

XX framework.
 XX Sequence 107 AA;

Query Match 80.4%; Score 45; DB 8; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33

RESULT 28

ADN49723
 ID ADN49723 standard; protein; 107 AA.

XX AC ADN49723;
 XX 15-JUL-2004 (first entry)

DT Variable light chain of a human immunoglobulin protein SeqID 51.
 DE human; erythropoietin; EPO; glycoconjugation; glycoPEGylated EPO peptide;

XX anaemia; antianaemic; haematocrit level; kidney dialysis; haematology.
 XX Homo sapiens.

XX WO2004033651-A2.
 XX 22-APR-2004.

XX 08-OCT-2003; 2003WO-US031974.
 XX 09-OCT-2002; 2002WO-US032263.

XX 05-NOV-2002; 2002US-00287994.
 XX 06-JAN-2003; 2003US-00360770.

XX 19-FEB-2003; 2003US-00360779.
 XX 09-APR-2003; 2003US-00410945.

XX (NEOS-) NEOSE TECHNOLOGIES INC.
 XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;

XX WPI; 2004-399848/37.
 XX Novel erythropoietin peptide comprising one or more glycans, having

XX glycoconjugate molecule covalently attached to peptide, useful for
 XX treating anemia in mammal such as human.

XX Disclosure; SEQ ID NO 51; 1018pp; English.
 XX This invention relates to novel erythropoietin (EPO) peptides and the

XX remodelling and glycoconjugation of these naturally occurring peptides
 XX thereof. Specifically, each EPO peptide comprises one or more glycans and

XX has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
 XX to it. Accordingly, the present invention provides glycoPEGylated EPO

XX peptides that have either monoantennary, biantennary or triantennary
 XX glycans covalently attached thereto. As such, these peptides are useful

XX for the treatment of anaemia, and hence exhibit antianaemic activities
 XX working to increase haematocrit levels in mammals, in particular in

XX humans i.e. increasing the relative volume of blood occupied by
 XX erythrocytes. Furthermore, EPO therapy can be used to treat kidney

XX dialysis patients. This polypeptide is a human protein sequence related
 XX to the field of haematology, given in an exemplification of the

XX invention.
 XX Sequence 107 AA;

Query Match 80.4%; Score 45; DB 8; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 24 RASQDINNLYL 33

RESULT 29

ADN49724
 ID ADN49724 standard; protein; 107 AA.

XX AC ADN49724;
 XX 15-JUL-2004 (first entry)

XX DE Variable light chain antiglycoprotein IiB/IIa murine antibody seqID 52.
XX KW murine; mouse; antibody; erythropoietin; EPO; glycoconjugation;
XX KW glycoPEGylated EPO peptide; anaemia; antianaemic; haematocrit level;
XX KW kidney dialysis; haematology.
XX OS Mus musculus.
XX PN WO2004033651-A2.
XX PD 22-APR-2004.
XX PF 08-OCT-2003; 2003WO-US031974.
XX PR 09-OCT-2002; 2002WO-US032263.
XX PR 05-NOV-2002; 2002US-00287994.
XX PR 06-JAN-2003; 2003US-00360770.
XX PR 19-FEB-2003; 2003US-00360779.
XX PR 09-APR-2003; 2003US-00410945.
XX PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX DR WPI; 2004-399848/37.
XX XX Novel erythropoietin peptide comprising one or more glycans, having
FT glycoconjugate molecule covalently attached to peptide, useful for
PT treating anemia in mammal such as human.
XX PS Disclosure; SEQ ID NO 52; 1018pp; English.
XX CC This invention relates to novel erythropoietin (EPO) peptides and the
CC remodelling and glycoconjugation of these naturally occurring peptides
CC thereof. Specifically, each EPO peptide comprises one or more glycans and
CC has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
CC to it. Accordingly, the present invention provides glycoPEGylated EPO
CC peptides that have either monoantennary, biantennary or triantennary
CC glycans covalently attached thereto. As such, these peptides are useful
CC for the treatment of anaemia, and hence exhibit antianaemic activities
CC working to increase haematocrit levels in mammals, in particular in
CC humans i.e. increasing the relative volume of blood occupied by
CC erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC dialysis patients. This polypeptide is a human protein sequence related
CC to the field of haematology, given in an exemplification of the
XX invention.
XX SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 8; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db ||||| |||
24 RASQDINNLY 33
RESULT 30
ADQ09630
ID ADQ09630 standard; protein; 107 AA.
XX AC ADQ09630;
XX XX 07-OCT-2004 (first entry)
XX DT
XX DE Variable light chain protein of murine anti-human GPR64-16 antibody ID16.
XX KW murine; mouse; antibody; GPR64; cytotoxic; ovarian cancer;
XX KW uterine cancer; Ewing's sarcoma; cell death; cytostatic; gene therapy;
XX KW immunotherapy; cellular proliferation.
XX FT

Mus sp.
XX PN WO2004058171-A2.
XX PD 15-JUL-2004.
XX PF 19-DEC-2003; 2003WO-US040820.
XX PR 20-DEC-2002; 2002US-0435618P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Law D, Wang Q, Dubridge R, Bhaskar V;
XX DR WPI; 2004-525780/50.
XX DR N-PSDB; ADQ09620.
XX XX New antibody that inhibits binding of a GPR64 polypeptide to an antibody
FT comprising GPR64-18, GPR64-81, GPR64-93 or GPR64-101, useful in preparing
PT a composition for diagnosing or treating ovarian cancer.
XX PS Example 2; SEQ ID NO 16; 75pp; English.
XX CC This invention relates to novel antibodies that bind to the G protein
CC coupled receptor protein identified as GPR64, namely GPR64-1, GPR64-16,
CC GPR64-18, GPR64-20 and GPR64-48. Specifically, it refers to the use of
CC these anti-GPR64 antibodies as selective cytotoxic agents against GPR64
CC expressing tumour cells such as those associated with ovarian cancer,
CC uterine cancer and Ewing's sarcoma. The present invention describes
CC epitope mapping of those antibodies that show high affinity binding to
CC GPR64 through competitive binding analyses, such that the antibodies can
CC be assessed for GPR64 dependent cell death in vitro. Accordingly, they
CC can be used to develop cytostatic compositions for gene therapy or
CC immunotherapy that inhibit cellular proliferation of an ovarian cancerous
CC cell and furthermore can diagnose and inhibit growth of tumour cells.
CC This polypeptide is encoded by a light chain variable region DNA sequence
XX of a murine anti-human GPR64 antibody of the invention.
XX SQ Sequence 107 AA;
Query Match 80.4%; Score 45; DB 8; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db ||||| |||
24 RASQDISNYL 33
RESULT 31
ADT02531
ID ADT02531 standard; protein; 107 AA.
XX AC ADT02531;
XX XX 30-DEC-2004 (first entry)
XX DT
XX DE Anti-CD22 low molecular weight scFv2 - RFB4 diabody protein Seq 11.
XX KW RFB4; low molecular weight antibody; CD22; apoptosis inducing agent;
XX KW anti-tumour agent; diabody; chronic myeloid leukaemia; Crohn's disease;
XX KW multiple sclerosis; tumour; lymphoma; cytostatic; antiinflammatory;
XX KW neuroprotective.
XX XX Unidentified.
XX OS
XX FH Key Location/Qualifiers
XX FT Region 24..34
XX FT /label= CDR1
XX FT Region 50..56
XX FT /label= CDR2
XX FT Region 89..97
XX FT /label= CDR3

XX PN WO2004087763-A1.
 XX PD 14-OCT-2004.
 XX PF 31-MAR-2004; 2004WO-JP004696.
 XX PR 31-MAR-2003; 2003JP-00096950.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Kimura N, Fukuda T;
 XX WPI; 2004-737671/72.
 DR N-PSDB; ADT02532.
 XX PT New low molecular weight antibody recognizing CD22, useful for inducing
 PT apoptosis in tumor cells.
 XX PS Claim 3; SEQ ID NO 11; 77pp; Japanese.
 XX CC This invention relates to a novel low molecular weight antibody that
 CC recognises CD22. Specifically, it refers to preparing an anti-CD22
 CC antibody (or diabody) in which variable regions of the heavy chain and
 CC the light chain are bonded together via a 5mer linker to produce a
 CC molecule that exhibits increased activity due to the reduced molecular
 CC weight. The present invention further describes apoptosis inducing agents
 CC and anti-tumour agents that each comprise this antibody as the active
 CC ingredient with apoptosis inducing activity. In particular, the diabody
 CC (defined as a recombinant antibody comprising two linked single chain
 CC antibodies) and can be useful in the treatment of chronic myeloid
 CC leukaemia, Crohn's disease and multiple sclerosis. Furthermore, it can be
 CC produced at a lower cost than conventional antibodies and exhibits a high
 CC specific activity with respect to tumour cells including lymphoma or
 CC leukaemia cells, in reduced dosage amounts. As such, the diabody can be
 CC used to prepare apoptosis-inducing agents and anti-tumour agents (e.g.
 CC for blood tumours) and hence these compositions exhibit cytostatic,
 CC antiinflammatory and neuroprotective activities. This polypeptide
 CC sequence is a single chain antibody protein of the CD22 diabody RPBA
 CC given in an exemplification of the invention.
 XX SQ Sequence 107 AA;
 Query Match 80.4%; Score 45; DB 8; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33
 RESULT 32
 ADU74399
 ID ADU74399 standard; protein; 107 AA.
 XX AC ADU74399;
 XX DT 10-FEB-2005 (first entry)
 XX DE Human immunoglobulin G variable region light chain.
 KW Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
 KW Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;
 KW Antinfertility; Antitubercular; Tuberculosstatic; protein engineering;
 KW bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
 KW infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
 KW osteoporosis; pulmonary fibrosis; tuberculosis; antibody.
 XX OS Homo sapiens.
 XX PN WO2004099231-A2.
 XX

PD 18-NOV-2004.
 XX 09-APR-2004; 2004WO-US011494.
 XX 09-APR-2003; 2003US-00410897.
 XX 09-APR-2003; 2003US-00410913.
 XX 09-APR-2003; 2003US-00410930.
 XX 09-APR-2003; 2003US-00410945.
 XX 09-APR-2003; 2003US-00410962.
 XX 09-APR-2003; 2003US-00410980.
 XX 09-APR-2003; 2003US-00410997.
 XX 09-APR-2003; 2003US-00411012.
 XX 09-APR-2003; 2003US-00411026.
 XX 09-APR-2003; 2003US-00411037.
 XX 09-APR-2003; 2003US-00411043.
 XX 09-APR-2003; 2003US-00411044.
 XX 09-APR-2003; 2003US-00411049.
 XX (NEOS-) NEOSE TECHNOLOGIES INC.
 XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
 WPI; 2004-833698/82.
 XX Cell-free in vitro method of remodeling peptide comprising poly(ethylene
 PT glycol) useful for generating glycopeptide suitable for therapeutic uses
 PT in mammal, involves addition or deletion of glycosyl groups to peptide.
 XX Disclosure; SEQ ID NO 51; 1024pp; English.
 XX The invention relates to a cell-free in vitro method (M1) of remodeling a
 CC peptide comprising poly(ethylene glycol). (M1) is useful for remodeling
 CC protein to generate glycopeptide having desired glycosylation pattern
 CC suitable for therapeutic use in mammal. (M1) is useful for remodeling
 CC peptides chosen from immunoglobulin, erythropoietin, tissue-type
 CC activator peptide, etc. (M1) is useful for remodeling (a) G-CSF which is
 CC useful for treating acute myeloid leukemia (AML), non-myeloid cancer
 CC patient receiving bone marrow transplant, (b) factor VII for treating
 CC bleeding episode, factor VIII deficiency, factor IX deficiency, liver
 CC cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in
 CC vitro fertilization and for infertile patient, (d) EPO for treating
 CC anemia, anemic patients having chronic renal insufficiency and end stage
 CC renal disease, anemic patient undergoing dialysis, (e) GM-CSF for
 CC treating acute myelogenous leukemia, (f) IFN-gamma for treating malignant
 CC osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis,
 CC etc. The glycopeptide produced using (M1) has specific customized or
 CC desired glycosylation pattern. (M1) allows efficient production of
 CC improved therapeutic moiety. The present sequence represents the amino
 CC acid sequence of a protein remodelled in the present invention
 XX SQ Sequence 107 AA;
 Query Match 80.4%; Score 45; DB 8; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDINNYL 33
 RESULT 33
 ADU74400
 ID ADU74400 standard; protein; 107 AA.
 XX AC ADU74400;
 XX DT 10-FEB-2005 (first entry)
 XX DE Mouse anti-glycoprotein IIb/IIIa antibody light chain.
 XX KW Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
 KW Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;

KW Antinfertility; Antitubercular; Tuberculostatic; protein engineering;
KW bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
KW infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
KW osteoporosis; pulmonary fibrosis; tuberculosis; antibody.
XX
XX Mus musculus.
XX OS
XX
XX W02004099231-A2.
XX PN
XX
XX 18-NOV-2004.
XX PD
XX
XX 09-APR-2004; 2004WO-US011494.
XX PF
XX
XX 09-APR-2003; 2003US-00410897.
XX PR
XX 09-APR-2003; 2003US-00410913.
XX PR
XX 09-APR-2003; 2003US-00410930.
XX PR
XX 09-APR-2003; 2003US-00410945.
XX PR
XX 09-APR-2003; 2003US-00410962.
XX PR
XX 09-APR-2003; 2003US-00410980.
XX PR
XX 09-APR-2003; 2003US-00410997.
XX PR
XX 09-APR-2003; 2003US-00411012.
XX PR
XX 09-APR-2003; 2003US-00411026.
XX PR
XX 09-APR-2003; 2003US-00411037.
XX PR
XX 09-APR-2003; 2003US-00411043.
XX PR
XX 09-APR-2003; 2003US-00411044.
XX PR
XX 09-APR-2003; 2003US-00411049.
XX
XX (NEOS-) NEOSE TECHNOLOGIES INC.
XX PA
XX
XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX PI
XX WPI; 2004-833698/82.
XX DR
XX
XX Cell-free in vitro method of remodeling peptide comprising poly(ethylene
PT glycol) useful for generating glycopeptide suitable for therapeutic uses
PT in mammal, involves addition or deletion of glycosyl groups to peptide.
PT
XX
XX Disclosure; SEQ ID NO 52; 1024pp; English.
XX PS
XX
XX The invention relates to a cell-free in vitro method (M1) of remodeling a
CC peptide comprising poly(ethylene glycol). (M1) is useful for remodeling a
CC protein to generate glycopeptide having desired glycosylation pattern
CC suitable for therapeutic use in mammal. (M1) is useful for remodeling
CC peptides chosen from immunoglobulin, erythropoietin, tissue-type
CC activator peptide, etc. (M1) is useful for remodeling (a) G-CSF which is
CC useful for treating acute myeloid leukemia (AML), non-myeloid cancer
CC patient receiving bone marrow transplant, (b) factor VII for treating
CC cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in
CC vitro fertilization and for infertile patient, (d) EPO for treating
CC anemia, anemic patients having chronic renal insufficiency and end stage
CC renal disease, anemic patient undergoing dialysis, (e) GM-CSF for
CC treating acute myelogenous leukemia, (f) IFN-gamma for treating malignant
CC osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis,
CC etc. The glycopeptide produced using (M1) has specific customized or
CC desired glycosylation pattern. (M1) allows efficient production of
CC improved therapeutic moiety. The present sequence represents the amino
XX acid sequence of a protein remodelled in the present invention
XX
XX Sequence 107 AA;
XX
XX Query Match 80.4%; Score 45; DB 8; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
Db ||||| |||
24 RASQDINSYL 33
XX
XX RESULT 34
ADW75670
XX ID ADW75670 standard; protein; 107 AA.

XX ADW75670;
XX AC
XX 24-MAR-2005 (first entry)
XX DT
XX DE
XX Novel modified immunoglobulin-related protein #5.
XX KW
XX antibody engineering; immunogenicity; FR; immunoglobulin.
XX OS
XX Unidentified.
XX XX
XX CN1429843-A.
XX PN
XX
XX 16-JUL-2003.
XX PD
XX 29-DEC-2001; 2001CN-00144894.
XX PF
XX 29-DEC-2001; 2001CN-00144894.
XX PR
XX (LIAN/) LIANG R.
XX PA
XX WPI; 2004-110046/12.
XX DR
XX Gene reform immune globulin with low immunogenicity and its application.
XX PT
XX Example 1; Page 14; 23pp; Chinese.
XX PS
XX This invention relates to a novel gene encoding a modified immunoglobulin
CC with low immunogenicity. The immunoglobulin features within the light-
CC chain or heavy-chain variable region, at least one mother FR subzone
CC sequence substituted or displaced by the relative FR subzone heterologous
CC to the mother antibody, and its specificity and affinity are increased 3-
CC fold. The present sequence is that of a protein which was used in the
CC exemplification of the invention.
XX
XX Sequence 107 AA;
XX
XX Query Match 80.4%; Score 45; DB 8; Length 107;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
Qy ||||| |||
24 RASQDINSYL 33
XX
XX RESULT 35
ADW75668
XX ID ADW75668 standard; protein; 107 AA.
XX AC
XX ADW75668;
XX AC
XX 24-MAR-2005 (first entry)
XX DT
XX DE
XX Novel modified immunoglobulin-related protein SeqID3.
XX KW
XX antibody engineering; immunogenicity; FR; immunoglobulin.
XX OS
XX Unidentified.
XX XX
XX CN1429843-A.
XX PN
XX
XX 16-JUL-2003.
XX PD
XX 29-DEC-2001; 2001CN-00144894.
XX PF
XX 29-DEC-2001; 2001CN-00144894.
XX PR
XX (LIAN/) LIANG R.
XX PA
XX WPI; 2004-110046/12.
XX DR
XX N-PSDB; ADW75666.
XX DR
XX

PT Gene reform immune globulin with low immunogenicity and its application.
 XX
 PS Example 1; SEQ ID NO 3; 23pp; Chinese.
 XX
 CC This invention relates to a novel gene encoding a modified immunoglobulin
 CC with low immunogenicity. The immunoglobulin features within the light-
 CC chain or heavy-chain variable region, at least one mother FR subzone
 CC sequence substituted or displaced by the relative FR subzone heterologous
 CC to the mother antibody, and its specificity and affinity are increased 3-
 CC fold. The present sequence is that of a protein which was used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 107 AA;
 Query Match 80.4%; Score 45; DB 8; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33
 RESULT 36
 ADY85028
 ID ADY85028 standard; protein; 107 AA.
 AC ADY85028;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Monoclonal antibody 10D4 HMGB1 Vkappa domain.
 XX
 KW High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
 KW anaphylactic; asthma; antiasthmatic; lupus erythematosus;
 KW antiinflammatory; inflammation; dermatological;
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;
 KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
 KW peritonitis; burns; vulnery; ischemia; vasotropic; Behcet's disease;
 KW graft versus host disease; inflammatory bowel disease;
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
 KW anabolic; infection; musculoskeletal disease; immune disorder;
 KW light chain variable region.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3
 XX
 PN WO2005026209-A2.
 XX
 PD 24-MAR-2005.
 XX
 PF 10-SEP-2004; 2004WO-US029527.
 XX
 PR 11-SEP-2003; 2003US-0502568P.
 XX
 PA (CRIT-) CRITICAL THERAPEUTICS INC.
 XX
 PI Newman W, Qin S, Okeefe T, Obar R;
 XX
 DR WPI; 2005-233483/24.
 DR N-PSDB; ADY85027.
 XX
 FT New antibody or its antigen-binding fragment specific to a vertebrate
 FT high mobility group box (HMGB) A box that inhibits release of a
 FT proinflammatory cytokine from a cell treated with HMGB protein, useful

PT for treating, e.g. sepsis.
 XX
 PS Example 4; SEQ ID NO 17; 123pp; English.
 XX
 CC The invention provides antibodies, or their antigen-binding fragments,
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
 CC methods of detecting and/or identifying an agent that binds to an HMGB
 CC polypeptide, methods of treating a condition in a subject characterized
 CC by activation of an inflammatory cytokine cascade, and methods of
 CC detecting an HMGB polypeptide in a sample. The antibody for antigen-
 CC binding fragment) binds to a vertebrate HMGB A box but does not
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
 CC protein. A method of treating a condition characterized by activation of
 CC an inflammatory cytokine cascade comprises administering an antibody of
 CC the invention, or its antigen-binding fragment. The condition is selected
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
 CC and cachexia, especially sepsis, arthritis, or lupus. The present
 CC sequence is the protein sequence of the light chain variable region
 CC (Vkappa) of an anti-HMGB1 monoclonal antibody produced by claimed murine
 CC hybridoma 10D4 HMGB1 (ATCC PTA-5435).
 XX
 SQ Sequence 107 AA;
 Query Match 80.4%; Score 45; DB 9; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33
 RESULT 37
 ADZ47655
 ID ADZ47655 standard; protein; 107 AA.
 XX
 AC ADZ47655;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Mouse anti-IL-1beta monoclonal antibody MAB201 VL #1, SEQ:4.
 XX
 KW Drug screening; antibody identification; cell signaling; inflammation;
 KW antiinflammatory; interleukin-beta; immunoglobulin; monoclonal antibody;
 KW light chain variable region.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /note= "Ser replaces Thr in the humanized VL"
 FT Misc-difference 8 /note= "Pro replaces Thr in the humanized VL"
 FT Misc-difference 15 /note= "Val replaces Leu in the humanized VL"
 FT Misc-difference 22 /note= "Thr replaces Ser in the humanized VL"
 FT Misc-difference 41 /note= "Gly replaces Asp in the humanized VL"
 FT Misc-difference 42 /note= "Lys replaces Gly in the humanized VL"
 FT Misc-difference 43 /note= "Ala replaces Thr in the humanized VL"
 FT Misc-difference 44 /note= "Pro replaces Val in the humanized VL"
 FT Misc-difference 71 /note= "Phe replaces Tyr in the humanized VL"
 FT Misc-difference 72 /note= "Thr replaces Phe in the humanized VL"

Qy	1	RASQDIGNYL 10	
Db	24	RASQDISNYL 33	
RESULT 38			
AEA50145			
ID	AEA50145	standard; protein; 107 AA.	
XX	AC	AEA50145;	
XX			
XX	11-AUG-2005	(first entry)	
DT			
XX			
DE	Anti-CD22	antibody VL.	
XX			
KW	Cytostatic; Antibody	therapy; complementarity determining region; CDR;	
KW	CD22; Pseudomonas	exotoxin; PE; antibody; cancer.	
XX	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO2005052006-A2.		
XX			
PD	09-JUN-2005.		
XX			
PF	24-NOV-2004; 2004WO-US039617.		
XX			
PR	25-NOV-2003; 2003US-0525371P.		
XX	(USSH)	US DEPT HEALTH & HUMAN SERVICES.	
XX	Pastan IH,	Ho M, Bang S;	
PI			
XX			
DR	WPI; 2005-405363/41.		
DR	N-PSDB; AEA50144.		
XX			
PT	New antibody	that specifically binds CD22, useful for the manufacture of	
PT	a medicament	to inhibit the growth of a CD22+ cancer cell, thus useful	
PT	for	treating cancer.	
XX			
PS	Disclosure; SEQ ID NO 2;	106pp; English.	
XX			
CC	This sequence	represents the light chain (VL) of the antibody, RFB4. This	
CC	antibody	was used in the design of the antibody of the invention which	
CC	specifically	binds CD22. The antibody of the invention may be used in the	
CC	generation	of a chimeric molecule, which may also comprise a therapeutic	
CC	moiety. The	therapeutic moiety is preferably a Pseudomonas exotoxin (PE)	
CC	A or its	cytotoxic fragment or mutant, where the PE has a Gly, Ala, Val,	
CC	Leu or Ile	in place of Arg at position 490 of the 613 amino acids wild	
CC	type PE	sequence. The antibody and chimeric molecule are useful for the	
CC	manufacture	of a medicament to inhibit the growth of a CD22+ cancer cell,	
CC	and	thus are useful for treating cancer.	
XX			
SQ	Sequence	107 AA;	
Query Match 80.4%; Score 45; DB 9; Length 107;			
Best Local Similarity 90.0%; Pred.No. 1.4;			
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	RASQDIGNYL 10	
Db	24	RASQDISNYL 33	
RESULT 39			
AEB19295			
ID	AEB19295	standard; protein; 107 AA.	
XX	AC	AEB19295;	
XX			
XX	08-SEP-2005	(first entry)	
DT			
XX			
DE	IGG kappa	light chain variable region polypeptide HBPAXK11.	

XX DNA amplification; expression; light chain variable region.
 KW Homo sapiens.
 OS WO2005060641-A2.
 XX 07-JUL-2005.
 XX 15-DEC-2004; 2004WO-US041945.
 XX 15-DEC-2003; 2003US-00737252.
 XX (ALEX-) ALEXION PHARM INC.
 XX Maruyama T, Frederickson S, Bowdish KS, Renshaw M, Lin Y;
 XX WPI; 2005-488575/49.
 XX Amplifying nucleic acid encoding portion of antibody, by annealing primer
 PT to template encoding antibody, synthesizing polynucleotide complementary
 PT to template, annealing template to polynucleotide and amplifying
 PT polynucleotide.
 XX Disclosure; SEQ ID NO 145; 76pp; English.
 XX The invention describes a method of amplifying a nucleic acid encoding a
 CC portion of an antibody, involving annealing a primer to a template that
 CC encodes a portion of the antibody, synthesizing a polynucleotide that is
 CC complementary to the portion of the template, separating the synthesized
 CC polynucleotide, annealing a template oligonucleotide to the synthesized
 CC polynucleotide, extending the synthesized polynucleotide and amplifying
 CC the polynucleotide. Also described are: producing (M2) an antibody
 CC library, involves providing a diverse population of templates that encode
 CC a portion of an IGA antibody, contacting the diverse population of
 CC templates with a primer, which has a first portion which anneals to the
 CC templates and a second portion of predetermined sequence which does not
 CC anneal to the templates, and carrying out steps (b)-(f) of (M1); a
 CC library of IGA antibodies prepared by (M2); identifying (M3) an antibody
 CC having a desired binding specificity, involves preparing a library of IGA
 CC antibodies by (M2), and screening the library to identify one or more IGA
 CC antibodies having a desired binding specificity; and an IGA antibody
 CC identified by (M3). (M1) is useful for amplifying nucleic acid encoding a
 CC portion of an antibody, and for producing an antibody library. (M2) is
 CC useful for identifying an antibody having a desired binding specificity.
 CC (M1) enables an improved nucleic acid amplification with decreased mis-
 CC priming and amplification of sequences other than the target sequence.
 CC This is the amino acid sequence of an IGG kappa light chain variable
 CC region comprising framework 1-CDR1-framework 2-CDR2.
 XX Sequence 107 AA;
 SQ
 Query Match 80.4%; Score 45; DB 9; Length 107;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 |||||
 DB 24 RASQDISNYL 33
 RESULT 40
 AAP81246
 ID AAP81246 standard; protein; 108 AA.
 XX AAP81246;
 AC
 XX 25-MAR-2003 (revised)
 DT 07-JAN-1991 (first entry)
 XX
 DE Anti-pseudomonas aeruginosa human type antibody L-chain contg. constant
 DE region of kappa and lambda types.
 XX

Pseudomonas aeruginosa P4; Pseudomonas aeruginosa HI; immunotherapy.
 KW Homo sapiens.
 OS JP63152984-A.
 XX 25-JUN-1988.
 XX 20-MAR-1986; 86JP-00064183.
 XX 18-AUG-1986; 86JP-00191687.
 PR 20-MAR-1987; 87JP-00064183.
 XX (WAKT) WAKUNAGA SEIYAKU KK.
 XX WPI; 1988-216877/31.
 DR N-PSDB; AAN81636.
 XX Anti-Pseudomonas aeruginosa type antibody L-chain coding DNA - contains
 PT constant kappa and lambda type regions, and versatile region recognising
 PT ps aeruginosa P4 and HI types.
 XX Claim 8; Page 602; 12pp; Japanese.
 XX It also contains a variable region recognising Ps.aeruginosa P4 and HI
 CC types. The Ab can be used for immunologic control of infection caused by
 CC Ps.aeruginosa. The antibody is made effective against various classes or
 CC subclasses of resistant Ps.aeruginosa by recombining corresp. DNA L-chain
 CC contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF
 CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX Sequence 108 AA;
 SQ
 Query Match 80.4%; Score 45; DB 1; Length 108;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 |||||
 DB 24 RASQDISNYL 33
 RESULT 41
 AARS4062
 ID AARS4062 standard; protein; 108 AA.
 XX AARS4062;
 AC
 XX 01-MAR-1995 (first entry)
 DT
 XX Anti-cancer monoclonal antibody light chain variable region.
 DE
 XX Antibody; hypervariable region; complementarity determining region;
 KW anti-cancer; CDR; CLN/SUZ H11 hybridoma; immunoglobulin kappa;
 KW light chain.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 28..34
 FT Region /label= hypervariable_region_1
 FT Region 50..56
 FT Region /label= hypervariable_region_2
 FT Region 91..96
 FT Region /label= hypervariable_region_3
 XX
 XX JP06141884-A.
 PN
 XX 24-MAY-1994.
 PD
 XX 06-NOV-1992; 92JP-00321418.
 PF
 XX

PR 06-NOV-1992; 92JP-00321418.
XX (HAGI/) HAGIWARA Y.
XX
XX WPI; 1994-205039/25.
XX N-PSDB; AAQ64060.
XX
XX Anti-cancer human monoclonal antibody - useful for the treatment,
PT prevention and diagnosis of human diseases.
XX
XX Claim 7; Page 3; 11pp; Japanese.
XX
XX An anti-cancer human monoclonal antibody produced by the human/human
CC hybridoma CLN/SUZ H11 has the kappa light chain variable region sequence
CC AAR54062
XX
XX Sequence 108 AA;
XX
XX Query Match 80.4%; Score 45; DB 2; Length 108;
XX Best Local Similarity 90.0%; Pred. No. 1.4;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
XX 24 RASQDISNYL 33
XX
XX RESULT 42
XX AAW04177
XX ID AAW04177 standard; protein; 108 AA.
XX AC AAW04177;
XX XX
XX 19-MAY-1997 (first entry)
XX
XX Variant variable light chain of Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus;
XX variant.
XX
XX Mus musculus.
XX OS
XX WO9629350-A1.
XX PN
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX DR
XX N-PSDB; AAT39550.
XX DR
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX DR
XX N-PSDB; AAT39550.
XX DR
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
XX Claim 20; Page 80-81; 133pp; Japanese.
XX
XX The present sequence is a variant light chain variable region of the anti
XX -human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by
XX the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The MAB recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX
XX Sequence 108 AA;
XX
XX Query Match 80.4%; Score 45; DB 2; Length 108;
XX Best Local Similarity 90.0%; Pred. No. 1.4;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
XX 24 RASQDISNYL 33
XX
XX RESULT 43
XX AAW00834
XX ID AAW00834 standard; protein; 108 AA.
XX AC AAW00834;
XX XX
XX 20-MAY-1997 (first entry)
XX
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
XX Mus musculus.
XX OS
XX WO9629350-A1.
XX PN
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX DR
XX N-PSDB; AAT39560.
XX DR
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
XX Claim 41; Page 93-94; 133pp; Japanese.
XX
XX The present sequence is the light chain variable region of the anti-human
XX Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by the
XX hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The MAB recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX
XX Sequence 108 AA;
XX
XX Query Match 80.4%; Score 45; DB 2; Length 108;
XX Best Local Similarity 90.0%; Pred. No. 1.4;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
XX 24 RASQDISNYL 33
XX
XX RESULT 43
XX AAW00834
XX ID AAW00834 standard; protein; 108 AA.
XX AC AAW00834;
XX XX
XX 20-MAY-1997 (first entry)
XX
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
XX Mus musculus.
XX OS
XX WO9629350-A1.
XX PN
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX DR
XX N-PSDB; AAT39560.
XX DR
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
XX Claim 20; Page 80-81; 133pp; Japanese.
XX
XX The present sequence is a variant light chain variable region of the anti
XX -human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by
XX the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The MAB recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX
XX Sequence 108 AA;
XX
XX Query Match 80.4%; Score 45; DB 2; Length 108;
XX Best Local Similarity 90.0%; Pred. No. 1.4;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
XX 24 RASQDISNYL 33
XX
XX RESULT 43
XX AAW00834
XX ID AAW00834 standard; protein; 108 AA.
XX AC AAW00834;
XX XX
XX 20-MAY-1997 (first entry)
XX
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
XX Mus musculus.
XX OS
XX WO9629350-A1.
XX PN
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX DR
XX N-PSDB; AAT39560.
XX DR
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
XX Claim 20; Page 80-81; 133pp; Japanese.
XX
XX The present sequence is a variant light chain variable region of the anti
XX -human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by
XX the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The MAB recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX
XX Sequence 108 AA;
XX
XX Query Match 80.4%; Score 45; DB 2; Length 108;
XX Best Local Similarity 90.0%; Pred. No. 1.4;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 RASQDIGNYL 10
XX 24 RASQDISNYL 33
XX
XX RESULT 43
XX AAW00834
XX ID AAW00834 standard; protein; 108 AA.
XX AC AAW00834;
XX XX
XX 20-MAY-1997 (first entry)
XX
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
XX Mus musculus.
XX OS
XX WO9629350-A1.
XX PN
XX 26-SEP-1996.
XX PD
XX 21-MAR-1996; 96WO-JP0000734.
XX PF
XX 20-MAR-1995; 95JP-00087420.
XX PR
XX 27-OCT-1995; 95JP-00303492.
XX PR
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PA
XX Kayagaki N, Yagita H,

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XX KW Antibody; RHAMM; receptor for hyaluronic acid mediated motility;
KW ras-dependent proliferation; leukaemia; cancer; lymphoma;
KW inflammatory disease; proliferative disease; psoriasis;
KW inflammatory bowel disease; rheumatoid arthritis;
KW proliferative cardiovascular disease; restenosis;
KW proliferative ocular disorder; diabetic retinopathy; haemangioma;
KW benign hyperproliferative disease; tumour formation; light chain;
KW variable region; 16E10.
XX OS Mus musculus.
XX PN WO200029447-A1.
XX PD 25-MAY-2000.
XX PF 19-NOV-1999; 99WO-US027565.
XX PR 19-NOV-1998; 98US-0109041P.
XX PR 14-JUL-1999; 99US-0143692P.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX PI Abrahamson JA, Holmes SD, Jackson JR;
XX DR WPI; 2000-387752/33.
XX DR N-PSDB; AAA27323.
XX PT Antibodies against receptor for hyaluronic acid mediated motility, useful
XX for treating or preventing proliferative diseases, e.g. cancer or
XX cardiovascular disease.
XX PS Claim 19; Page 33; 39pp; English.
XX CC The present sequence is the protein sequence for the murine 16E10 light
XX chain variable region. This forms part of the monoclonal antibody 16E10,
XX and can be used against the receptor for hyaluronic acid mediated
XX motility (RHAMM). RHAMM is required for ras-transformation of cells,
XX which leads to tumour formation, and so the antibody can be used to treat
XX proliferative disorders such as leukaemias, solid tumour cancers and
XX metastases including lymphomas, soft tissue, brain, oesophageal, stomach,
XX pancreatic, liver, lung, bladder, bone, prostate, ovarian, cervical,
XX uterine, skin, breast, testicular, kidney, head and neck and colon
XX cancers, chronic inflammatory diseases such as psoriasis, inflammatory
XX bowel disease and rheumatoid arthritis, proliferative cardiovascular
XX diseases such as restenosis, proliferative ocular disorders such as
XX diabetic retinopathy and benign hyperproliferative diseases such as
XX haemangiomas
XX SQ Sequence 108 AA;

Query Match 80.4%; Score 45; DB 3; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 46
ABO10817
ID ABO10817 standard; protein; 108 AA.
XX AC ABO10817;
XX .DT 21-AUG-2003 (first entry)
XX XX Human germline region variable region VK-1018/08.
XX KW Human; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; AIDS;
KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;

XX KW Anti-human FasL antibody (NOK1) light chain variable region.
XX Light chain; variable region; mouse; murine; human; Fas ligand; FasL;
XX monoclonal antibody; MAb; hybridoma; treatment; hepatitis;
XX hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;
XX glutamate oxaloacetate; pyruvate transaminase.
XX OS Mus sp.
XX PN WO9715326-A1.
XX PD 01-MAY-1997.
XX PF 24-OCT-1996; 96WO-JP003089.
XX PR 27-OCT-1995; 95JP-00303491.
XX PA (SUME ) SUMITOMO ELECTRIC IND CO.
XX PI Seino K, Kayagaki N, Yagita H, Okumura K, Nakata M;
XX DR WPI; 1997-258767/23.
XX DR N-PSDB; AAT66710.
XX PT Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in
XX liver cells and improves liver function.
XX PS Claim 6; Page 30-31; 51pp; Japanese.
XX CC The present sequence is the light chain variable region of the murine
XX anti-human Fas ligand (FasL) monoclonal antibody (MAb) NOK1, which is
XX expressed by the hybridoma NOK1 (FERM BP-5044). The MAb can be used in
XX the preparation of a composition for the effective oral or parenteral
XX treatment of hepatitis, including hepatitis caused by hepatitis B or C
XX virus. The composition controls apoptosis in liver cells caused by the
XX binding of FasL to Fas expressing liver cells, and improves liver
XX function by improving blood glutamate oxaloacetate and pyruvate
XX transaminase levels. The composition is given in a dosage of 0.0001-1000,
XX preferably 0.01-600 mg/day. Spleen cells from mice immunised with FasL
XX expressing COS cells were fused with mouse myeloma cells to produce
XX hybridomas. The hybridomas were screened for anti-FasL activity, and the
XX active clones NOK1-5 isolated
XX SQ Sequence 108 AA;

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 45
AAV94216
ID AAV94216 standard; protein; 108 AA.
XX AC AAV94216;
XX XX Murine consensus 16E10 light chain variable region.
XX DT 08-AUG-2000 (first entry)
XX DE Murine consensus 16E10 light chain variable region.

```


asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
 chronic fatigue syndrome; coronary condition; congestive heart failure;
 cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
 graft versus host disease; haemorrhagic shock; inflammatory condition;
 inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
 ischaemia; stroke; lung disease; adult respiratory distress syndrome;
 multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
 reperfusion injury; sleep disturbance; uveitis; infection; antibody;
 MAB201; germline variable region.

Homo sapiens.

US2003026806-A1.

06-FEB-2003.

29-OCT-2001; 2001US-00011931.

27-OCT-2000; 2000US-0244118P.

(AMGE-) AMGEN INC.

Witte A, Varnum BC, Qian X, Vezina C;

WPI; 2003-479525/45.

Treating interleukin-1 mediated disease, by administering an IL-1
 selective binding agent that binds to IL-1alpha or IL-1beta, such that
 the complex binds to IL-1 receptor without activating the receptor.

Example 2; Fig 6A; 39pp; English.

The invention relates to treating interleukin-1 (IL-1)-mediated disease,
 or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
 involving administering an IL-1 selective binding agent (e.g. a humanised
 mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
 1beta, where the selective binding agent-IL-1 complex is capable of
 binding to IL-1 receptor without activating the receptor. The activities
 of mouse, chimaeric and humanised monoclonal antibody (MAB)201 in
 blocking formation of IL-1beta/IL-1 receptor/IL-1Racp complex were
 studied. The results showed that anti-IL-1beta antibody MAB201 is the
 most effective inhibitor of IL-1beta signalling. The method is useful for
 treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
 lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
 pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
 fatigue syndrome, Clostridium associated illness, coronary conditions
 (e.g. congestive heart failure, coronary restenosis, myocardial
 infarction, myocardial dysfunction and coronary artery bypass graft),
 cancer, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
 glomerulonephritis, graft versus host disease; haemorrhagic shock,
 inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
 psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
 ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
 learning impairment, lung diseases (adult respiratory distress syndrome
 (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
 pain, Parkinson's disease, periodontal disease, preterm labour,
 psoriasis, reperfusion injury, septic shock, side effects from radiation
 therapy, temporal mandibular joint disease, sleep disturbance, uveitis
 and inflammatory conditions resulting from strain, sprain, cartilage
 damage, trauma, orthopaedic surgery and infection. The present sequence
 is a human germline variable region used to determine which residues or
 CDRs required to be changed in mouse anti-IL-1 monoclonal antibody MAB201
 in order to humanise it or make it into a chimaeric molecule with human
 CDR (complementarity determining region) sequences

Sequence 108 AA;

Query Match 80.4%; Score 45; DB 6; Length 108;
 Best Local Similarity 90.0%; Pred. NO. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 RASQDISNYL 10
 ||||| |||

Db 24 RASQDISNYL 33

RESULT 47

ABO10815

ID ABO10815 standard; protein; 108 AA.

XX ABO10815;

AC ABO10815;

XX 21-AUG-2003 (first entry)

XX Mouse monoclonal antibody MAB201 light chain.

XX Mouse; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;
 amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;
 asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
 chronic fatigue syndrome; coronary condition; congestive heart failure;
 cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
 graft versus host disease; haemorrhagic shock; inflammatory condition;
 inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
 ischaemia; stroke; lung disease; adult respiratory distress syndrome;
 multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
 reperfusion injury; sleep disturbance; uveitis; infection; antibody;
 MAB201.

XX Mus sp.

OS US2003026806-A1.

PN 06-FEB-2003.

XX 29-OCT-2001; 2001US-00011931.

XX 27-OCT-2000; 2000US-0244118P.

PR (AMGE-) AMGEN INC.

XX Witte A, Varnum BC, Qian X, Vezina C;

XX WPI; 2003-479525/45.

DR Treating interleukin-1 mediated disease, by administering an IL-1
 selective binding agent that binds to IL-1alpha or IL-1beta, such that
 the complex binds to IL-1 receptor without activating the receptor.

XX Example 2; Fig 6A; 39pp; English.

XX The invention relates to treating interleukin-1 (IL-1)-mediated disease,
 or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
 involving administering an IL-1 selective binding agent (e.g. a humanised
 mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
 1beta, where the selective binding agent-IL-1 complex is capable of
 binding to IL-1 receptor without activating the receptor. The activities
 of mouse, chimaeric and humanised monoclonal antibody (MAB)201 in
 blocking formation of IL-1beta/IL-1 receptor/IL-1Racp complex were
 studied. The results showed that anti-IL-1beta antibody MAB201 is the
 most effective inhibitor of IL-1beta signalling. The method is useful for
 treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
 lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
 pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
 fatigue syndrome, Clostridium associated illness, coronary conditions
 (e.g. congestive heart failure, coronary restenosis, myocardial
 infarction, myocardial dysfunction and coronary artery bypass graft),
 cancer, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
 glomerulonephritis, graft versus host disease; haemorrhagic shock,
 inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
 psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
 ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
 learning impairment, lung diseases (adult respiratory distress syndrome
 (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
 pain, Parkinson's disease, periodontal disease, preterm labour,
 psoriasis, reperfusion injury, septic shock, side effects from radiation
 therapy, temporal mandibular joint disease, sleep disturbance, uveitis
 and inflammatory conditions resulting from strain, sprain, cartilage
 damage, trauma, orthopaedic surgery and infection. The present sequence
 is a human germline variable region used to determine which residues or
 CDRs required to be changed in mouse anti-IL-1 monoclonal antibody MAB201
 in order to humanise it or make it into a chimaeric molecule with human
 CDR (complementarity determining region) sequences

CC and inflammatory conditions resulting from strain, sprain, cartilage
 CC damage, trauma, orthopaedic surgery and infection. The present sequence
 CC is a heavy, light or kappa chain of the mouse anti-IL-1 monoclonal
 CC antibody MAB201 which was humanised or made into a chimaeric molecule
 CC with human CDR (complementarity determining region) sequences
 XX
 XX Sequence 108 AA;
 SQ
 Query Match 80.4%; Score 45; DB 6; Length 108;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33
 RESULT 48
 ABO10816
 ID ABO10816 standard; protein; 108 AA.
 XX
 XX ABO10816;
 AC
 DT 21-AUG-2003 (first entry)
 XX
 XX Human germline region variable region VK-1 A20.
 DE
 XX Human; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;
 KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;
 KW asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;
 KW chronic fatigue syndrome; coronary condition; congestive heart failure;
 KW cancer; diabetes; endometriosis; fever; glomerulonephritis; ARDS;
 KW graft versus host disease; haemorrhagic shock; inflammatory condition;
 KW inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;
 KW ischaemia; stroke; lung disease; adult respiratory distress syndrome;
 KW multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;
 KW reperfusion injury; sleep disturbance; uveitis; infection; antibody;
 KW MAB201; germline variable region.
 XX
 XX Homo sapiens.
 OS
 XX US2003026806-A1.
 PN
 XX
 PD 06-FEB-2003.
 XX
 XX 29-OCT-2001; 2001US-00011931.
 PF
 XX
 XX 27-OCT-2000; 2000US-0244118P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Witte A, Varnum BC, Qian X, Vezina C;
 PI
 XX WPI; 2003-479525/45.
 DR
 XX
 XX Treating interleukin-1 mediated disease, by administering an IL-1
 PT selective binding agent that binds to IL-1alpha or IL-1beta, such that
 PT the complex binds to IL-1 receptor without activating the receptor.
 PT
 XX Example 2; Fig 6A; 39pp; English.
 PS
 XX The invention relates to treating interleukin-1 (IL-1)-mediated disease,
 CC or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
 CC involving administering an IL-1 selective binding agent (e.g. a humanised
 CC mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
 CC 1beta, where the selective binding agent-IL-1 complex is capable of
 CC binding to IL-1 receptor without activating the receptor. The activities
 CC of mouse, chimaeric and humanised monoclonal antibody (MAB)201 in
 CC blocking formation of IL-1beta/IL-1 receptor/IL-1racp complex were
 CC studied. The results showed that anti-IL-1beta antibody MAB201 is the
 CC most effective inhibitor of IL-1beta signalling. The method is useful for
 CC treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
 CC lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,

CC pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
 CC fatigue syndrome, Clostridium associated illness, coronary conditions
 CC (e.g. congestive heart failure, coronary restenosis, myocardial
 CC infarction, myocardial dysfunction and coronary artery bypass graft),
 CC cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
 CC glomerulonephritis, graft versus host disease; haemorrhagic shock,
 CC inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
 CC psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
 CC ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
 CC learning impairment, lung diseases (adult respiratory distress syndrome
 CC (ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
 CC pain, Parkinson's disease, periodontal disease, preterm labour,
 CC psoriasis, reperfusion injury, septic shock, side effects from radiation
 CC therapy, temporal mandibular joint disease, sleep disturbance, uveitis
 CC and inflammatory conditions resulting from strain, sprain, cartilage
 CC damage, trauma, orthopaedic surgery and infection. The present sequence
 CC is a human germline variable region used to determine which residues or
 CC CDRs required to be changed in mouse anti-IL-1 monoclonal antibody MAB201
 CC in order to humanise it or make it into a chimaeric molecule with human
 CC CDR (complementarity determining region) sequences
 XX
 XX Sequence 108 AA;
 SQ
 Query Match 80.4%; Score 45; DB 6; Length 108;
 Best Local Similarity 90.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 DB 24 RASQDISNYL 33
 RESULT 49
 ADH50842
 ID ADH50842 standard; protein; 108 AA.
 XX
 XX ADH50842;
 AC
 XX 25-MAR-2004 (first entry)
 DT
 XX Human VL#19 with grafted anti-CD22 RFB4 binding specificity.
 DE
 XX Humanized antibody; antibody; mouse; CD22; RFB4; human.
 KW
 XX Chimeric.
 OS
 XX Mus sp.
 OS
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 3
 FT /note= "Back-mutated to mouse donor amino acid residue"
 FT Region 24..34
 FT /label= CDR1
 FT Misc-difference 40
 FT /note= "Back-mutated to mouse donor amino acid residue"
 FT Misc-difference 46
 FT /note= "Back-mutated to mouse donor amino acid residue"
 FT Misc-difference 49
 FT /note= "Back-mutated to mouse donor amino acid residue"
 FT Region 50..56
 FT /label= CDR2
 FT Misc-difference 71
 FT /note= "Back-mutated to mouse donor amino acid residue"
 FT Region 89..97
 FT /label= CDR3
 PN WO2003105782-A2.
 XX
 XX 24-DEC-2003.
 PD
 XX 17-JUN-2003; 2003WO-US019333.
 PF
 XX 17-JUN-2002; 2002US-0390033P.
 PR

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYRE-) UNIV READING.
XX Rybak S, Krauss J, Arndt M, Martin ACR;
XX WPI; 2004-082055/08.
XX New heavy or light chain variable useful for specificity grafting, or for
PT generating humanized antibody which in turn is useful for treating
PT lymphocytic leukemia.
XX Disclosure; SEQ ID NO 19; 74pp; English.
XX The present sequence is the protein sequence of a human light chain
CC variable region (VL) framework, denoted VL#19 ADH50825, with grafted
CC complementarity determining regions (CDRs) from mouse anti-human CD22
CC antibody RFB4 VH ADH50840, and with additional human framework residues
CC back-mutated to the mouse donor residue. Claimed humanised antibodies
CC comprise human variable chain framework regions with CDRs from a donor
CC antibody, especially RFB4. RFB4 humanised scFv antibodies have been
CC constructed. Claimed immunoconjugates comprise a humanised antibody
CC linked to a detectable or therapeutic (especially cytotoxic) moiety. The
CC invention also provides a new method of identifying framework acceptor
CC regions in framework sequences for back-mutation to graft a donor
CC sequence to the human framework.
XX Sequence 108 AA;
SQ

Query Match 80.4%; Score 45; DB 8; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
||||| |||
Db 24 RASQDISNYL 33

RESULT 50
ADZ47742
ID ADZ47742 standard; protein; 108 AA.
XX
AC ADZ47742;
XX
DT 30-JUN-2005 (first entry)
XX
DE Mouse anti-IL-1beta monoclonal antibody MAB201 VL #2.
XX
XX Drug screening; antibody identification; cell signaling; inflammation;
KW antiinflammatory; interleukin-1beta; immunoglobulin; monoclonal antibody;
KW light chain variable region.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH
FT Misc-difference 7 /note= "Ser replaces Thr in the humanized VL"
FT
FT Misc-difference 8 /note= "Pro replaces Thr in the humanized VL"
FT
FT Misc-difference 15 /note= "Val replaces Leu in the humanized VL"
FT
FT Misc-difference 22 /note= "Thr replaces Ser in the humanized VL"
FT
FT Misc-difference 41 /note= "Gly replaces Asp in the humanized VL"
FT
FT Misc-difference 42 /note= "Lys replaces Gly in the humanized VL"
FT
FT Misc-difference 43 /note= "Ala replaces Thr in the humanized VL"
FT
FT Misc-difference 44 /note= "Pro replaces Val in the humanized VL"
FT
FT Misc-difference 71 /note= "Phe replaces Tyr in the humanized VL"
FT

Misc-difference 72 /note= "Thr replaces Phe in the humanized VL"
FT
FT Misc-difference 77 /note= "Ser replaces Asn in the humanized VL"
FT
FT Misc-difference 79 /note= "Gln replaces Glu in the humanized VL"
FT
FT Misc-difference 80 /note= "Pro replaces Gln in the humanized VL"
FT
FT Misc-difference 87 /note= "Tyr replaces Phe in the humanized VL"
FT
FT Misc-difference 100 /note= "Gln replaces Gly in the humanized VL"
FT
FT Misc-difference 104 /note= "Val replaces Leu in the humanized VL"
FT
XX US2005084493-A1.
XX 21-APR-2005.
XX 09-NOV-2004; 2004US-00985299.
XX 27-OCT-2000; 2000US-0244118P.
PR 29-OCT-2001; 2001US-00011931.
XX (AMGE-) AMGEN INC.
XX Witte A, Varnum BC, Qian X, Vezina C;
XX WPI; 2005-313939/32.
DR Screening antibodies and other selective interleukin-1 IL-1 binding
XX agents that bind to IL-1 receptor, by detecting binding of IL-1alpha/IL-
FT beta to IL-1R1 in presence of test agent and selecting agent that
FT decreases IL-1 activity.
XX
XX Example 2; Fig 6A; 55pp; English.
XX
XX The invention relates to methods of screening for antibodies or other
CC agents which selectively bind to the pro-inflammatory cytokine
CC interleukin-1 (IL-1) to form an antagonist complex which can still bind
CC to IL-1 receptor type I (IL-1R1) but which cannot activate it. The agents
CC identified using the methods act by blocking the recruitment of the IL-1
CC receptor accessory protein (IL-1RACp) by the IL-1/IL-1R1 complex,
CC preventing IL-1 signaling and thereby reducing inflammatory responses.
CC One screening method of the invention involves detecting the binding of
CC IL-1alpha or IL-1beta to IL-1R1 in the presence of a test agent,
CC detecting IL-1R1 activity in cells comprising IL-1R1 and IL-1alpha or IL-
CC beta, and selecting the test agent which allows IL-1alpha or IL-1beta to
CC bind to IL-1R1 but which decreases IL-1 activity. A second method
CC involves detecting the binding of IL-1RACp to IL-1R1 in the presence of
CC IL-1alpha or IL-1beta and a test agent, and selecting the test agent
CC whose presence correlates with decreased binding to IL-1RACp to IL-1R1.
CC The methods are useful for screening for antibodies and other selective
CC IL-1 binding agents which can be used in the treatment of a variety of
CC acute and chronic IL-1-mediated diseases (including rheumatoid arthritis,
CC Alzheimer's disease, acute pancreatitis, diabetes, graft-versus-host
CC disease, osteoporosis, Parkinson's disease, psoriasis, septic shock, and
CC uveitis), or an inflammatory condition resulting from trauma, cartilage
CC damage, surgery or infection. The present sequence represents the light
CC chain variable region (VL) of the murine anti-IL-1beta monoclonal
CC antibody MAB201, which is capable of blocking the formation of the IL-
CC beta/IL-1 receptor/IL-1RACp complex. The MAB201 VL and heavy chain
CC variable region (VH) were used as the basis for the construction of
CC mouse/human chimeric and CDR-grafted (humanized) versions of the MAB201
CC antibody in an example of the invention. Note: The present sequence
CC differs from SEQ ID NO:4 of the sequence listing (ADZ47655) which is also
CC referred to as a murine monoclonal antibody MAB201 light chain variable
XX region.
XX Sequence 108 AA;
SQ

Query Match 80.4%; Score 45; DB 9; Length 108;
Best Local Similarity 90.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10

Db 24 RASQDISNYL 33

Search completed: May 11, 2006, 16:26:55
Job time : 122.705 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 16.2295 Seconds

(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-4

Perfect score: 56

Sequence: 1 RASQDIGNYLRL 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	80.4	93	2	S38564
2	45	80.4	107	2	S69901
3	45	80.4	107	2	S32188
4	45	80.4	107	2	A28044
5	45	80.4	107	2	D48677
6	45	80.4	107	2	B28044
7	45	80.4	107	2	B49026
8	45	80.4	107	2	S69906
9	45	80.4	108	1	KVMSAR
10	45	80.4	108	2	PL0282
11	45	80.4	108	2	C26405
12	45	80.4	108	2	B26405
13	45	80.4	108	2	S38862
14	45	80.4	108	2	S69902
15	45	80.4	108	2	S69900
16	45	80.4	108	2	S19970
17	45	80.4	108	2	S69903
18	45	80.4	115	2	S53276
19	45	80.4	115	2	JI0080
20	45	80.4	122	2	A29380
21	45	80.4	126	2	A34904
22	45	80.4	127	2	PH1224
23	45	80.4	128	2	A26406
24	44	78.6	139	2	S40365
25	43	76.8	95	2	PH0865
26	43	76.8	109	2	PH0888
27	42	75.0	98	2	PH1065
28	42	75.0	127	2	S52447
29	41	73.2	62	2	S42265

30	41	73.2	87	2	I52592	Ig kappa chain v r
31	41	73.2	88	2	S34087	Ig kappa chain v r
32	41	73.2	88	2	S34088	Ig kappa chain v r
33	41	73.2	95	2	PH0862	Ig kappa chain v r
34	41	73.2	106	2	PL0262	Ig kappa chain v r
35	41	73.2	107	2	I69017	anti-HIV1 envelope
36	41	73.2	108	2	B30551	Ig kappa chain v r
37	41	73.2	108	2	S11124	Ig kappa chain v r
38	41	73.2	110	2	S44118	Ig kappa chain v-J
39	41	73.2	111	2	B37266	Ig kappa chain v r
40	41	73.2	117	2	S42263	Ig kappa chain v r
41	41	73.2	117	2	S43528	Ig kappa chain v r
42	41	73.2	129	2	S52789	Ig kappa chain v r
43	40	71.4	108	1	KVMS73	Ig kappa chain v r
44	40	71.4	109	2	S32001	Ig kappa chain - h
45	40	71.4	109	2	S31980	Ig kappa chain - h
46	40	71.4	109	2	S31979	Ig kappa chain - h
47	40	71.4	125	2	S04936	Ig kappa chain pre
48	40	71.4	130	2	PL0113	Ig kappa chain pre
49	39	69.6	105	2	PH0087	Ig kappa chain v r
50	39	69.6	106	2	PL0267	Ig kappa chain v r
51	39	69.6	108	2	S19674	Ig kappa chain v r
52	39	69.6	109	2	S31981	Ig kappa chain - h
53	39	69.6	122	2	S40314	Ig kappa chain - h
54	39	69.6	123	2	S35479	Ig kappa chain pre
55	39	69.6	127	2	S40367	Ig kappa chain v-J
56	39	69.6	129	1	K1HUKK	Ig kappa chain pre
57	39	69.6	129	2	S40317	Ig kappa chain - h
58	39	69.6	129	2	S29627	Ig kappa chain v r
59	38	67.9	43	2	S21065	Ig kappa chain v r
60	38	67.9	71	2	S21526	Ig kappa chain v r
61	38	67.9	88	2	S21525	Ig kappa chain v r
62	38	67.9	95	2	PH0866	Ig kappa chain v r
63	38	67.9	95	2	PH0863	Ig kappa chain v r
64	38	67.9	101	2	S44117	Ig kappa chain v-J
65	38	67.9	106	2	PC4282	Ig kappa chain (an
66	38	67.9	107	2	S36275	Ig lambda chain v
67	38	67.9	107	2	S40366	Ig kappa chain v-J
68	38	67.9	107	2	B48677	Ig kappa chain v-J
69	38	67.9	107	2	C48677	Ig light chain v-J
70	38	67.9	107	2	A48677	Ig kappa chain v-J
71	38	67.9	111	2	C38740	Ig kappa chain v r
72	38	67.9	117	2	C21056	Ig kappa chain pre
73	38	67.9	129	2	B23986	Ig kappa chain pre
74	38	67.9	131	2	S40352	Ig kappa chain v-J
75	38	67.9	241	2	H81327	hypothetical prote
76	37	66.1	88	2	PL0261	Ig kappa chain v r
77	37	66.1	89	2	A22775	Ig kappa chain pre
78	37	66.1	106	2	PL0260	Ig kappa chain v r
79	37	66.1	106	2	S20652	Ig kappa chain v r
80	37	66.1	108	1	KVMSAA	Ig kappa chain v r
81	37	66.1	111	2	I38740	Ig kappa chain v r
82	37	66.1	115	1	KVMSL6	Ig kappa chain pre
83	37	66.1	115	2	S10146	Ig kappa chain pre
84	37	66.1	117	1	KVMS3B	Ig kappa chain pre
85	37	66.1	128	1	KVMS71	Ig kappa chain pre
86	37	66.1	128	2	PL0101	Ig kappa chain pre
87	37	66.1	130	1	KVMSM4	Ig kappa chain pre
88	37	66.1	162	1	CFMWA	C-phycocyanin alph
89	37	66.1	162	2	T11978	phycocyanin alpha
90	37	66.1	163	2	B35126	Ig kappa chain pre
91	37	66.1	234	2	S14237	Ig kappa chain pre
92	37	66.1	470	2	T29380	hypothetical prote
93	37	66.1	520	2	A35883	laccase (EC 1.10.3
94	37	66.1	520	2	B35883	ligninolytic pheno
95	37	66.1	623	2	S46427	botulinum neurotox
96	37	66.1	2188	2	A70984	probable polyketid
97	37	66.1	10797	2	T30192	probable peptide s
98	36	64.3	92	2	D28840	Ig kappa chain v r
99	36	64.3	95	2	PH0867	Ig kappa chain v r
100	36	64.3	101	2	C28840	Ig kappa chain v r
101	36	64.3	101	2	B28840	Ig kappa chain v r
102	36	64.3	106	2	C33936	Ig kappa chain v r

103	36	64.3	106	2	PL0259	Ig kappa chain V r	176	34	60.7	482	2	AB1421	beta-glucosidase h
104	36	64.3	108	1	KIHUAG	Ig kappa chain V-I	177	34	60.7	538	2	C90406	conserved hypothet
105	36	64.3	108	1	KIHUAG	Ig kappa chain V-I	178	34	60.7	709	2	A97218	uncharacterized co
106	36	64.3	108	2	I39154	Ig kappa chain (BR	179	34	60.7	901	1	WMNVN	104K glycoprotein
107	36	64.3	135	2	S24330	Ig kappa chain pre	180	34	60.7	1035	2	G97273	isoleucyl-tRNA syn
108	36	64.3	162	1	CFYCA3	R-phycocyanin ii a	181	34	60.7	1116	2	T30828	RNA-directed RNA p
109	36	64.3	163	2	A29674	phycocyanin alpha	182	34	60.7	1398	2	T18350	probable pol polyph
110	36	64.3	163	2	AH1872	phycocyanin alpha	183	33.5	59.8	108	2	E30609	Ig kappa chain V-I
111	36	64.3	416	2	S19382	probable membrane	184	33	58.9	39	2	PH0878	Ig kappa chain V r
112	36	64.3	1033	2	S19247	cell adhesion prot	185	33	58.9	53	2	PH0881	Ig kappa chain V r
113	35	62.5	85	2	S76972	hypothetical prote	186	33	58.9	54	2	E36943	chemoreceptor prot
114	35	62.5	91	2	S37511	Ig kappa chain V r	187	33	58.9	78	2	S34102	Ig kappa chain V r
115	35	62.5	91	2	S17622	Ig kappa chain V r	188	33	58.9	82	2	S34090	Ig kappa chain V r
116	35	62.5	98	2	PH1062	Ig light chain V r	189	33	58.9	86	2	S16837	Ig kappa chain V r
117	35	62.5	101	2	S13701	Ig kappa chain V r	190	33	58.9	86	2	S16830	Ig kappa chain V r
118	35	62.5	103	2	S13703	Ig kappa chain V r	191	33	58.9	86	2	S16833	Ig kappa chain V-I
119	35	62.5	104	2	S13700	Ig kappa chain V r	192	33	58.9	86	2	S16826	Ig kappa chain V r
120	35	62.5	108	1	KIHUWS	Ig kappa chain V-I	193	33	58.9	87	2	S21523	Ig kappa chain V r
121	35	62.5	108	2	S40330	Ig kappa chain V-J	194	33	58.9	88	2	S21520	Ig kappa chain V r
122	35	62.5	108	4	B47271	nitrophenyl phosph	195	33	58.9	88	2	S34104	Ig kappa chain V r
123	35	62.5	117	2	S46376	Ig kappa chain V-J	196	33	58.9	88	2	S21524	Ig kappa chain V r
124	35	62.5	125	2	S40315	Ig kappa chain - h	197	33	58.9	88	2	S38562	Ig kappa chain V r
125	35	62.5	129	2	S40332	Ig kappa chain - h	198	33	58.9	92	2	S37506	Ig kappa chain V r
126	35	62.5	421	2	H81843	conserved hypothet	199	33	58.9	92	2	S37512	Ig kappa chain V r
127	35	62.5	421	2	D81098	gcpE protein NMB13	200	33	58.9	92	2	S37522	Ig kappa chain V r
128	35	62.5	561	2	T34368	hypothetical prote	201	33	58.9	92	2	S37516	Ig kappa chain V r
129	35	62.5	573	2	E84687	hypothetical prote	202	33	58.9	95	2	S45324	Ig kappa chain V r
130	35	62.5	1777	2	T34369	hypothetical prote	203	33	58.9	106	2	PC2397	anti-tetanus toxin
131	34.5	61.6	92	2	S37507	Ig kappa chain V r	204	33	58.9	108	2	G44151	Ig kappa chain V r
132	34	60.7	53	2	T23548	hypothetical prote	205	33	58.9	108	2	S34007	Ig kappa chain V r
133	34	60.7	67	2	AC1954	hypothetical prote	206	33	58.9	108	2	S30521	Ig kappa chain V r
134	34	60.7	72	2	H36025	Ig heavy chain V r	207	33	58.9	111	2	S23628	Ig kappa chain V r
135	34	60.7	81	2	G36025	Ig light chain V r	208	33	58.9	111	2	A38740	Ig kappa chain V r
136	34	60.7	85	2	F36025	Ig light chain V r	209	33	58.9	111	2	E38740	Ig kappa chain V r
137	34	60.7	86	2	S34086	Ig kappa chain V r	210	33	58.9	111	2	C38740	Ig kappa chain V r
138	34	60.7	87	2	S34084	Ig kappa chain V r	211	33	58.9	114	2	S54905	Ig kappa chain V r
139	34	60.7	87	2	S34083	Ig kappa chain V r	212	33	58.9	115	1	K3HUVG	Ig kappa chain pre
140	34	60.7	88	2	S21522	Ig kappa chain V r	213	33	58.9	117	2	S41810	Ig kappa chain V r
141	34	60.7	88	2	S21528	Ig kappa chain V r	214	33	58.9	124	2	S40318	Ig kappa chain V r
142	34	60.7	94	2	E33750	Ig kappa chain V r	215	33	58.9	124	2	S40336	Ig kappa chain V-J
143	34	60.7	96	2	G33730	Ig kappa chain V r	216	33	58.9	127	2	A23986	Ig kappa chain pre
144	34	60.7	97	2	PH1064	Ig light chain V r	217	33	58.9	128	2	S46372	Ig light chain var
145	34	60.7	101	2	B37262	Ig kappa chain V r	218	33	58.9	128	2	A56701	Ig kappa chain V r
146	34	60.7	103	2	S44121	Ig kappa chain V-J	219	33	58.9	128	2	S40379	Ig kappa chain V-J
147	34	60.7	103	2	S19975	Ig kappa chain V r	220	33	58.9	129	2	S52792	Ig kappa chain V r
148	34	60.7	104	2	S26330	Ig kappa chain V r	221	33	58.9	129	2	S40363	Ig kappa chain - h
149	34	60.7	104	2	S26329	Ig kappa chain V r	222	33	58.9	130	2	S40368	Ig kappa chain - h
150	34	60.7	107	2	S36264	Ig lambda chain V	223	33	58.9	132	2	S38646	Ig kappa chain - h
151	34	60.7	107	2	S47183	Ig kappa chain - h	224	33	58.9	132	2	S40334	Ig kappa chain - h
152	34	60.7	108	1	KIHUHU	Ig kappa chain V-I	225	33	58.9	142	2	E95176	acetyltransferase,
153	34	60.7	108	2	S44122	Ig kappa chain V r	226	33	58.9	144	2	PL0106	Ig kappa chain pre
154	34	60.7	108	2	S47182	Ig kappa chain - h	227	33	58.9	160	2	G98042	hypothetical prote
155	34	60.7	108	2	B49047	Ig kappa chain V r	228	33	58.9	201	2	D81519	hypothetical prote
156	34	60.7	116	2	A27594	Ig kappa chain pre	229	33	58.9	201	2	G81182	hypothetical prote
157	34	60.7	117	2	S24206	Ig kappa chain V r	230	33	58.9	228	2	H90098	translation initia
158	34	60.7	122	2	S40351	Ig kappa chain V-J	231	33	58.9	235	2	S14675	Ig lambda chain -
159	34	60.7	123	2	S40331	Ig kappa chain - h	232	33	58.9	240	1	A37769	hlyX protein - Act
160	34	60.7	125	2	S40353	Ig kappa chain V-J	233	33	58.9	250	1	RGECE	transcription regu
161	34	60.7	125	2	S09365	Ig kappa chain - m	234	33	58.9	250	2	A49310	etrA protein - She
162	34	60.7	158	2	A97262	uncharacterized co	235	33	58.9	250	2	C90868	transcription regu
163	34	60.7	162	1	CFPKA	C-phycocyanin alph	236	33	58.9	250	2	F85750	=transcription reg
164	34	60.7	162	1	CFYCAA	C-phycocyanin alph	237	33	58.9	250	2	F82199	fumarate and nitra
165	34	60.7	162	2	S30940	phycocyanin alpha	238	33	58.9	250	2	AB0280	fumarate and nitra
166	34	60.7	162	2	S73239	phycocyanin alpha	239	33	58.9	257	2	E64122	regulatory protein
167	34	60.7	162	2	S43238	R-phycocyanin I al	240	33	58.9	284	2	AB0662	fumarate and nitra
168	34	60.7	162	2	S75317	phycocyanin alpha	241	33	58.9	309	2	S78291	probable transcrip
169	34	60.7	162	2	TF0968	C-phycocyanin alph	242	33	58.9	353	2	A70798	probable transcrip
170	34	60.7	163	1	CFYCAA	C-phycocyanin alph	243	33	58.9	363	2	D64640	hypothetical prote
171	34	60.7	230	2	S33151	Ig kappa chain - s	244	33	58.9	366	2	S76662	S-adenosylmethoni
172	34	60.7	242	2	AG1823	hypothetical prote	245	33	58.9	385	2	S54705	transcription fact
173	34	60.7	342	2	E70463	conserved hypothet	246	33	58.9	385	2	H97335	Na+ ABC transporte
174	34	60.7	349	2	F84246	hypothetical prote	247	33	58.9	424	2	AC2975	oxidoreductase ord
175	34	60.7	411	2	T36526	probable cytochrom	248	33	58.9	424	2	H98307	probable oxidoredu

249	33	58.9	425	2	B95389	probable oxidoredu	322	57.1	516	2	T37066	probable integral
250	33	58.9	438	2	H84711	hypothetical prote	323	57.1	527	2	T07607	phosphate transpor
251	33	58.9	449	2	I52630	GABAA receptor del	324	57.1	528	2	T05724	probable inorganic
252	33	58.9	449	2	A36303	gamma-aminobutyric	325	57.1	532	2	B82354	deoxycytidylate de
253	33	58.9	449	2	A34625	probable ABC subet	326	57.1	536	2	A10278	probable AMP nucle
254	33	58.9	470	2	B82943	probable ABC subet	327	57.1	554	2	AC0320	asparagine synthas
255	33	58.9	507	2	F86033	probable sugar upt	328	57.1	586	2	B83790	hypothetical prote
256	33	58.9	557	2	A32694	interferon alpha/b	329	57.1	618	2	D75502	cell division prot
257	33	58.9	560	2	S27387	interferon alpha r	330	57.1	630	2	T00351	hypothetical prote
258	33	58.9	566	2	C18170	probable single-st	331	57.1	658	2	A11385	exonuclease ABC (
259	33	58.9	566	2	G81151	single-stranded-DN	332	57.1	658	2	AC1761	excinuclease ABC (
260	33	58.9	590	2	A45283	interferon alpha/b	333	57.1	685	1	SXBPT4	NAD+-protein ADP-r
261	33	58.9	619	2	F81324	glucose inhibited	334	57.1	697	2	C71850	probable outer mem
262	33	58.9	695	2	T40717	hypothetical prote	335	57.1	814	1	C40618	fibriular outer mem
263	33	58.9	792	2	B82756	organic solvent to	336	57.1	818	2	S58333	probable membrane
264	33	58.9	835	2	T35763	probable aminopept	337	57.1	838	2	AC1064	outer membrane fil
265	33	58.9	1114	2	T30819	RNA-directed RNA p	338	57.1	912	2	C64107	transferrin-bindin
266	33	58.9	1140	2	S73786	hypothetical prote	339	57.1	1012	2	T13712	dof protein - frui
267	33	58.9	1164	2	C86238	protein T10024.5 [340	57.1	1144	2	T13749	dof protein - frui
268	33	58.9	1231	2	S30185	insulin receptor s	341	57.1	1463	2	T30290	AAS surface protei
269	33	58.9	1458	2	S36014	dynein heavy chain	342	57.1	1622	2	T45240	hypothetical prote
270	32.5	58.0	108	1	K3HUB6	ig kappa chain V-I	343	55.4	55	2	G86706	hypothetical prote
271	32.5	58.0	409	2	B71198	hypothetical prote	344	55.4	82	2	C69013	hypothetical prote
272	32	57.1	75	2	A71423	hypothetical prote	345	55.4	86	2	C28195	ig kappa chain V r
273	32	57.1	86	2	S16825	ig kappa chain V r	346	55.4	95	2	PH0864	ig kappa chain V r
274	32	57.1	92	2	T45409	hypothetical prote	347	55.4	98	2	S36068	ig lambda chain -
275	32	57.1	107	2	S57444	ig kappa chain V-J	348	55.4	100	2	E90330	hypothetical prote
276	32	57.1	108	1	K1HUBN	ig kappa chain V-I	349	55.4	107	2	B28195	ig kappa chain V r
277	32	57.1	108	1	KVRB12	ig kappa chain V r	350	55.4	107	2	A28195	ig kappa chain V r
278	32	57.1	115	2	S11697	ig kappa chain pre	351	55.4	108	1	K1HUOU	ig kappa chain V-I
279	32	57.1	125	2	S40344	ig kappa chain V-J	352	55.4	108	1	K1HURW	ig kappa chain V-I
280	32	57.1	129	2	E95189	hypothetical prote	353	55.4	108	1	K1HUSW	ig kappa chain V-I
281	32	57.1	152	2	H83578	hypothetical prote	354	55.4	108	1	KVRB2K	ig kappa chain V r
282	32	57.1	154	2	A11231	hypothetical prote	355	55.4	108	2	S36277	ig lambda chain V
283	32	57.1	154	2	AH1585	hypothetical prote	356	55.4	108	2	S31977	ig kappa chain - h
284	32	57.1	155	2	S78774	perlucin - Haloti	357	55.4	108	2	S77752	probable phosphor
285	32	57.1	157	2	E84433	hypothetical prote	358	55.4	108	2	S19112	ig kappa chain V r
286	32	57.1	162	1	B28539	c-phycocyanin 2 al	359	55.4	109	2	S31998	ig kappa chain - h
287	32	57.1	164	2	S43779	phycocerythrin I al	360	55.4	112	2	I51578	gene wnt-88 protei
288	32	57.1	164	2	G45045	phycocerythrin I al	361	55.4	114	2	S00996	ig kappa chain pre
289	32	57.1	167	2	I58352	pl6INK4a - mouse	362	55.4	115	1	KVMSK2	ig kappa chain pre
290	32	57.1	171	2	T13554	hypothetical prote	363	55.4	117	2	S04525	ig lambda chain pr
291	32	57.1	176	2	T50767	peptidylprolyl iso	364	55.4	125	2	S40350	ig kappa chain - h
292	32	57.1	181	2	S65230	hypothetical prote	365	55.4	128	2	A47159	ig lambda chain V
293	32	57.1	210	2	S34135	ribosomal protein	366	55.4	129	2	S52793	ig kappa chain V r
294	32	57.1	212	1	RSHS1	ribosomal protein	367	55.4	129	2	A42692	T-cell receptor al
295	32	57.1	219	2	AG2036	hypothetical prote	368	55.4	136	2	A12084	hypothetical prote
296	32	57.1	221	2	T15782	hypothetical prote	369	55.4	143	2	S72515	PTS system mannito
297	32	57.1	223	2	S16652	hypothetical prote	370	55.4	143	2	A96819	hypothetical prote
298	32	57.1	287	2	A10782	probable transcript	371	55.4	146	2	S60698	gag protein - huma
299	32	57.1	290	2	AG0159	probable lysR-fami	372	55.4	146	2	S60704	gag protein - huma
300	32	57.1	293	2	D64984	hypothetical trans	373	55.4	146	2	S60702	gag protein - huma
301	32	57.1	293	2	C85854	probable transcript	374	55.4	146	2	S60703	gag protein - huma
302	32	57.1	293	2	A98010	probable transcript	375	55.4	154	2	B89699	conserved hypotet
303	32	57.1	311	2	G97403	methionyl-tRNA for	376	55.4	158	2	S15263	finA protein - Dic
304	32	57.1	311	2	AG2621	probable membrane	377	55.4	160	2	S00714	phycocyanin 1 alph
305	32	57.1	337	2	S42416	probable membrane	378	55.4	162	2	S05712	phycocyanin 3 alph
306	32	57.1	353	2	S43134	hypothetical prote	379	55.4	176	2	S12914	calponin - turkey
307	32	57.1	365	2	I50690	wnt-8C - chicken	380	55.4	180	2	AP2397	hypothetical prote
308	32	57.1	365	2	H82749	magnesium and coba	381	55.4	180	2	T41300	protein involved i
309	32	57.1	366	2	G64449	modification methy	382	55.4	182	2	E37246	hypothetical prote
310	32	57.1	382	2	A82173	probable ABC trans	383	55.4	185	2	S63457	hypothetical prote
311	32	57.1	391	2	A71936	hypothetical prote	384	55.4	190	2	T07895	prosyetamin - pept
312	32	57.1	391	2	B64648	conserved hypotet	385	55.4	203	2	AC3344	hypothetical prote
313	32	57.1	406	2	S40774	ribonucleoprotein	386	55.4	203	2	T18679	hypothetical prote
314	32	57.1	428	2	A83642	hypothetical prote	387	55.4	237	2	A84997	N-acetylmuramoyl-L
315	32	57.1	460	2	G85686	sensor protein Pho	388	55.4	241	2	A49926	transcription regu
316	32	57.1	484	2	AD0199	sensor protein kin	389	55.4	253	2	D75193	hypothetical prote
317	32	57.1	486	1	B41966	sensor kinase phoQ	390	55.4	286	2	A82159	hypothetical prote
318	32	57.1	486	2	A99829	sensor protein Pho	391	55.4	290	2	AG2216	hypothetical prote
319	32	57.1	487	1	VZE8PT	sensor kinase phoQ	392	55.4	292	1	A39871	calponin alpha, sm
320	32	57.1	487	2	AG0646	sensor protein Pho	393	55.4	297	2	B82972	probable transcrip
321	32	57.1	516	2	AH0178	conserved hypotet	394	55.4	310	2	D71679	UDP-n-acetylenolpy

395	31	55.4	312	2	B96512	hypothetical prote	468	31	55.4	735	2	AC0858	conserved hypothet
396	31	55.4	326	1	B70164	thioredoxin-disulf	469	31	55.4	782	2	D84514	dynamain-like prote
397	31	55.4	329	1	I64160	hypothetical prote	470	31	55.4	808	2	T25748	hypothetical prote
398	31	55.4	339	2	B70024	hypothetical prote	471	31	55.4	870	2	AB0570	outer membrane ush
399	31	55.4	341	1	RGO0BE	GTP-binding regula	472	31	55.4	873	2	B83148	leucyl-tRNA synthet
400	31	55.4	341	2	S34348	GTP-binding regula	473	31	55.4	880	2	S51473	probable membrane
401	31	55.4	348	2	G71681	hypothetical prote	474	31	55.4	927	2	T47827	squamosa promoter
402	31	55.4	351	2	AD2599	hypothetical prote	475	31	55.4	1011	2	T13669	neuromusculin - fr
403	31	55.4	351	2	E97381	myrin endopeptida	476	31	55.4	1039	2	T22982	hypothetical prote
404	31	55.4	357	2	C97744	hypothetical prote	477	31	55.4	1148	2	T00016	minor outer capsid
405	31	55.4	358	2	I50506	gene wnt8b protein	478	31	55.4	1192	2	H88293	protein F59B10.1 [
406	31	55.4	361	2	I50505	gene wnt8 protein	479	31	55.4	1469	2	B36665	slit protein 2 pre
407	31	55.4	376	2	T34734	hypothetical prote	480	31	55.4	1480	2	A36665	slit protein 1 pre
408	31	55.4	379	2	C90987	probable polysacch	481	31	55.4	1480	2	B36665	hypothetical prote
409	31	55.4	379	2	E64972	probable polysacch	482	31	55.4	3263	2	E82410	hypothetical prote
410	31	55.4	379	2	F85832	probable polysacch	483	31	53.6	67	2	T1854	hypothetical prote
411	31	55.4	379	2	A83404	hypothetical prote	484	31	53.6	79	2	D97811	hypothetical prote
412	31	55.4	379	2	E97198	methyl-accepting c	485	31	53.6	84	2	B81930	hypothetical prote
413	31	55.4	383	2	G84597	probable XAP-5 pro	486	31	53.6	86	2	S78488	hypothetical prote
414	31	55.4	387	2	S18771	developmental regu	487	31	53.6	91	2	PH1071	hypothetical prote
415	31	55.4	387	2	E75184	hypothetical prote	488	31	53.6	96	2	PH1070	hypothetical prote
416	31	55.4	391	2	S23507	pyruvate dehydroge	489	31	53.6	102	2	PH1079	hypothetical prote
417	31	55.4	394	2	F75462	conserved hypothet	490	31	53.6	102	2	S26346	hypothetical prote
418	31	55.4	406	2	B32029	hypothetical prote	491	31	53.6	104	2	B43413	hypothetical prote
419	31	55.4	413	2	A54127	dolichyl-diphospho	492	31	53.6	104	2	B43413	hypothetical prote
420	31	55.4	414	2	A44654	dolichyl-diphospho	493	31	53.6	107	1	K1HUAR	hypothetical prote
421	31	55.4	422	2	A26328	cyclin A - Atlanti	494	31	53.6	107	2	PL0268	hypothetical prote
422	31	55.4	423	2	AC3553	4-aminobutyrate tr	495	31	53.6	107	2	B45722	anti-glycoprotein
423	31	55.4	425	2	A70394	hypothetical prote	496	31	53.6	107	2	A45722	anti-glycoprotein
424	31	55.4	427	2	AE2512	hypothetical prote	497	31	53.6	107	2	S12954	hypothetical prote
425	31	55.4	428	2	I51680	Xwnt-8b - African	498	31	53.6	108	1	K1HUBI	hypothetical prote
426	31	55.4	430	2	T09061	PBX2 protein - mou	499	31	53.6	108	2	C30502	hypothetical prote
427	31	55.4	430	2	A56002	pre-B-cell leukemi	500	31	53.6	111	1	KVMS50	hypothetical prote
428	31	55.4	445	2	A45139	oligosaccharyltran	501	31	53.6	111	1	KVMS80	hypothetical prote
429	31	55.4	446	2	F64172	hypothetical prote	502	31	53.6	111	2	S09969	hypothetical prote
430	31	55.4	447	2	G85614	probable polynucle	503	31	53.6	115	2	A25924	hypothetical prote
431	31	55.4	447	2	AH0611	conserevd hypothet	504	31	53.6	117	2	S42466	hypothetical prote
432	31	55.4	447	2	C64828	probable polynucle	505	31	53.6	120	2	S06732	hypothetical prote
433	31	55.4	447	2	A99751	probable polynucle	506	31	53.6	125	2	AF1134	hypothetical prote
434	31	55.4	447	2	A99751	probable polynucle	507	31	53.6	127	2	S04577	hypothetical prote
435	31	55.4	449	2	G82241	probable ATPase pr	508	31	53.6	128	2	B64764	hypothetical prote
436	31	55.4	450	2	T39088	conserved hypothet	509	31	53.6	129	2	S32806	hypothetical prote
437	31	55.4	451	2	T47824	hypothetical prote	510	31	53.6	129	2	A81980	hypothetical prote
438	31	55.4	475	2	T35697	arabinofuranosidas	511	31	53.6	129	2	A81035	conserved hypothet
439	31	55.4	482	2	B69780	transcription regu	512	31	53.6	138	2	A26471	Ig kappa chain pre
440	31	55.4	483	2	T16443	hypothetical prote	513	31	53.6	138	2	B55479	CDK4 inhibitor p14
441	31	55.4	497	1	F0LJND	gag polyprotein -	514	31	53.6	150	2	E90302	hypothetical prote
442	31	55.4	499	2	H83148	AMP nucleosidase P	515	31	53.6	151	2	C86352	hypothetical prote
443	31	55.4	502	1	FOVWA2	gag polyprotein -	516	31	53.6	153	2	A87400	conserved hypothet
444	31	55.4	508	2	T22954	hypothetical prote	517	31	53.6	160	2	T30571	hypothetical prote
445	31	55.4	515	1	VHNZB3	nucleocapsid prote	518	31	53.6	160	2	A82020	probable periplasm
446	31	55.4	515	1	VHNZP3	nucleocapsid prote	519	31	53.6	160	2	D81247	thioredoxin-relate
447	31	55.4	520	2	JC5356	laccase [EC 1.10.3	520	31	53.6	180	2	D87754	protein C43E11.9 [
448	31	55.4	520	2	S59533	laccase [EC 1.10.3	521	31	53.6	180	2	E64009	hypothetical prote
449	31	55.4	524	1	VHNZP1	nucleocapsid prote	522	31	53.6	180	2	B95391	protein [imported
450	31	55.4	524	1	A48341	nucleocapsid prote	523	31	53.6	197	2	D71145	hypothetical prote
451	31	55.4	524	1	VHNZSV	nucleocapsid prote	524	31	53.6	221	2	T50958	hypothetical prote
452	31	55.4	524	1	VHNZT1	nucleocapsid prote	525	31	53.6	222	2	T50958	hypothetical prote
453	31	55.4	524	2	S72317	nucleocapsid prote	526	31	53.6	223	2	A90523	hypothetical prote
454	31	55.4	524	2	S72316	nucleocapsid prote	527	31	53.6	223	2	B90088	similar to proteas
455	31	55.4	544	2	B75379	CTP synthase - Dei	528	31	53.6	246	2	S50731	hypothetical prote
456	31	55.4	549	2	T17525	proline-rich prote	529	31	53.6	254	2	C75219	probable myo-inosi
457	31	55.4	573	2	D90202	methionyl-tRNA syn	530	31	53.6	254	2	E71203	hypothetical prote
458	31	55.4	581	2	T29830	hypothetical prote	531	31	53.6	259	2	H81159	conserved hypothet
459	31	55.4	587	2	JH0464	DM-GRASP precursor	532	31	53.6	259	2	B81945	hypothetical prote
460	31	55.4	588	2	JH0506	adhesion molecule	533	31	53.6	263	2	AD0590	endonuclease VIII,
461	31	55.4	588	2	A45254	surface glycoprote	534	31	53.6	263	2	A85572	hypothetical prote
462	31	55.4	593	2	AB0046	probable N-acetyl	535	31	53.6	263	2	C90721	hypothetical prote
463	31	55.4	624	2	A83237	hypothetical prote	536	31	53.6	263	2	A64807	endonuclease VIII
464	31	55.4	632	2	C86922	probable membrane	537	31	53.6	271	1	ONGAPA	egg-laying hormone
465	31	55.4	695	2	G84137	methyl-accepting c	538	31	53.6	275	2	E91111	probable adherence
466	31	55.4	715	2	E71073	hypothetical prote	539	31	53.6	275	2	A85957	probable cytotoxin
467	31	55.4	720	2	F64079	ornithine decarbox	540	31	53.6	282	2	F71076	hypothetical prote
													5,10-methyltetra

541	30	53.6	292	2	A64487	modification methy	614	30	53.6	560	2	T08202	L-amino-acid oxida
542	30	53.6	293	2	AC3451	pantoate-beta-alan	615	30	53.6	562	2	S56145	BSG9 protein - hum
543	30	53.6	301	2	T19672	hypothetical prote	616	30	53.6	583	2	I39428	alcam - human
544	30	53.6	301	2	T50001	hypothetical prote	617	30	53.6	585	2	G96995	ATP-dependent RNA
545	30	53.6	309	2	G72365	conserved hypotet	618	30	53.6	590	2	D69722	thiamin biosynthes
546	30	53.6	312	2	B69303	hypothetical prote	619	30	53.6	594	2	T31744	hypothetical prote
547	30	53.6	315	2	S58171	bifunctional cycla	620	30	53.6	599	1	WBP92	gene 9 protein - p
548	30	53.6	328	2	S47800	hypothetical 36k p	621	30	53.6	605	2	D82434	probable conserved
549	30	53.6	332	2	C90607	hypothetical prote	622	30	53.6	614	1	T19539	hypothetical prote
550	30	53.6	333	2	AF1924	succinate dehydrog	623	30	53.6	619	1	KGNCLO	laccase (EC 1.10.3
551	30	53.6	333	2	H83364	hypothetical prote	624	30	53.6	619	1	KGNCLO	laccase (EC 1.10.3
552	30	53.6	334	2	C22735	hypothetical nox2	625	30	53.6	624	2	S74222	alpha-galactosidas
553	30	53.6	334	2	AH03000	conserved hypotet	626	30	53.6	631	2	G64048	heat shock protein
554	30	53.6	335	2	G88640	protein F52C12.3 [627	30	53.6	633	2	S23151	glycine transporte
555	30	53.6	338	2	T47427	hypothetical prote	628	30	53.6	638	2	I77912	glycine transporte
556	30	53.6	345	2	T46962	8-oxoguanine DNA-g	629	30	53.6	641	2	A24075	lipase precursor -
557	30	53.6	346	2	T35215	hypothetical prote	630	30	53.6	666	2	C82932	exonuclease ABC s
558	30	53.6	348	2	D82114	flagellar motor sw	631	30	53.6	667	2	B96575	hypothetical prote
559	30	53.6	350	1	RGH071	GTP-binding regula	632	30	53.6	680	2	T27078	hypothetical prote
560	30	53.6	350	1	RGH071	GTP-binding regula	633	30	53.6	682	2	AG2118	serine/threonine k
561	30	53.6	350	1	RGH071	GTP-binding regula	634	30	53.6	692	2	I57956	glycine transporte
562	30	53.6	353	2	T48310	hypothetical prote	635	30	53.6	703	2	T41065	RNA binding protei
563	30	53.6	354	1	RGH072	GTP-binding regula	636	30	53.6	705	2	S34155	gene Mx protein -
564	30	53.6	354	2	S24352	gustducin - rat	637	30	53.6	719	2	T49434	hypothetical prote
565	30	53.6	354	2	C82110	probable permease	638	30	53.6	723	2	S51788	malate synthase [S
566	30	53.6	354	2	E83751	ABC transporter (A	639	30	53.6	730	2	B83592	hypothetical prote
567	30	53.6	357	2	H83519	conserved hypotet	640	30	53.6	755	1	S74695	hypothetical prote
568	30	53.6	358	2	G64230	pyruvate dehydroge	641	30	53.6	755	2	E95302	FixI2 E1-E2 type C
569	30	53.6	360	2	G84060	hypothetical prote	642	30	53.6	756	2	AC2378	penicillin-binding
570	30	53.6	377	2	T21170	hypothetical prote	643	30	53.6	758	2	S37855	hypothetical prote
571	30	53.6	380	2	H90261	hypothetical prote	644	30	53.6	773	1	QRRBG	secretory componen
572	30	53.6	382	2	C85725	probable outer mem	645	30	53.6	787	2	C81166	phenylalanyl-tRNA
573	30	53.6	382	2	JQ1122	gas-vesicle operon	646	30	53.6	791	2	A81940	probable phenylala
574	30	53.6	382	2	T08243	gas-vesicle operon	647	30	53.6	791	2	E81906	probable ribonucle
575	30	53.6	382	2	F90892	probable outer mem	648	30	53.6	791	2	G81109	ribonuclease II fa
576	30	53.6	382	2	D64904	outer membrane uah	649	30	53.6	820	2	G86246	hypothetical prote
577	30	53.6	384	2	A12962	cellulose syntheti	650	30	53.6	837	2	B82932	preproteol translo
578	30	53.6	388	2	G82150	mannose-6-phosphat	651	30	53.6	843	2	S33442	EF protein - Strep
579	30	53.6	389	2	E98320	hypothetical prote	652	30	53.6	868	1	A45391	mRNA guanylyltrans
580	30	53.6	390	2	I64149	hypothetical prote	653	30	53.6	876	2	G89952	DNA polymerase I [
581	30	53.6	391	2	AH1968	phosphoribosylglyc	654	30	53.6	882	2	B96788	protein T4O12.15 [
582	30	53.6	391	2	T08338	conserved hypotet	655	30	53.6	883	2	B85725	probable fibinrial
583	30	53.6	400	1	B65075	probable monooxyge	656	30	53.6	884	2	S61569	hypothetical prote
584	30	53.6	400	2	E85946	hypothetical prote	657	30	53.6	904	2	G90563	lipoprotein (impor
585	30	53.6	400	2	A98101	hypothetical prote	658	30	53.6	925	1	TVHUBD	transforming prote
586	30	53.6	405	2	T40300	histone deacetylase	659	30	53.6	939	2	AR2275	hypothetical prote
587	30	53.6	407	2	D66721	hypothetical prote	660	30	53.6	982	1	VCLJLK	env polypeptin -
588	30	53.6	413	2	F96743	probable C2H2-type	661	30	53.6	1004	2	A48821	wnt-5 protein - fr
589	30	53.6	415	2	C87328	conserved hypotet	662	30	53.6	1057	2	T04874	hypothetical prote
590	30	53.6	416	2	C97197	Zn-dependent prote	663	30	53.6	1059	2	G83706	lanthibiotic merasc
591	30	53.6	421	2	I49375	serotonin receptor	664	30	53.6	1162	2	PC4184	leptin receptor, O
592	30	53.6	421	2	T00955	hypothetical prote	665	30	53.6	1289	2	T46486	chromosomal protei
593	30	53.6	422	2	I38209	serotonin receptor	666	30	53.6	1290	2	A57190	ebnerin precursor
594	30	53.6	422	2	JH0315	serotonin receptor	667	30	53.6	1358	2	B86241	hypothetical prote
595	30	53.6	438	2	T45602	glucosyltransferase	668	30	53.6	1441	1	GNVULC	M polyprotein prec
596	30	53.6	440	2	T07676	cyclin b1-type, mi	669	30	53.6	1444	1	A30588	140K adhesin precu
597	30	53.6	440	2	C97376	probable transport	670	30	53.6	1464	2	T07050	hypothetical prote
598	30	53.6	440	2	A12593	MPS permease limpo	671	30	53.6	1493	2	S49777	probable membrane
599	30	53.6	444	2	AH0346	putative Hyd fami	672	30	53.6	1529	2	T20986	hypothetical prote
600	30	53.6	447	2	AG0393	NADH2 dehydrogenas	673	30	53.6	1594	2	T30549	hensin - rabbit
601	30	53.6	451	2	F89130	protein F52E1.10 [674	30	53.6	1784	2	T43167	EF protein - Strep
602	30	53.6	455	2	C84133	glutamine syntheta	675	30	53.6	1822	2	S33441	N conserved hypoth
603	30	53.6	477	2	T52382	zinc finger protei	676	30	53.6	1948	2	B69511	CRP-ductin-alpha p
604	30	53.6	479	2	F84179	hypothetical prote	677	30	53.6	2083	2	T42721	genome polyprotein
605	30	53.6	484	2	AC0756	AMP nucleosidase [678	30	53.6	2344	2	S64740	genome polyprotein
606	30	53.6	484	2	C90976	AMP nucleosidase [679	30	53.6	2344	2	S55399	genome polyprotein
607	30	53.6	484	2	H64962	AMP nucleosidase [680	30	53.6	2344	2	S55399	genome polyprotein
608	30	53.6	484	2	A85823	AMP nucleosidase [681	30	53.6	2348	2	AD1841	hypothetical prote
609	30	53.6	532	2	T08205	nucleocapsid prote	682	30	53.6	2403	2	A59386	sanko - human
610	30	53.6	535	2	T52048	probable beta-gluc	683	30	53.6	2491	2	A57036	talin - slime mold
611	30	53.6	547	2	AE1884	hypothetical prote	684	30	53.6	2630	2	T08868	polyprotein P1-A
612	30	53.6	548	2	S18746	laccase (EC 1.10.3	685	30	53.6	2693	2	A40743	IP3 receptor, XIP3
613	30	53.6	554	2	E90601	hypothetical prote	686	30	53.6	2695	2	S54974	type 1 inositol 1,

687	30	53.6	2713	2	A55713	inositol 1,4,5-tri	760	29	51.8	227	2	B64617	hypothetical prote
688	30	53.6	2734	2	B36579	inositol 1,4,5-tri	761	29	51.8	228	2	S75999	hypothetical prote
689	30	53.6	2749	1	ACMS57	inositol 1,4,5-tri	762	29	51.8	228	2	C87184	conserved hypothet
690	30	53.6	2749	2	A36579	inositol 1,4,5-tri	763	29	51.8	230	2	F81231	30S ribosomal prot
691	30	53.6	7962	2	I38346	elastic titin - hu	764	29	51.8	231	2	E86338	protein F5M15.16 [
692	30	53.6	13055	2	T16580	hypothetical prote	765	29	51.8	233	2	C70128	hypothetical prote
693	29.5	52.7	311	2	F70599	hypothetical prote	766	29	51.8	240	2	A70463	rRNA methylase - A
694	29.5	52.7	407	2	E75158	hypothetical prote	767	29	51.8	241	2	H72226	conserved hypothet
695	29.5	52.7	930	2	T32017	hypothetical prote	768	29	51.8	244	1	S16307	transcription acti
696	29	51.8	68	2	E98055	hypothetical prote	769	29	51.8	244	1	S37397	regulatory protein
697	29	51.8	76	2	B64660	hypothetical prote	770	29	51.8	251	2	D83517	hypothetical prote
698	29	51.8	82	2	I36928	gene MHC DQ-beta 2	771	29	51.8	260	2	B64367	hypothetical prote
699	29	51.8	82	2	I61811	gene MHC DQ-beta 1	772	29	51.8	263	2	G90294	hypothetical prote
700	29	51.8	82	2	I61813	gene MHC DQ-beta 1	773	29	51.8	267	2	H90368	hypothetical prote
701	29	51.8	86	2	S16840	ig kappa chain v r	774	29	51.8	270	2	B69379	chemotaxis protein
702	29	51.8	92	2	S37504	ig kappa chain v r	775	29	51.8	272	2	D90597	conserved hypothet
703	29	51.8	96	2	T21301	hypothetical prote	776	29	51.8	272	2	C86383	probable Myb-like
704	29	51.8	97	2	PH1068	ig light chain v r	777	29	51.8	278	2	D96513	unknown protein, 6
705	29	51.8	98	2	S41813	ig kappa chain v r	778	29	51.8	278	2	G64393	hypothetical prote
706	29	51.8	98	2	PH1069	ig light chain v r	779	29	51.8	281	2	G97439	transcription regu
707	29	51.8	98	2	PH1083	ig light chain v r	780	29	51.8	284	2	B88508	protein H14A12.3 [
708	29	51.8	99	2	S36058	ig lambda chain -	781	29	51.8	284	2	F90016	conserved hypothet
709	29	51.8	101	2	S20810	ig kappa chain v r	782	29	51.8	291	2	AB2939	hypothetical prote
710	29	51.8	106	2	S26345	ig light chain v r	783	29	51.8	291	2	E98343	hypothetical prote
711	29	51.8	106	2	B47329	ig kappa chain v r	784	29	51.8	293	2	AH0633	probable transcrip
712	29	51.8	107	2	C45722	anti-glycoprotein	785	29	51.8	297	2	B70894	probable lipu prot
713	29	51.8	107	2	S24290	ig kappa chain v r	786	29	51.8	299	2	AB2658	transcription regu
714	29	51.8	108	1	KWMS49	ig kappa chain v r	787	29	51.8	300	2	B75619	probable cobalamin
715	29	51.8	108	2	S36283	ig lambda chain v	788	29	51.8	301	2	A58928	phosducin-like pro
716	29	51.8	110	2	PN0535	ig kappa chain v r	789	29	51.8	304	2	H83636	hypothetical prote
717	29	51.8	111	1	KVRB36	ig kappa chain v r	790	29	51.8	307	2	AF2402	hypothetical prote
718	29	51.8	115	1	K3HUCI	ig kappa chain pre	791	29	51.8	308	2	C83220	probable transcrip
719	29	51.8	115	2	A30553	ig kappa chain pre	792	29	51.8	310	2	F97112	methionyl-tRNA for
720	29	51.8	117	1	KLHU2	ig kappa chain pre	793	29	51.8	310	2	AD2557	hypothetical prote
721	29	51.8	117	1	K4RBF2	ig kappa chain pre	794	29	51.8	312	1	S29756	nitrogen fixation
722	29	51.8	117	2	S21668	ig kappa chain v r	795	29	51.8	312	2	F70376	exopolysphatase
723	29	51.8	117	2	S24207	ig kappa chain v r	796	29	51.8	314	2	C70562	probable DTPD-Gluc
724	29	51.8	120	2	S21667	ig kappa chain v r	797	29	51.8	318	2	S76773	hypothetical prote
725	29	51.8	120	2	S21666	ig kappa chain v r	798	29	51.8	322	2	H84299	phytoene synthase
726	29	51.8	122	2	S40370	ig kappa chain - h	799	29	51.8	323	2	F89845	hypothetical prote
727	29	51.8	124	2	S40348	ig kappa chain v-J	800	29	51.8	329	2	A48715	gal-beta(1-3)-gluc
728	29	51.8	125	2	S40333	ig kappa chain v-J	801	29	51.8	332	2	A49879	alpha-2,3-sialyltr
729	29	51.8	127	2	S04574	ig kappa chain pre	802	29	51.8	342	2	G84197	glucose-1-phosphat
730	29	51.8	127	2	AH2536	single-strand DNA	803	29	51.8	346	2	S73894	tryptophan-tRNA li
731	29	51.8	127	2	T21302	hypothetical prote	804	29	51.8	346	2	AI2266	hypothetical prote
732	29	51.8	128	2	S31488	ig kappa chain pre	805	29	51.8	348	2	T31916	hypothetical prote
733	29	51.8	132	2	F97185	hypothetical prote	806	29	51.8	353	2	F84031	hypothetical prote
734	29	51.8	139	2	H84809	hypothetical prote	807	29	51.8	355	2	E97740	multidrug resistan
735	29	51.8	141	2	F69948	phage-related prot	808	29	51.8	357	2	G70960	probable fadB3 pro
736	29	51.8	144	2	G90107	ubiquitin-conjugat	809	29	51.8	357	2	E83205	hypothetical prote
737	29	51.8	146	2	S73551	ribosomal protein	810	29	51.8	358	2	T40703	probable DNA polym
738	29	51.8	147	2	H90177	conserved hypothet	811	29	51.8	359	2	T24539	hypothetical prote
739	29	51.8	148	2	S75206	hypothetical prote	812	29	51.8	360	2	S06280	decorin precursor
740	29	51.8	149	2	S64114	hypothetical prote	813	29	51.8	363	2	S66727	hypothetical prote
741	29	51.8	158	2	T14078	hypothetical prote	814	29	51.8	367	2	T10352	protein gp41 - Org
742	29	51.8	162	2	T18855	hypothetical prote	815	29	51.8	369	2	F96969	malate dehydrogena
743	29	51.8	163	2	S67038	ribosomal protein	816	29	51.8	374	2	H75002	probable GTP-bindi
744	29	51.8	164	1	CFXCA	C-phycoerythrin al	817	29	51.8	376	2	C71286	probable polysacch
745	29	51.8	164	2	S18526	phycoerythrin alph	818	29	51.8	379	2	AC0770	42.4K protein Kln
746	29	51.8	169	2	D25973	pertussis toxin ch	819	29	51.8	380	1	TVB812	pqg protein - Kle
747	29	51.8	175	2	H97785	probable transposo	820	29	51.8	380	2	S20457	hypothetical prote
748	29	51.8	181	2	G90166	hypothetical prote	821	29	51.8	383	2	T23057	hypothetical prote
749	29	51.8	186	2	H75106	hypothetical prote	822	29	51.8	388	2	S74985	hpaA-2 protein - S
750	29	51.8	187	2	S76728	hypothetical prote	823	29	51.8	390	2	E40362	tryptophan synthas
751	29	51.8	201	2	G90134	hypothetical prote	824	29	51.8	397	2	AE1142	penicillin-binding
752	29	51.8	209	1	TVBYH1	transforming prote	825	29	51.8	399	2	C83563	tyrosyl-tRNA synth
753	29	51.8	209	2	C96999	hypothetical prote	826	29	51.8	400	2	A96996	tyrosyl-tRNA liga
754	29	51.8	214	2	T20056	hypothetical prote	827	29	51.8	401	1	D64132	tyrosine-tRNA synth
755	29	51.8	225	2	AI3595	frnE protein [impo	828	29	51.8	404	2	A42677	interleukin-1 beta
756	29	51.8	225	2	AB2415	hypothetical prote	829	29	51.8	412	2	H81713	tyrosyl-tRNA synth
757	29	51.8	226	1	MEBR2P	pertussis toxin ch	830	29	51.8	418	2	E82840	tyrosyl-tRNA synth
758	29	51.8	226	2	C25973	pertussis toxin ch	831	29	51.8	419	2	AC2340	hypothetical prote
759	29	51.8	227	2	F71898	hypothetical prote	832	29	51.8	419	2	T50517	hypothetical prote

833	29	51.8	424	2	H96963	dihydroorotase [im	906	29	51.8	678	2	F70451	hypothetical prote
834	29	51.8	426	2	H71603	FAD-dependent oxid	907	29	51.8	683	1	QBEM8	gene 29 protein -
835	29	51.8	440	2	G72317	chromosomal replic	908	29	51.8	689	2	A83036	conserved hypothet
836	29	51.8	440	2	S58302	hypothetical prote	909	29	51.8	690	2	F71239	hypothetical prote
837	29	51.8	450	2	C88700	protein K02B2.1 [i	910	29	51.8	708	2	B86470	F21H2.11 protein -
838	29	51.8	451	1	S27617	glucarate dehydrat	911	29	51.8	712	1	S69782	outer membrane pro
839	29	51.8	451	2	T24018	hypothetical prote	912	29	51.8	723	1	AG0887	conserved hypothet
840	29	51.8	452	2	JC4888	phenylalanine 4-mo	913	29	51.8	729	1	AG0006	coat protein VP1 -
841	29	51.8	453	1	A42271	tryptophan 5-monoo	914	29	51.8	729	1	VCPVNA	coat protein VP1 -
842	29	51.8	453	2	JQ0766	phenylalanine 4-mo	915	29	51.8	729	2	S73093	probable oxidoredu
843	29	51.8	469	2	S05602	keratin K7, type I	916	29	51.8	755	1	S20922	photosystem I prot
844	29	51.8	480	1	C69378	4-hydroxyphenylace	917	29	51.8	757	2	C32052	FixI protein - Rhi
845	29	51.8	480	2	A34720	keratin 8, type II	918	29	51.8	757	2	C35344	FixII copper trans
846	29	51.8	487	2	JU0407	keratin 8, type II	919	29	51.8	763	2	AGZ764	nitrogen fixation
847	29	51.8	487	2	B83120	probable outer mem	920	29	51.8	763	2	E97545	nitrogen fixation
848	29	51.8	488	1	H64313	corrinoid/iron-sul	921	29	51.8	772	2	B82888	phenylalanine-tRNA
849	29	51.8	489	2	B24177	keratin, 55K type	922	29	51.8	788	2	I40776	paralysed flagellu
850	29	51.8	489	2	S51428	hypothetical prote	923	29	51.8	800	2	T23247	hypothetical prote
851	29	51.8	490	2	J80658	cytokeratin Endox	924	29	51.8	808	2	J02205	UL47h protein - Ma
852	29	51.8	491	2	AH3416	AMP nucleosidase (925	29	51.8	811	2	B69512	cell division cont
853	29	51.8	492	2	S83855	stage IV sporulati	926	29	51.8	814	2	I40048	S-layer protein pr
854	29	51.8	497	2	F86150	F22M8.2 protein -	927	29	51.8	830	1	RNEGB2	DNA-directed RNA p
855	29	51.8	498	2	T11683	probable iron-sulf	928	29	51.8	836	2	S61570	regulatory protein
856	29	51.8	500	2	F97025	spvB related memb	929	29	51.8	856	2	G96814	hypothetical prote
857	29	51.8	504	1	S23558	ubiquinol-cytochro	930	29	51.8	856	2	T52415	polycarb protein B
858	29	51.8	504	2	S51590	mitochondrial proc	931	29	51.8	880	2	F83386	hypothetical prote
859	29	51.8	504	2	I40811	uroporphyrinogen-I	932	29	51.8	881	2	I84737	kinesin heavy chai
860	29	51.8	506	2	T41623	probable protein k	933	29	51.8	891	2	T40417	hypothetical prote
861	29	51.8	512	2	T00870	probable cytochrom	934	29	51.8	894	2	C86756	prophage p12 prote
862	29	51.8	515	2	T43152	hypothetical prote	935	29	51.8	895	2	A55514	pyruvate dehydroge
863	29	51.8	524	2	H69099	conserved hypothet	936	29	51.8	895	2	F75608	conserved hypothet
864	29	51.8	527	2	E72016	lysine-tRNA ligase	937	29	51.8	896	2	S61996	probable membrane
865	29	51.8	527	2	A86607	lysyl tRNA synthet	938	29	51.8	896	2	H86762	ABC transporter pe
866	29	51.8	533	2	AG2384	hypothetical prote	939	29	51.8	898	2	T21179	hypothetical prote
867	29	51.8	535	2	B84590	hypothetical prote	940	29	51.8	898	2	T01503	hypothetical prote
868	29	51.8	535	2	T32139	hypothetical prote	941	29	51.8	918	2	A99221	protein T27F2.2 [i
869	29	51.8	537	2	F75149	CTP synthase (pyrg	942	29	51.8	924	2	T21738	hypothetical prote
870	29	51.8	539	2	T01513	CTP synthase (EC 6	943	29	51.8	932	2	F84465	hypothetical prote
871	29	51.8	542	2	T20457	hypothetical prote	944	29	51.8	941	1	TVMVMD	protein-tyrosine k
872	29	51.8	545	2	F84562	Mutator-like trans	945	29	51.8	942	2	T38649	hypothetical homeo
873	29	51.8	550	2	D87462	CTP synthase [limp	946	29	51.8	944	2	A89624	protein F21A10.2 [
874	29	51.8	553	2	B84334	CTP synthase [limp	947	29	51.8	963	1	A41919	kinesin heavy chai
875	29	51.8	553	2	T05340	CTP synthase (EC 6	948	29	51.8	967	1	A35075	kinesin heavy chai
876	29	51.8	554	1	AJECN	asparagine synthas	949	29	51.8	980	1	TVCTMD	macrophage colony-
877	29	51.8	554	2	AE0584	asparagine synthet	950	29	51.8	985	1	VCLJSP	env polyprotein -
878	29	51.8	578	2	H90716	asparagine synthet	951	29	51.8	1028	2	T34360	hypothetical prote
879	29	51.8	554	2	H85566	asparagine synthet	952	29	51.8	1039	2	T28644	hypothetical prote
880	29	51.8	557	2	T47723	mandelonitrile lya	953	29	51.8	1058	2	T19282	Y4jO protein - Rhi
881	29	51.8	557	2	H71189	probable CTP synth	954	29	51.8	1074	2	JC5928	hypothetical prote
882	29	51.8	558	2	D64507	methyl coenzyme M	955	29	51.8	1131	2	F96662	semaphorin F precu
883	29	51.8	564	2	S57124	CTP synthase (EC 6	956	29	51.8	1178	2	S30431	hypothetical prote
884	29	51.8	578	2	AC1041	Vi polysaccharide	957	29	51.8	1193	2	T32016	hypothetical prote
885	29	51.8	578	2	S28492	Vi polysaccharide	958	29	51.8	1218	2	AD0837	probable ABC trans
886	29	51.8	578	2	E36892	CTP synthase (EC 6	959	29	51.8	1232	2	B70556	probable respiraco
887	29	51.8	579	2	S50291	CTP synthase (EC 6	960	29	51.8	1297	2	C82521	hemolysin-type cal
888	29	51.8	580	2	T43732	CTP synthase (EC 6	961	29	51.8	1307	2	G96711	unknown protein, 9
889	29	51.8	591	1	SVHUTP	CTP synthase (EC 6	962	29	51.8	1407	1	T00558	probable ABC trans
890	29	51.8	595	2	E83891	thiamin biosynthes	963	29	51.8	1408	2	T47671	P-glycoprotein-like
891	29	51.8	597	2	T00471	CTP synthase (EC 6	964	29	51.8	1486	2	E85618	hypothetical prote
892	29	51.8	599	2	T26252	hypothetical prote	965	29	51.8	1486	2	G90754	kinesin-like cell
893	29	51.8	600	2	T37497	probable CTP synth	966	29	51.8	1486	2	C64832	cell division prot
894	29	51.8	602	2	T19898	aryl hydrocarbon r	967	29	51.8	1534	2	JH0228	hypothetical prote
895	29	51.8	605	2	D84687	hypothetical prote	968	29	51.8	1593	2	T22028	cell division prot
896	29	51.8	607	1	S52629	catechol oxidase (969	29	51.8	1603	1	BVASA1	3-dehydroquinatase
897	29	51.8	610	2	A81365	C1ab protein Cj091	970	29	51.8	1638	2	D87749	protein unc-73b [i
898	29	51.8	616	2	C95861	probable ABC trans	971	29	51.8	1645	2	A37792	spectrin beta-H ch
899	29	51.8	620	2	T52389	hypothetical prote	972	29	51.8	1653	2	T14758	hypothetical prote
900	29	51.8	626	2	T03547	probable ferrous i	973	29	51.8	1666	2	T09072	probable translati
901	29	51.8	630	2	B32935	hypothetical prote	974	29	51.8	2154	2	F83068	hypothetical prote
902	29	51.8	650	2	G87883	protein C41G7.5 [i	975	29	51.8	2163	2	S50675	pre-mRNA splicing
903	29	51.8	654	2	A69656	methyl-accepting c	976	29	51.8	2261	1	A42548	genome polyprotein
904	29	51.8	655	2	A57681	hypothetical prote	977	29	51.8	2354	2	T13288	mei-41 protein - f
905	29	51.8	660	1	G6BP74	baseplate protein	978	29	51.8	2388	2	J80271	beta spectrin, bet

979 29 51.8 2488 2 T42739 guanine nucleotide
980 29 51.8 3386 1 GNWVDF genome polypeptide
981 29 51.8 4063 2 T42993 probable spectrin
982 29 51.8 4101 2 T23630 hypothetical prote
983 29 51.8 4572 2 S57908 hypothetical 527K
984 29 51.8 5175 2 T20992 hypothetical prote
985 29 51.8 5198 2 T43290 hemicentin precurs
986 28.5 50.9 109 1 K3HUPM Ig kappa chain V-I
987 28.5 50.9 129 2 S40325 Ig kappa chain - h
988 28.5 50.9 177 2 S45878 hypothetical prote
989 28.5 50.9 256 2 C7I546 probable glucose-6
990 28.5 50.9 300 2 T43137 hypothetical prote
991 28.5 50.9 335 2 T41354 nucleoporin GLFG h
992 28.5 50.9 441 2 C86378 protein F21Q9.6 [i
993 28.5 50.9 559 2 R86479 hypothetical prote
994 28.5 50.9 807 2 A86740 telchoic acid bios
995 28 50.0 25 2 FN0632 biphenyl dioxygena
996 28.5 50.0 61 2 D84213 50S ribosomal prot
997 28 50.0 86 2 S16832 Ig kappa chain V r
998 28 50.0 87 2 PH1082 Ig light chain V r
999 28 50.0 91 2 S37521 Ig kappa chain V r
1000 28 50.0 102 2 H82071 conserved hypothet

ALIGNMENTS

RESULT 1
S38564
Ig kappa chain V region (ASWU1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38564
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38564
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <MON>
A;Cross-references: UNIPARC:UPI00001161CA; EMBL:X75105; NID:G414153; PIDN:CAA52996.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 93;
Best Local Similarity 90.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 2
S69901
Ig kappa chain (clone KL2.21) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69901
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75; 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69901
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <WYS>

A;Cross-references: UNIPARC:UPI0000115EA4; EMBL:X55042; NID:G511025; PIDN:CAA38882.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 3
S32188
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32188
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32188
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: UNIPARC:UPI0000116101; EMBL:X70090; NID:G288253; PIDN:CAA49695.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 4
A28044
Ig kappa chain V region (22B5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
C;Accession: A28044
R;Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
A;Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
A;Reference number: A94179; MUID:87317629; PMID:3114744
A;Accession: A28044
A;Molecule type: mRNA
A;Residues: 1-107 <MEE>
A;Cross-references: UNIPARC:UPI0000176B2A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 5
D48677
Ig kappa chain V-J region (24) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C;Accession: D48677
R;Taasogon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsenate antibodies
A;Reference number: A48677; MUID:94022404; PMID:8415731

A:Accession: D49677
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <TAS>
 A:Cross-references: UNIPARC:UPI0000176CBF
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 1;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33

RESULT 6

B28044
 Ig kappa chain V region (GPI) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jan-2000
 C:Accession: B28044
 R:Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
 A:Title: Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
 A:Reference number: A94179; MUID:87317629; PMID:3114744
 A:Accession: B28044

A:Molecule type: mRNA
 A:Residues: 1-107 <ME>
 A:Cross-references: UNIPARC:UPI0000176B29
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 1;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33

RESULT 7

B49026
 Ig kappa chain V region, anti-idiotypic monoclonal antibody - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B49026; PLO220
 R:Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
 Eur. J. Immunol. 21, 2185-2193, 1991
 A:Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MRL-lpr/lpr mice.
 A:Reference number: A49026; MUID:91364791; PMID:1909645
 A:Accession: B49026

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <KOI>
 A:Cross-references: UNIPARC:UPI0000176D3F
 A:Experimental source: MRL-lpr/lpr
 A:Note: sequence extracted from NCBI backbone (NCBI:60876)
 R:Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz, J.; Barrett, K.J.; Schwartz, J. Exp. Med. 171, 1919-1930, 1990

A:Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies
 A:Reference number: PLO220; MUID:90278348; PMID:1693654
 A:Accession: PLO220

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <PUC>
 A:Cross-references: UNIPARC:UPI0000176D3F

A:Experimental source: strain lupus-prone MRL-lpr/lpr mouse
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:50-56/Region: complementarity-determining 2
 F:89-97/Region: complementarity-determining 3

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0; Indels 1;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33

RESULT 8

S69906
 Ig kappa chain (clone KL4A1) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69906
 R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992
 A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
 A:Reference number: S69900; MUID:92165291; PMID:1537587
 A:Status: preliminary; translation not shown
 A:Accession: S69906

A:Molecule type: DNA
 A:Residues: 1-107 <WYS>
 A:Cross-references: UNIPARC:UPI0000115EA6; EMBL:X55047; NID:9511035; PIDN:CAA38887.1; P
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 Db 24 RASQDISNYL 33

RESULT 9

KVMSAR
 Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
 C:Accession: A01927
 R:Siegelman, M.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
 A:Title: Complete amino acid sequence of light chain variable regions derived from five
 A:Reference number: A01927; MUID:82150934; PMID:6801658
 A:Accession: A01927

A:Molecule type: protein
 A:Residues: 1-108 <SIB>
 A:Cross-references: UNIPROT:P01644; UNIPARC:UPI000002A0C5
 A:Experimental source: strain A/J
 A:Note: hp 93G7 differs in having 93-Met; HP 12386 differs in having 7-Ser, 92-Tyr, and
 Arg, 84-Ser, and 93-Ala

C:Comment: The sequence shown is HP R16.7.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer

F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match 80.4%; Score 45; DB 1; Length 108;
 Best Local Similarity 90.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||

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Db          24 RASQDISNYL 33

RESULT 10
PL0282
Ig kappa chain V region (45-49, anti p-azophenylarsonate) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Accession: PL0282
R;Wysocki, L.J.; Geffter, M.L.; Margolies, M.N.
J. Exp. Med. 172, 315-323, 1990
A;Title: Parallel evolution of antibody variable regions by somatic processes: Consecuti
y point mutation and selection rather than by gene conversion.
A;Reference number: PL0281; MUID:90293694; PMID:2358780
A;Accession: PL0282
A;Molecule type: mRNA
A;Residues: 1-108 <WYS>
A;Cross-references: UNIPARC:UPI0000176B45
A;Experimental source: A/J mice
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
    ||||| |||
Db 24 RASQDISNYL 33

RESULT 11
C26405
Ig kappa chain V region (3D10) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: C26405
R;Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987
A;Title: Complete amino acid sequences of the heavy and light chain variable regions fro
A;Reference number: A90518; MUID:87157677; PMID:3103682
A;Accession: C26405
A;Molecule type: protein
A;Residues: 1-108 <SMI>
A;Cross-references: UNIPARC:UPI00001769E9
A;Experimental source: strain A/J
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
    ||||| |||
Db 24 RASQDISNYL 33

RESULT 12
B26405
Ig kappa chain V region (1F6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: B26405
R;Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987
A;Title: Complete amino acid sequences of the heavy and light chain variable regions fro
A;Reference number: A90518; MUID:87157677; PMID:3103682
A;Accession: B26405
```

```
A;Molecule type: protein
A;Residues: 1-108 <SMI>
A;Cross-references: UNIPARC:UPI00001769E7
A;Experimental source: strain A/J
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
    ||||| |||
Db 24 RASQDISNYL 33

RESULT 13
S38862
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S38862
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
A;Accession: S38862
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <FIS>
A;Cross-references: UNIPARC:UPI00001161D1; EMBL:X75854; NID:9429109; PID:9429110
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
    ||||| |||
Db 24 RASQDISNYL 33

RESULT 14
S69902
Ig kappa chain (clone KL2.28) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69902
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69902
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: UNIPARC:UPI0000115EA5; EMBL:X55043; NID:9511027; PIDN:CAA38883.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
    ||||| |||
Db 24 RASQDISNYL 33

RESULT 15
```


S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69900; S69907; S69908
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; PMID:92165291; PMID:1537587
A:Accession: S69900
A:Molecule type: DNA
A>Status: preliminary; translation not shown
A:Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PI
A:Residues: 1-108 <WYS>
A:Accession: S69907
A:Molecule type: DNA
A>Status: preliminary; translation not shown
A:Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55048; NID:G511037; PIDN:CAA38888.1; PI
A:Residues: 1-108 <WY2>
A:Accession: S69908
A:Molecule type: DNA
A>Status: preliminary; translation not shown
A:Cross-references: UNIPARC:UPI0000115EA3; EMBL:X55049; NID:G511039; PIDN:CAA38889.1; PI
A:Residues: 1-108 <WY3>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 16
S19970
Ig kappa chain V region (M-T151) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19970
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19970
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <WEI>
A:Cross-references: UNIPARC:UPI0000116033; EMBL:X65095; NID:G52286; PIDN:CAA46223.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 17
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin

A:Reference number: S69900; PMID:92165291; PMID:1537587
A:Accession: S69903
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: UNIPARC:UPI0000115227; EMBL:X55044; NID:G511029; PIDN:CAA38884.1; PI
A:Accession: S69904
A:Molecule type: DNA
A>Status: preliminary; translation not shown
A:Cross-references: UNIPARC:UPI0000115227; EMBL:X55045; NID:G511031; PIDN:CAA38885.1; PI
A:Residues: 1-108 <WY2>
A:Accession: S69905
A:Molecule type: DNA
A>Status: preliminary; translation not shown
A:Cross-references: UNIPARC:UPI0000115227; EMBL:X55046; NID:G511033; PIDN:CAA38886.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 18
AS3276
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A53276
R:Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb, P.D.
Immunogenetics 34, 231-241, 1991
A:Title: Polymorphism in V kappa 10 genes encoding L chains of antibodies bearing the A
A:Reference number: A53276; PMID:92010099; PMID:1916951
A:Accession: A53276
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <KIM>
A:Cross-references: UNIPARC:UPI000011D106
A:Experimental source: AJ1 strain
A:Note: sequence extracted from NCBI backbone (NCBIN:62777, NCBIIP:62780)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 19
JL0080
Ig kappa chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0080
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A:Reference number: JL0076; PMID:89096973; PMID:3211160
A:Accession: JL0080
A:Molecule type: mRNA
A:Residues: 1-115 <KAA>
A:Cross-references: UNIPARC:UPI0000114EB9; GB:M27793; NID:G197161; PIDN:AAA38937.1; PID
A:Note: the authors translated the codon AGG for residue 30 as Ser

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>
 F;7-115/Product: Ig light chain #status predicted <MAT>
 F;22-96/Domain: immunoglobulin homology <IMM>
 F;30-40/Region: complementarity-determining 1
 F;56-62/Region: complementarity-determining 2

Query Match 80.4%; Score 45; DB 2; Length 115;
 Best Local Similarity 90.0%; Pred. No. 0.24; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| ||||
 Db 30 RASQDISNYL 39

RESULT 20
 A29380
 Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
 C;Accession: A29380
 R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 J. Biol. Chem. 262, 13579-13583, 1987
 A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
 A;Reference number: A92612; MUID:88007582; PMID:3115981
 A;Accession: A29380
 A;Molecule type: mRNA
 A;Residues: 1-122 <CHE>
 A;Cross-references: UNIPARC:UPI000011677C; GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38
 A;Note: the authors translated the codon TTC for residue 1 as Leu
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 122;
 Best Local Similarity 90.0%; Pred. No. 0.26; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| ||||
 Db 38 RASQDINNLY 47

RESULT 21
 A34904
 Ig kappa chain precursor V region (5-27) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
 C;Accession: A34904
 R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
 J. Biol. Chem. 265, 133-138, 1990
 A;Title: Active site structure and antigen binding properties of idiotypically cross-reac
 A;Reference number: A34903; MUID:90094387; PMID:2104617
 A;Accession: A34904
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-126 <BED>
 A;Cross-references: UNIPROT:Q91WF8; UNIPARC:UPI000017679E
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;33-109/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 126;
 Best Local Similarity 90.0%; Pred. No. 0.26; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| ||||
 Db 43 RASQDINNLY 52

RESULT 22
 PH1224

Ig kappa chain precursor V region (M-T151) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
 C;Accession: PH1224
 R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz
 Gene 121, 271-278, 1992
 A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on

A;Reference number: PH1224; MUID:93077041; PMID:1446824

A;Accession: PH1224

A;Molecule type: mRNA

A;Residues: 1-127 <WEI>

A;Cross-references: UNIPARC:UPI00001153EC; GB:S50261; NID:g260761; PIDN:AAB24318.1; PID:

A;Note: this mouse sequence was hybridized and fused with a human constant region gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-127/Product: Ig light chain V region #status predicted <MAT>

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 127;
 Best Local Similarity 90.0%; Pred. No. 0.27; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| ||||
 Db 44 RASQDINNLY 53

RESULT 23
 A26406

Ig kappa chain V region (Ara-A) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: A26406

R;Sanz, I.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987

A;Title: V-K and J-K gene segments of A/J Ara-A antibodies: somatic recombination genera

A;Reference number: A26406; MUID:87147197; PMID:3103124

A;Accession: A26406

A;Molecule type: DNA

A;Residues: 1-128 <SAN>

A;Cross-references: UNIPROT:Q91WF8; UNIPARC:UPI000017679C; GB:M15519

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 128;
 Best Local Similarity 90.0%; Pred. No. 0.27; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 ||||| ||||
 Db 44 RASQDISNYL 53

RESULT 24
 S40365

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40365

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40365

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-139 <KLE>

A;Cross-references: UNIPARC:UPI0000116173; EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 44; DB 2; Length 139;
Best Local Similarity 80.0%; Pred. No. 0.46;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 39 QATQDIGNYL 48

RESULT 25

PH0865
Ig kappa chain V region (anti-DNA, I-2a) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0865
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A:Reference number: PH0862; MUID:92078875; PMID:1660528
A:Accession: PH0865
A:Molecule type: DNA
A:Residues: 1-95 <MAN>
A:CROSS-references: UNIPARC:UPI0000176DA1
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-95/Region: complementarity-determining 3

Query Match 76.8%; Score 43; DB 2; Length 95;
Best Local Similarity 90.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 RASQDIRNYL 33

RESULT 26

PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0888
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
A:Reference number: PH0885; MUID:92113462; PMID:1346155
A:Accession: PH0888
A:Molecule type: mRNA
A:Residues: 1-109 <SHA>
A:CROSS-references: UNIPARC:UPI0000176B2B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 43; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 RASQDIRNYL 33

RESULT 27

PH1065
Ig kappa chain V region (clone 163.47) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PH1065
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1065
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98 <TIL>
A:CROSS-references: UNIPARC:UPI0000176AB5
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 75.0%; Score 42; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.78;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 28

S52447
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52447
R:Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged germline
A:Reference number: S52445
A:Accession: S52447
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <BER>
A:CROSS-references: UNIPARC:UPI0000116206; EMBL:X82688; NID:g673443; PIDN:CAA58009.1; PI
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 42; DB 2; Length 127;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 44 KASQDINNYL 53

RESULT 29

S42265
Ig kappa chain V region (018) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42265
R:Scott, M.G.; Crammins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A:Reference number: S42263; MUID:92043792; PMID:1940382
A:Accession: S42265
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SCO>
A:CROSS-references: UNIPARC:UPI0000176D84; EMBL:M64856

C;Genetics:

A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 73.2%; Score 41; DB 2; Length 62;
Best Local Similarity 80.0%; Pred. No. 0.77;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 30

Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I52592
R;Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A;Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio
A;Reference number: I52592; MUID:94264318; PMID:8204889
A;Accession: I52592
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-87 <RES>
A;Cross-references: UNIPARC:UPI0000113F67; GB:S71057; NID:G547053; PIDN:AAB30971.1; PID:
C;Genetics:
A;Gene: IGKV
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 87;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 17 QASQDISNYL 26

RESULT 31

Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34087
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9B; EMBL:X67171
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 88;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 17 QASQDISNYL 26

RESULT 32

S34088

Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34088
R;Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9A; EMBL:X67172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 88;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 17 QASQDISNYL 26

RESULT 33

PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9C
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: complementarity-determining 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match 73.2%; Score 41; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 34

IG kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PLO262
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PLO231; MUID:9011618; PMID:2104919
A;Accession: PLO262
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>

A;Cross-references: UNIPARC:UPI0000176CC2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 73.2%; Score 41; DB 2; Length 106;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||:|
Db 24 RASQDIGGYL 33

RESULT 35

I69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (E
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I69017
R;Chn, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A;Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A;Reference number: 154563; MUID:95237884; PMID:7721339
A;Accession: I69017

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <RES>

A;Cross-references: UNIPARC:UPI0000113P9C; GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:
C;Genetics:
A;Gene: Ig Vkappa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||:|
Db 24 RASHDIGSYL 33

RESULT 36

B30551
Ig kappa chain V region (36-71) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30551
R;Sharon, J.; Gefter, M.L.; Wysocki, L.J.; Margolies, M.N.
J. Immunol. 142, 596-601, 1989
A;Title: Recurrent somatic mutations in mouse antibodies to p-azophenylarsonate increase
A;Reference number: A30551; MUID:89093946; PMID:2911012
A;Accession: B30551

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 <SHA>
A;Cross-references: UNIPARC:UPI0000114FA1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||:|
Db 24 RASQDINNFL 33

RESULT 37

S11124
Ig kappa chain V region (clone NQ5-89.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11124
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolon
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11124

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <KAA>
A;Cross-references: UNIPARC:UPI0000176EA7
A;Note: 87-Phe was also found
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||:|
Db 24 RXSQDISNYL 33

RESULT 38

S44118
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44118
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, P.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44118

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Cross-references: UNIPARC:UPI0000116635; EMBL:Z31395; NID:G472972; PIDN:CAA83270.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||:|
Db 24 QASQDISNYL 33

RESULT 39

B37266
Ig kappa chain V region (2G8) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: B37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: B37266
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPARC:UPI0000176B07
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 111;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 27 KASQDVSNYL 36

RESULT 40

S42263
Ig kappa chain V region (08) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42263
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus influenzae
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B51; EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PI
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 46 QASQDISNYL 55

RESULT 41

S43528
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S43528
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus influenzae
A;Reference number: S43528
A;Accession: S43528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B52; EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 46 QASQDISNYL 55

RESULT 42

S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: UNIPARC:UPI0000116220; EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 129;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 46 QASQDISNYL 55

RESULT 43

KVMS73
Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01926
R;Schiff, C.; Fougereau, M.
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid
A;Reference number: A01926; MUID:76091934; PMID:812696
A;Accession: A01926
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01643; UNIPARC:UPI000002A0C4
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 71.4%; Score 40; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 10
:|||||
Db 25 ASQSIGNYL 33

RESULT 44

S32001
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32001
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S32001
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116498; EMBL:Z15082; NID:G38503; PIDN:CAA78791.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 40; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||:|
Db 24 RASQNIKYL 33

RESULT 45
S31980
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31980; S32000
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31980
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116493; EMBL:Z15076; NID:G38491; PIDN:CAA78785.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 40; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||:|
Db 24 RASQNIKYL 33

RESULT 46
S31979
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31979
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31979
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116492; EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 40; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||:|
Db 24 RASQNIKYL 33

RESULT 47
S04936

Ig kappa chain precursor V-J region (IH1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S04936
R;Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
J. Exp. Med. 168, 475-489, 1988
A;Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
A;Reference number: S04936; MUID:88316166; PMID:3045247
A;Accession: S04936
A;Molecule type: mRNA
A;Residues: 1-125 <LEV>
A;Cross-references: UNIPARC:UPI0000115DD3; EMBL:X13076; NID:G33173; PIDN:CAA31477.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-125/Product: Ig kappa chain (fragment) #status predicted <MAT>
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 40; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||:|
Db 41 RASQSIGNWL 50

RESULT 48
PL0113
Ig kappa chain precursor V-I region (CJ) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PL0113
R;Levy, S.; Mendel, E.; Kon, S.; Avnur, Z.; Levy, R.
J. Exp. Med. 168, 475-489, 1988
A;Title: Mutational hot spots in Ig V region genes of human follicular lymphomas.
A;Reference number: S04936; MUID:88316166; PMID:3045247
A;Accession: PL0113
A;Molecule type: mRNA
A;Residues: 1-130 <LEV>
A;Cross-references: UNIPARC:UPI00001767A3
A;Experimental source: follicular lymphoma cells
A;Note: the sequence shown here is derived from the consensus nucleotide sequence of the
om tumor cells of a single patient
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V-I region CJ #status predicted <MAT>
F;38-112/Domain: immunoglobulin homology <IMM>
F;46-56/Region: complementarity-determining 1
F;72-78/Region: complementarity-determining 2
F;111-130/Region: complementarity-determining 3
F;118-130/Region: J1

Query Match 71.4%; Score 40; DB 2; Length 130;
Best Local Similarity 80.0%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||:|
Db 46 RASQSIGNWL 55

RESULT 49
PH0087
Ig kappa chain V region (anti-cyclosporin C and D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accession: PH0087
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Queeniaux, V.F.J.; v
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240

A;Accession: PH0087
A;Molecule type: mRNA
A;Residues: 1-105 <SCH>
A;Cross-references: UNIPARC:UPI0000115EE7; GB:X57639; NID:g296839; PIDN:CAA40857.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3

Query Match 69.6%; Score 39; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISTYL 33

RESULT 50
PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0267
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 263-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0267
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
A;Cross-references: UNIPARC:UPI0000176805
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

Query Match 69.6%; Score 39; DB 2; Length 106;
Best Local Similarity 80.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISTYL 33

Search completed: May 11, 2006, 16:37:39
Job time : 30.2295 secs

GenCore version 5.1.8

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 101.705 Seconds

(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-4

Perfect score: 56

Sequence: 1 RASQDIGNYLIR 11

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	80.4	108	1	KV5K_MOUSE
2	45	80.4	108	1	KV5L_MOUSE
3	45	80.4	108	1	KV5M_MOUSE
4	45	80.4	108	1	KV5N_MOUSE
5	45	80.4	108	1	KV5O_MOUSE
6	45	80.4	236	2	Q723Y4_HUMAN
7	44	78.6	283	2	Q6FMX7_CANGA
8	42	75.0	2188	2	Q7D6F1_MYCTU
9	41	73.2	50	2	Q6L8V5_HUMAN
10	41	73.2	316	1	TNP11_MOUSE
11	41	73.2	451	2	Q751I5_ASHGO
12	40	71.4	108	1	KV1Y_HUMAN
13	40	71.4	108	1	KV5J_MOUSE
14	40	71.4	108	1	KV5U_MOUSE
15	40	71.4	234	2	Q5FEF6_HUMAN
16	40	71.4	234	2	Q72473_HUMAN
17	40	71.4	236	2	Q6GMX0_HUMAN
18	40	71.4	2008	2	Q4ZD65_9VIRU
19	40	71.4	2033	2	Q7RQ61_PLAYO
20	39	69.6	107	2	Q9UL81_HUMAN
21	39	69.6	129	1	KV1V_HUMAN
22	39	69.6	443	2	Q7N5S4_PHOLL
23	39	69.6	937	2	Q4INP3_GIBZE
24	38	67.9	94	2	Q5F0M1_9CYAN
25	38	67.9	95	2	Q5M0T4_STRT1
26	38	67.9	108	2	Q9UL70_HUMAN
27	38	67.9	236	2	Q5HTQ0_CAMJR
28	38	67.9	241	2	Q9PN81_CAMJE
29	38	67.9	318	1	TNP11_RAT
30	38	67.9	348	2	Q75D24_ASHBYA
31	38	67.9	409	2	Q9BLX6_CIOIN

32	38	67.9	524	2	Q6TH77_9APHY	Q6th77	trametes	sp
33	38	67.9	733	2	Q70KQ6_CIOIN	Q70kq6	ciona	intes
34	38	67.9	1009	2	Q818Y2_ANOGA	Q818y2	anopheles	g
35	38	67.9	1009	2	Q7PS90_ANOGA	Q7ps90	anopheles	g
36	37	66.1	101	2	Q9F2E8_9CVAN	Q9f2e8	spirulina	s
37	37	66.1	102	2	Q50318_MICAE	Q50318	microcystis	s
38	37	66.1	108	1	KV5P_MOUSE	P01649	mus musculus	
39	37	66.1	115	1	KV5F_MOUSE	P01638	mus musculus	
40	37	66.1	117	1	KV5H_MOUSE	P01641	mus musculus	
41	37	66.1	125	2	Q6RX70_SPIPL	Q6rx70	spirulina	p
42	37	66.1	130	1	KV5E_MOUSE	P01637	mus musculus	
43	37	66.1	138	1	KV5G_MOUSE	P01639	mus musculus	
44	37	66.1	161	1	PHRA_SYNPY	O02182	synecococc	
45	37	66.1	162	1	PHCA_CYACA	O19910	cyanidium c	
46	37	66.1	162	1	PHCA_NASLA	P00307	mastigoclad	
47	37	66.1	162	1	PHCA_SYNY1	P20776	synecocyst	
48	37	66.1	162	2	Q82RA8_STRAW	Q82ra8	streptomyce	
49	37	66.1	195	2	Q8PVD9_METMA	Q8pvd9	methanosarc	
50	37	66.1	201	2	Q7PVR5_ANOGA	Q7pvr5	anopheles	g
51	37	66.1	230	2	Q4HH06_CAMCO	Q4hh06	campylobact	
52	37	66.1	236	2	Q7TS98_MOUSE	Q7ts98	mus musculus	
53	37	66.1	374	2	O05107_ECTVA	O05107	ectothiorho	
54	37	66.1	384	2	Q7NFI2_GLOVI	Q7nfi2	gloeobacter	
55	37	66.1	392	2	Q5C8D3_9PEZI	Q5c8d3	chaetosphae	
56	37	66.1	396	2	Q5SL67_BACLD	Q5sl67	bacillus li	
57	37	66.1	470	1	VATH2_CABEL	Q22494	caenorhabdi	
58	37	66.1	470	2	Q619W5_CABER	Q619w5	caenorhabdi	
59	37	66.1	514	2	Q5MBH3_9APHY	Q5mbh3	trametes	sp
60	37	66.1	517	2	Q9HDQ0_9APHY	Q9hdq0	funalia tro	
61	37	66.1	520	1	LAC1_TRAHI	Q02497	trametes hi	
62	37	66.1	520	2	Q5MBH6_9APHY	Q5mbh6	trametes	sp
63	37	66.1	530	2	Q7SEPO_NEUCR	Q7sepo	neurospora	
64	37	66.1	560	1	INARI_SHEEP	P46085	ovis aries	
65	37	66.1	623	1	HA70_CLOBO	P46085	c hemagglut	
66	37	66.1	623	2	Q786X9_CBDP	Q786x9	clostridium	
67	37	66.1	623	2	Q9ZX79_CBDP	Q9zx79	clostridium	
68	37	66.1	623	2	Q9LBR5_CLOBO	Q9lbr5	clostridium	
69	37	66.1	623	2	Q9LBT1_CLOBO	Q9lbt1	clostridium	
70	37	66.1	623	2	Q7DHI7_CLOBO	Q7dhi7	clostridium	
71	37	66.1	626	2	Q45877_CLOBO	Q45877	clostridium	
72	37	66.1	1161	2	Q6BMG3_DBBHA	Q6bmj3	debaromyce	
73	37	66.1	2188	2	P96202_MYCTU	P96202	mycobacteri	
74	37	66.1	2188	2	Q7TLX8_MYCBO	Q7tlx8	mycobacteri	
75	37	66.1	4912	2	Q94116_AURPU	O94116	ureobasidi	
76	36	64.3	93	2	Q68GP6_9NOST	Q68gp6	anabaena so	
77	36	64.3	93	2	Q68GN6_9NOST	Q68gn6	anabaena ki	
78	36	64.3	93	2	Q68GN0_9NOST	Q68gn0	anabaena el	
79	36	64.3	93	2	Q68GL0_9NOST	Q68gl0	anabaena me	
80	36	64.3	93	2	Q68GR0_9NOST	Q68gr0	anabaena pl	
81	36	64.3	93	2	Q68GP4_9NOST	Q68gp4	anabaena sm	
82	36	64.3	93	2	Q68GM0_9NOST	Q68gm0	anabaena uc	
83	36	64.3	93	2	Q68GK6_9NOST	Q68gk6	anabaena le	
84	36	64.3	94	2	Q93NN6_9NOST	Q93nn6	aphanizomen	
85	36	64.3	94	2	Q939H8_APHFL	Q939h8	aphanizomen	
86	36	64.3	95	2	Q93NN2_9NOST	Q93nn2	nodularia h	
87	36	64.3	95	2	Q9S4Z5_NODSP	Q9s4z5	nodularia s	
88	36	64.3	95	2	Q9S4Z9_NODSP	Q9s4z9	nodularia s	
89	36	64.3	95	2	Q93NN4_NODSP	Q93nn4	nodularia s	
90	36	64.3	95	2	Q9S4Z7_NODSP	Q9s4z7	nodularia s	
91	36	64.3	95	2	Q9S4Z4_NODSP	Q9s4z4	nodularia s	
92	36	64.3	95	2	Q9R310_NODSP	Q9r310	nodularia s	
93	36	64.3	98	2	Q8RLN9_9NOST	Q8rln9	cyllindrospe	
94	36	64.3	98	2	Q8KPY8_9NOST	Q8kpy8	anabaena ci	
95	36	64.3	98	2	Q8RLN8_9NOST	Q8rln8	cyllindrospe	
96	36	64.3	98	2	Q84FY6_9NOST	Q84fy6	nostocaceae	
97	36	64.3	99	2	Q5F0M2_NOSLI	Q5f0m2	nostoc linc	
98	36	64.3	99	2	Q5F0K1_9CYAN	Q5f0k1	phormidium	
99	36	64.3	103	2	Q58QL7_9NOST	Q58ql7	anabaena le	
100	36	64.3	103	2	Q58QN7_9NOST	Q58qn7	anabaena le	
101	36	64.3	105	2	Q58QL4_9NOST	Q58ql4	anabaena so	
102	36	64.3	105	2	Q58QL5_9NOST	Q58ql5	anabaena so	
103	36	64.3	105	2	Q58QL6_9NOST	Q58ql6	anabaena so	
104	36	64.3	105	2	Q58QN3_9NOST	Q58qn3	anabaena so	

105	36	64.3	107	2	Q58Q9_9NOST	Q58qm9 anabaena le	178	35	62.5	624	2	Q8SW03_ENCCU	Q8sw03 encephalito
106	36	64.3	108	1	KV1A_HUMAN	P01593 homo sapien	179	35	62.5	634	2	Q8H150_ARATH	Q8h150 arabidopsis
107	36	64.3	108	1	KV1B_HUMAN	P01594 homo sapien	180	35	62.5	634	2	Q8FN91_ARATH	Q8fn91 arabidopsis
108	36	64.3	116	2	Q96PF6_HUMAN	Q96pf6 homo sapien	181	35	62.5	654	2	Q873H9_NEUCR	Q873h9 neurospora
109	36	64.3	161	1	PHCA_SYNPN	P27288 synechococc	182	35	62.5	660	1	KUPL1_LACPL	Q88242 lactobacill
110	36	64.3	161	1	PHRA_SYNPN	P11394 synechococc	183	35	62.5	674	2	Q98F52_RHILO	Q98f52 thizobium l
111	36	64.3	162	2	Q85G43_CVAME	Q85g43 cyanidiosch	184	35	62.5	693	2	Q6CN50_KLULA	Q6cn50 kluyveromyc
112	36	64.3	162	2	Q7U4P4_SYNPN	Q7u4p4 synechococc	185	35	62.5	693	2	Q7V967_PROMM	Q7v967 prochloroc
113	36	64.3	163	1	PHCA_ANASP	P07121 anabaena sp	186	35	62.5	767	2	Q75K46_ORYSA	Q75k46 oryza sativ
114	36	64.3	185	2	Q4LR04_9EURK	Q4lr04 burkholderi	187	35	62.5	782	2	Q5FTF6_GLUOX	Q5ftf6 gluconobact
115	36	64.3	199	2	Q65V01_MANSM	Q65v01 manheimia	188	35	62.5	817	2	Q813Y1_PLAF7	Q813y1 plasmodium
116	36	64.3	261	2	Q7PJPA_ANOGA	Q7pjpa anopheles g	189	35	62.5	1161	2	Q5DTZ0_MOUSE	Q5dtz0 mus musculu
117	36	64.3	278	2	Q51QC1_MAGGR	Q51qcl magnaporth	190	35	62.5	1216	1	REC04_MOUSE	Q75nr7 mus musculu
118	36	64.3	292	2	Q9LVH1_ARATH	Q9lvh1 arabidopsis	191	35	62.5	1257	2	Q6CAA7_YARLI	Q6caa7 varrowia li
119	36	64.3	365	2	Q65SH6_MANSM	Q65sh6 manheimia	192	35	62.5	1475	1	R1_CITRE	Q8ald9 citrus reti
120	36	64.3	371	2	Q5QXP7_IDILO	Q5qxp7 idiomarina	193	35	62.5	1844	2	Q22579_CABEL	Q22579 caenorhabdi
121	36	64.3	381	2	Q90ZA3_AMBME	Q90za3 ambystoma m	194	35	62.5	2275	2	Q8QSA1_9BETA	Q8qsa1 pongine her
122	36	64.3	416	1	PBN1_YEAST	P25580 saccharomyc	195	34.5	61.6	405	2	Q8TZU1_PYRFU	Q8tzul pyrococcus
123	36	64.3	427	2	Q6MI22_BDEBA	Q6mi22 bdellovibri	196	34	60.7	53	2	Q9XVL2_CABEL	Q9xvl2 caenorhabdi
124	36	64.3	430	2	Q7R2X0_GIALA	Q7r2x0 giardia lam	197	34	60.7	67	2	Q8YXN0_ANASP	Q8yxno anabaena sp
125	36	64.3	449	2	Q7QG40_ANOGA	Q7qg40 anopheles g	198	34	60.7	81	2	Q9NPB5_HUMAN	Q9npb5 homo sapien
126	36	64.3	492	2	Q9LH83_ARATH	Q9lh83 arabidopsis	199	34	60.7	93	2	Q8VMZ6_9CHRO	Q8vmz6 microcystis
127	36	64.3	515	2	Q6CPB4_KLULA	Q6cpb4 kluyveromyc	200	34	60.7	93	2	Q8VMW26_9CHRO	Q8vmw26 microcystis
128	36	64.3	528	2	Q91FE4_IRV6	Q91fe4 chilo iride	201	34	60.7	93	2	Q8VM32_9CHRO	Q8vm32 microcystis
129	36	64.3	635	2	Q4R897_WACFA	Q4r897 macaca fasc	202	34	60.7	93	2	Q8VM35_9CHRO	Q8vm35 microcystis
130	36	64.3	635	2	Q4R6D6_WACFA	Q4r6d6 macaca fasc	203	34	60.7	93	2	Q8VM31_MICAB	Q8vm31 microcystis
131	36	64.3	653	2	Q4P819_USTMA	Q4p819 utiilago ma	204	34	60.7	93	2	Q8VM34_MICAB	Q8vm34 microcystis
132	36	64.3	694	2	Q51XW4_MAGGR	Q51xw4 magnaporth	205	34	60.7	93	2	Q8VLC6_MICAB	Q8vlc6 microcystis
133	36	64.3	716	2	Q6C489_YARLI	Q6c489 yarrowia li	206	34	60.7	93	2	Q8VLA48_9CHRO	Q8vlla48 microcystis
134	36	64.3	944	2	Q9HE41_NEUCR	Q9he41 neurospora	207	34	60.7	93	2	Q5MPE4_9CHRO	Q5mpe4 microcystis
135	36	64.3	1033	2	Q9V643_DROME	Q9v643 drosophila	208	34	60.7	93	2	Q5MPE2_9CHRO	Q5mpe2 microcystis
136	36	64.3	1033	2	Q24327_DROME	Q24327 drosophila	209	34	60.7	93	2	Q5MPE0_9CHRO	Q5mpe0 microcystis
137	36	64.3	1442	2	Q4NU14_9DELT	Q4nu14 anaeromyxob	210	34	60.7	93	2	Q5MPD8_9CHRO	Q5mpd8 microcystis
138	36	64.3	1697	2	Q8JUG7_9CALI	Q8jg7 normal-lik	211	34	60.7	93	2	Q5MPD6_9CHRO	Q5mpd6 microcystis
139	36	64.3	1697	2	Q8JUI0_9CALI	Q8ji10 normal-lik	212	34	60.7	93	2	Q5MPD4_9CHRO	Q5mpd4 microcystis
140	36	64.3	1699	2	Q8JX16_9CALI	Q8jx16 normal-lik	213	34	60.7	93	2	Q5MPD2_9CHRO	Q5mpd2 microcystis
141	36	64.3	2009	2	Q7R8P2_PLAYO	Q7r8p2 plasmodium	214	34	60.7	93	2	Q5MPD0_9CHRO	Q5mpd0 microcystis
142	35	62.5	89	2	Q6NMX7_DROME	Q6nm7 drosophila	215	34	60.7	93	2	Q52MB8_9CHRO	Q52mb8 microcystis
143	35	62.5	89	2	Q9VEA7_DROME	Q9vea7 drosophila	216	34	60.7	93	2	Q52MB6_9CHRO	Q52mb6 microcystis
144	35	62.5	108	1	KVIS_HUMAN	P01611 homo sapien	217	34	60.7	93	2	Q52MB4_9CHRO	Q52mb4 microcystis
145	35	62.5	116	2	Q5SMN9_ORYSA	Q5smn9 oryza sativ	218	34	60.7	93	2	Q8VIL96_MICAB	Q8vil96 microcystis
146	35	62.5	120	2	Q8GGI8_LACPL	Q8ggi8 lactobacill	219	34	60.7	93	2	Q8VILA4_MICAB	Q8vlla4 microcystis
147	35	62.5	124	2	Q9RLT0_9HIV1	Q9rlt0 lactobacill	220	34	60.7	94	2	Q4TQM1_9SPHN	Q4tqm1 erythroba
148	35	62.5	133	2	Q9QOV6_9HIV1	Q9qov6 homo immun	221	34	60.7	94	2	Q5F0L7_9CYAN	Q5f0l7 phormidium
149	35	62.5	140	2	Q4XR24_PLACH	Q4xr24 plasmodium	222	34	60.7	95	2	Q5F0L3_9CYAN	Q5f0l3 phormidium
150	35	62.5	142	2	Q8RHH8_FUSNN	Q8rhh8 fusobacteri	223	34	60.7	95	2	Q5F0K5_9CYAN	Q5f0k5 lyngbya aer
151	35	62.5	146	2	Q8ISA1_ONCVO	Q8isa1 onchocerca	224	34	60.7	95	2	Q5F0K3_9CYAN	Q5f0k3 phormidium
152	35	62.5	162	2	Q85491_SYNC	Q85491 synechocyst	225	34	60.7	97	2	Q9F9D8_MICAB	Q9f9d8 microcystis
153	35	62.5	189	2	Q8NSF5_CORGL	Q8nsf5 corynebacte	226	34	60.7	97	2	Q9F9D6_MICAB	Q9f9d6 microcystis
154	35	62.5	196	2	Q7PX18_ANOGA	Q7px18 anopheles g	227	34	60.7	97	2	Q5F0L5_9CYAN	Q5f0l5 phormidium
155	35	62.5	247	1	MINC_SYNPN	Q55901 synechocyst	228	34	60.7	98	2	Q9RLG3_PLARU	Q9rlg3 planktothri
156	35	62.5	247	2	Q93I51_9EURK	Q93i51 sphaerotilu	229	34	60.7	98	2	Q8KXK6_9CHRO	Q8kpk6 microcystis
157	35	62.5	277	2	Q6D9B7_ERWCT	Q6d9b7 erwinia car	230	34	60.7	98	2	Q9F9E4_9CHRO	Q9f9e6 microcystis
158	35	62.5	328	2	Q5QQ39_CHICK	Q5qq39 gallus gall	231	34	60.7	98	2	Q8KPY0_9CHRO	Q8kpy0 microcystis
159	35	62.5	381	2	Q7N440_PHOLI	Q7n440 photorhabd	232	34	60.7	98	2	Q9F9E2_9CHRO	Q9f9e2 microcystis
160	35	62.5	411	2	Q4WFK5_ASPFU	Q4wfk5 aspergillus	233	34	60.7	98	2	Q8KPY2_9CHRO	Q8kpy2 microcystis
161	35	62.5	421	1	ISPG_NEIG1	Q5f913 neisseria g	234	34	60.7	98	2	Q9F9C6_MICAB	Q9f9c6 microcystis
162	35	62.5	421	1	ISPG_NEIMA	Q9ju34 neisseria m	235	34	60.7	98	2	Q8KXK2_9CHRO	Q8kpk2 microcystis
163	35	62.5	421	1	ISPG_NEIMA	Q9ju34 neisseria m	236	34	60.7	98	2	Q9F9E4_9CHRO	Q9f9e6 microcystis
164	35	62.5	422	2	Q86ND3_CABEL	Q86nd3 caenorhabdi	237	34	60.7	98	2	Q9F9E8_MICAB	Q9f9e8 microcystis
165	35	62.5	440	1	GBRP_HUMAN	Q00591 homo sapien	238	34	60.7	98	2	Q8KPY4_MICAB	Q8kpy4 microcystis
166	35	62.5	440	2	Q5EA06_BOVIN	Q5ea06 bos taurus	239	34	60.7	98	2	Q9F9C9_MICAB	Q9f9c9 microcystis
167	35	62.5	471	2	Q394E4_9ADEN	Q394e4 porcine ade	240	34	60.7	98	2	Q8KPY6_9CHRO	Q8kpy6 microcystis
168	35	62.5	481	2	Q413R5_GIBZE	Q413r5 gibberella	241	34	60.7	98	2	Q9ETB4_MICAB	Q9etb4 microcystis
169	35	62.5	484	2	Q979H9_THEVO	Q979h9 thetoplas	242	34	60.7	98	2	Q9ETB3_9CHRO	Q9etb3 microcystis
170	35	62.5	500	2	Q5S2S1_9HIV1	Q5s2s1 human immun	243	34	60.7	98	2	Q9ETG6_MICAB	Q9etg6 microcystis
171	35	62.5	516	2	Q86ND4_CABEL	Q86nd4 caenorhabdi	244	34	60.7	98	2	Q5F0L9_9CYAN	Q5f0l9 phormidium
172	35	62.5	518	2	Q8A171_BACTN	Q8a171 bacteroides	245	34	60.7	98	2	Q5F0K9_9CYAN	Q5f0k9 phormidium
173	35	62.5	547	2	Q6MRP6_BDEBA	Q6mrp6 bdellovibri	246	34	60.7	99	2	Q9F9D2_MICAB	Q9f9d2 microcystis
174	35	62.5	573	2	Q9S1B0_ARATH	Q9s1b0 arabidopsis	247	34	60.7	99	2	Q9F9C2_9CHRO	Q9f9c2 microcystis
175	35	62.5	586	2	Q6LIW1_PROPR	Q6liw1 photobacter	248	34	60.7	99	2	Q5GJ63_ACMR	Q5gj63 acaryochlor
176	35	62.5	610	2	Q86ND6_CABEL	Q86nd6 caenorhabdi	249	34	60.7	100	2	Q9F9D1_MICAB	Q9f9d1 microcystis
177	35	62.5	616	2	Q4RNB2_TETNG	Q4rnb2 tetraodon n	250	34	60.7	101	2	Q9F4Y2_9CYAN	Q9f4y2 arthrospira

251	34	60.7	101	2	Q9F4X2_9CYAN	Q9F4x2	arthrospira	324	34	60.7	105	2	Q6Q0U3_MICAE	Q6Q0u3	microcystis
252	34	60.7	101	2	Q9F4Y6_9CYAN	Q9F4y6	arthrospira	325	34	60.7	105	2	Q6Q0U1_MICAE	Q6Q0u1	microcystis
253	34	60.7	101	2	Q9F4Z4_9CYAN	Q9F4z4	arthrospira	326	34	60.7	105	2	Q6Q0T9_MICAE	Q6Q0t9	microcystis
254	34	60.7	101	2	Q9F4Z0_9CYAN	Q9F4z0	lyngbya aea	327	34	60.7	105	2	Q6Q0T7_MICAE	Q6Q0t7	microcystis
255	34	60.7	101	2	Q9F4W8_9CYAN	Q9F4w8	arthrospira	328	34	60.7	105	2	Q6Q0T5_MICAE	Q6Q0t5	microcystis
256	34	60.7	101	2	Q9F4Z8_9CYAN	Q9F4z8	arthrospira	329	34	60.7	105	2	Q6Q0T3_MICAE	Q6Q0t3	microcystis
257	34	60.7	101	2	Q9F4Z6_9CYAN	Q9F4z6	arthrospira	330	34	60.7	105	2	Q6Q0T1_MICAE	Q6Q0t1	microcystis
258	34	60.7	101	2	Q9F9C0_9CHRO	Q9F9c0	microcystis	331	34	60.7	105	2	Q546Z8_MICAE	Q546z8	microcystis
259	34	60.7	101	2	Q9F3Z0_9CYAN	Q9F3z0	oscillatori	332	34	60.7	105	2	Q54554_MICAE	Q54554	microcystis
260	34	60.7	101	2	Q9F4Y0_9CYAN	Q9F4y0	arthrospira	333	34	60.7	105	2	Q54555_MICAE	Q54555	microcystis
261	34	60.7	101	2	Q9F4X0_9CYAN	Q9F4x0	arthrospira	334	34	60.7	106	2	Q54586_9CHRO	Q54586	microcystis
262	34	60.7	101	2	Q9F4X6_9CYAN	Q9F4x6	arthrospira	335	34	60.7	107	2	Q96SA9_HUMAN	Q96sa9	homo sapien
263	34	60.7	101	2	Q9AF76_9CYAN	Q9AF76	arthrospira	336	34	60.7	108	2	Q9UL77_HUMAN	Q9ul77	homo sapien
264	34	60.7	101	2	Q9F4Z2_9CYAN	Q9F4z2	arthrospira	337	34	60.7	108	2	Q925S9_MOUSE	Q925s9	mus musculus
265	34	60.7	101	2	Q9F4Z0_9CYAN	Q9F4z0	arthrospira	338	34	60.7	127	2	Q925S9_MOUSE	Q925s9	mus musculus
266	34	60.7	101	2	Q9F4Y8_9CYAN	Q9F4y8	arthrospira	339	34	60.7	158	1	LUXS_CLOAB	Q97f13	clostridium
267	34	60.7	101	2	Q9AF74_9CYAN	Q9AF74	arthrospira	340	34	60.7	162	1	PHCA1_SYNPF6	P03038	synecococc
268	34	60.7	101	2	Q9F9C8_MICAE	Q9F9c8	microcystis	341	34	60.7	162	1	PHCA2_SYNPF6	P03043	synecococc
269	34	60.7	101	2	Q9AF72_9CYAN	Q9AF72	arthrospira	342	34	60.7	162	1	PHCA_AGLNE	P28557	aglaothamni
270	34	60.7	101	2	Q9F4X4_9CYAN	Q9F4x4	arthrospira	343	34	60.7	162	1	PHCA_CYPAPA	P05730	cyanophora
271	34	60.7	101	2	Q9F4W6_9CYAN	Q9F4w6	arthrospira	344	34	60.7	162	1	PHCA_GALUSU	P03066	gaidieria s
272	34	60.7	101	2	Q9F4Y4_9CYAN	Q9F4y4	arthrospira	345	34	60.7	162	1	PHCA_POLUR	P59858	polyisiphoni
273	34	60.7	101	2	Q9F4W4_9CYAN	Q9F4w4	arthrospira	346	34	60.7	162	1	PHCA_PORCR	P37207	porphyridiu
274	34	60.7	101	2	Q9F4X8_9CYAN	Q9F4x8	arthrospira	347	34	60.7	162	1	PHCA_PORPU	P51378	porphyra pu
275	34	60.7	101	2	Q6WS47_9CHRO	Q6ws47	microcystis	348	34	60.7	162	1	PHCA_RHOVL	Q36699	rhodella vi
276	34	60.7	101	2	Q6WS45_9CHRO	Q6ws45	microcystis	349	34	60.7	162	1	PHCA_SPIPL	P72509	spirulina p
277	34	60.7	101	2	Q6WS43_9CHRO	Q6ws43	microcystis	350	34	60.7	162	1	PHCA_SYNEL	P50032	synecococc
278	34	60.7	101	2	Q6WS41_9CHRO	Q6ws41	microcystis	351	34	60.7	162	1	PHCA_SYNPF7	P03943	synecococc
279	34	60.7	101	2	Q6WS39_9CHRO	Q6ws39	microcystis	352	34	60.7	162	1	PHCA_SYNPF3	P13530	synecococc
280	34	60.7	101	2	Q6WS37_9CHRO	Q6ws37	microcystis	353	34	60.7	162	1	PHCA_SYNPF3	P13530	synecococc
281	34	60.7	101	2	Q6WS35_9CHRO	Q6ws35	microcystis	354	34	60.7	162	1	Q6B8L6_GRATL	Q6B8l6	gracilaria
282	34	60.7	101	2	Q6WS33_9CHRO	Q6ws33	microcystis	355	34	60.7	162	2	Q9AM02_SYNVU	Q9am02	synecococc
283	34	60.7	101	2	Q6WS31_9CHRO	Q6ws31	microcystis	356	34	60.7	162	2	Q8VV08_SYNY4	Q8vv08	synecocyst
284	34	60.7	101	2	Q6WS29_9CHRO	Q6ws29	microcystis	357	34	60.7	162	2	Q8VRJ2_SFIMA	Q8vrj2	spirulina m
285	34	60.7	101	2	Q6WS27_MICAE	Q6ws27	microcystis	358	34	60.7	163	2	Q76N39_SYNSP	Q76n39	synecococc
286	34	60.7	101	2	Q6WS25_MICAE	Q6ws25	microcystis	359	34	60.7	167	2	Q7OUG1_GIALA	Q7oug1	giardia lam
287	34	60.7	101	2	Q6WS23_9CHRO	Q6ws23	microcystis	360	34	60.7	179	2	Q6Z8L7_CAEBR	Q6z8l7	caenorhabdi
288	34	60.7	101	2	Q6WS21_9CHRO	Q6ws21	microcystis	361	34	60.7	202	2	Q3P97_9SPHI	Q3p97	microscilla
289	34	60.7	101	2	Q6WS19_9CHRO	Q6ws19	microcystis	362	34	60.7	207	2	Q6X0G4_9HIV1	Q6x0g4	human immun
290	34	60.7	101	2	Q6WS17_9CHRO	Q6ws17	microcystis	363	34	60.7	215	2	Q89Q87_BRAJA	Q89q87	bradyrhizob
291	34	60.7	101	2	Q6WS15_9CHRO	Q6ws15	microcystis	364	34	60.7	221	2	Q9ZAP4_PHOLE	Q9zap4	photobacter
292	34	60.7	102	2	Q9F9F0_MICAE	Q9F9f0	microcystis	365	34	60.7	241	2	Q921A6_MOUSE	Q921a6	mus musculus
293	34	60.7	103	2	Q9F9C4_MICAE	Q9F9c4	microcystis	366	34	60.7	244	2	Q8Z0G1_ANASP	Q8z0g1	anabaena sp
294	34	60.7	103	2	Q6Q0V4_MICAE	Q6Q0v4	microcystis	367	34	60.7	255	2	Q6MM15_BDEBA	Q6mm15	bdellovibri
295	34	60.7	103	2	Q6Q0V4_MICAE	Q6Q0v4	microcystis	368	34	60.7	256	2	Q7ZXN2_XENLA	Q7zxnn2	xenopus lae
296	34	60.7	104	2	Q6J9A3_9CHRO	Q6j9a3	uncultured	369	34	60.7	260	2	Q4LUD5_9BURK	Q4lud5	burkholderi
297	34	60.7	105	2	Q50364_MICAE	Q50364	microcystis	370	34	60.7	262	1	CAPZA_CANGA	Q6fn48	candida gla
298	34	60.7	105	2	Q50362_MICAE	Q50362	microcystis	371	34	60.7	269	2	Q83VY9_9PROT	Q83vr9	methylobaci
299	34	60.7	105	2	Q50359_MICAE	Q50359	microcystis	372	34	60.7	282	2	Q73WY2_MYCPA	Q73wy2	mycobacteri
300	34	60.7	105	2	Q712U9_9SYNC	Q712u9	synecocyst	373	34	60.7	290	2	Q6D3M0_ERWCT	Q6d3m0	erwinia car
301	34	60.7	105	2	Q6QUW8_9CHRO	Q6quw8	microcystis	374	34	60.7	290	2	Q5QX14_IDILO	Q5qx14	idiomarina
302	34	60.7	105	2	Q6QUW6_9CHRO	Q6quw6	microcystis	375	34	60.7	299	2	Q6FQB5_CANGA	Q6fqb5	candida gla
303	34	60.7	105	2	Q6QUW4_9CHRO	Q6quw4	microcystis	376	34	60.7	299	2	Q8EE29_SHEON	Q8ee29	shewanella
304	34	60.7	105	2	Q6QUW2_9CHRO	Q6quw2	microcystis	377	34	60.7	304	2	Q4MK58_BACCE	Q4mk58	bacillus ce
305	34	60.7	105	2	Q6Q0Y6_MICAE	Q6Q0y6	microcystis	378	34	60.7	304	2	Q63DR3_BACCE	Q63dr3	bacillus ce
306	34	60.7	105	2	Q6Q0Y2_MICAE	Q6Q0y2	microcystis	379	34	60.7	304	2	Q6HL86_BACHK	Q6hl86	bacillus th
307	34	60.7	105	2	Q6Q0Y0_MICAE	Q6Q0y0	microcystis	380	34	60.7	304	2	Q73B27_BACCI	Q73b27	bacillus th
308	34	60.7	105	2	Q6Q0X8_MICAE	Q6Q0x8	microcystis	381	34	60.7	304	2	Q81T03_BACAN	Q81t03	bacillus an
309	34	60.7	105	2	Q6Q0X6_9CHRO	Q6Q0x6	microcystis	382	34	60.7	335	2	Q4FVY9_LEIMA	Q4fvy9	leishmania
310	34	60.7	105	2	Q6Q0X4_9CHRO	Q6Q0x4	microcystis	383	34	60.7	342	2	Q67735_AQUAE	Q67735	aquifex aeo
311	34	60.7	105	2	Q6Q0X2_MICAE	Q6Q0x2	microcystis	384	34	60.7	349	2	Q9HR20_HALSA	Q9hr20	halobacteri
312	34	60.7	105	2	Q6Q0X0_MICAE	Q6Q0x0	microcystis	385	34	60.7	362	2	Q6BSL4_DEBHA	Q6bsl4	debaryomyce
313	34	60.7	105	2	Q6Q0W8_MICAE	Q6Q0w8	microcystis	386	34	60.7	365	2	Q72KY0_THET2	Q72ky0	thermus the
314	34	60.7	105	2	Q6Q0W6_9CHRO	Q6Q0w6	microcystis	387	34	60.7	373	2	Q9JKN9_MARMO	Q9jkn9	marmota mon
315	34	60.7	105	2	Q6Q0W4_MICAE	Q6Q0w4	microcystis	388	34	60.7	379	2	Q5GF26_9POKV	Q5gf26	diachasmaim
316	34	60.7	105	2	Q6Q0W2_9CHRO	Q6Q0w2	microcystis	389	34	60.7	385	2	Q5NH20_FRANT	Q5nh20	francisella
317	34	60.7	105	2	Q6Q0W0_9CHRO	Q6Q0w0	microcystis	390	34	60.7	390	2	Q7KZR4_HUMAN	Q7kzr4	homo sapien
318	34	60.7	105	2	Q6Q0V8_MICAE	Q6Q0v8	microcystis	391	34	60.7	396	2	Q9H6K3_HUMAN	Q9h6k3	homo sapien
319	34	60.7	105	2	Q6Q0V6_MICAE	Q6Q0v6	microcystis	392	34	60.7	405	2	Q96VN6_GLOIN	Q96vn6	glomus intr
320	34	60.7	105	2	Q6Q0V4_MICAE	Q6Q0v4	microcystis	393	34	60.7	407	2	Q6M9K8_PARUW	Q6m9k8	parachlamyd
321	34	60.7	105	2	Q6Q0V2_MICAE	Q6Q0v2	microcystis	394	34	60.7	411	2	Q96BR8_HUMAN	Q96br8	homo sapien
322	34	60.7	105	2	Q6Q0U8_9CHRO	Q6Q0u8	microcystis	395	34	60.7	425	2	Q9X8Q3_STRCO	Q9x8q3	streptomyce
323	34	60.7	105	2	Q6Q0U5_MICAE	Q6Q0u5	microcystis	396	34	60.7	449	2	Q5P939_AZOSE	Q5p939	azocarcus sp
													Q41F10_GIBZE	Q41f10	gibberella

397 34 60.7 458 2 Q7PW77 ANOGA Q7pw77 anopheles g
398 34 60.7 471 2 Q5NE99 FRATT Q5nes9 francisella
399 34 60.7 479 2 Q5B1X5 XENLA Q5bix5 xenopus lae
400 34 60.7 479 2 Q4RH53 TETNG Q4rh53 tetradon n
401 34 60.7 482 2 Q4RV20 LISMF Q4rv20 listeria mo
402 34 60.7 482 2 Q8Y3R2 LISMO Q8y3r2 listeria mo
403 34 60.7 494 2 Q5AXM8 EMENI Q5axm8 aspergillus
404 34 60.7 521 2 Q8X1F6 GLOIN Q8x1f6 glomus intr
405 34 60.7 528 2 Q5KR92 NEOP Q5kr92 hodotermops
406 34 60.7 535 2 Q82289 CHLCV Q82289 chlamydomphi
407 34 60.7 538 2 Q97W82 SULSO Q97w82 sulfolobus
408 34 60.7 542 2 Q9QZT6 MOUSE Q9qzt6 mus musculus
409 34 60.7 556 2 Q6BHQ0 DEBHA Q6bhq0 debaryomyce
410 34 60.7 612 2 Q7RYF1 NEUCR Q7ryf1 neurospora
411 34 60.7 623 2 Q872P3 NEUCR Q872p3 neurospora
412 34 60.7 624 2 Q5X46 CRYNE Q5x46 cryptococcu
413 34 60.7 624 2 Q5KMT6 CRYNE Q5kmt6 cryptococcu
414 34 60.7 640 1 COG8 MOUSE COG8 mus musculus
415 34 60.7 640 2 Q8BFW5 MOUSE Q8bfw5 m mus muscu
416 34 60.7 709 2 Q97F21 CLOAB Q97f21 clostridium
417 34 60.7 728 2 Q9RLJ8 RAT Q9rlj8 rattus norv
418 34 60.7 736 2 Q9HC86 HUMAN Q9hc86 homo sapien
419 34 60.7 736 2 Q96S15 HUMAN Q96s15 homo sapien
420 34 60.7 739 2 Q96SK8 HUMAN Q96sk8 homo sapien
421 34 60.7 739 2 Q8CFI3 MOUSE Q8cfi3 mus musculus
422 34 60.7 742 2 Q9CWK5 MOUSE Q9cwk5 mus musculus
423 34 60.7 747 2 Q9QZT7 MOUSE Q9qzt7 mus musculus
424 34 60.7 804 2 Q96SN3 HUMAN Q96sn3 homo sapien
425 34 60.7 901 1 VEF GVPU VEF GVPU
426 34 60.7 901 2 Q9DXA2 GVCF Q9dxa2 gvcp
427 34 60.7 901 2 Q8TPR8 METAC Q8tpr8 methanosarc
428 34 60.7 919 2 Q4ULL1 RICPE Q4ull1 rickettsia
429 34 60.7 949 2 Q5MPG7 SAUR Q5mpg7 feylinia po
430 34 60.7 956 2 Q6BQ78 DEBHA Q6bq78 debaryomyce
431 34 60.7 1024 2 Q9TESO CLOAB Q9teso clostridum
432 34 60.7 1035 2 Q4P236 USTMA Q4p236 ustilago ma
433 34 60.7 1088 2 Q9ZRV7 TOBAC Q9zrv7 nicotiana t
434 34 60.7 1116 2 Q4I3Q3 GIBZE Q4i3q3 gibberella
435 34 60.7 1141 2 Q4RF12 TETNG Q4rf12 tetradon n
436 34 60.7 1145 2 Q4P3M1 USTMA Q4p3m1 ustilago ma
437 34 60.7 1297 2 Q9P3Y3 PICFA Q9p3y3 pichia fari
438 34 60.7 1398 2 Q5AI83 CANAL Q5ai83 candida alb
439 34 60.7 1404 2 Q5AJ13 CANAL Q5aj13 candida alb
440 34 60.7 1404 2 Q9P2P1 HUMAN Q9p2p1 homo sapien
441 34 60.7 1819 2 Q8Q891 LEPMC Q8q891 leptosphaer
442 34 60.7 2028 2 Q5AZ32 EMENI Q5az32 aspergillus
443 34 60.7 2517 2 Q46587 DESUVIBR Q46587 desulfovibr
444 33 58.9 57 2 Q8K691 STRP3 Q8k691 streptococc
445 33 58.9 91 2 FNR CAPCP FNR CAPCP
446 33 58.9 92 1 FNR HAEP8 FNR HAEP8
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448 33 58.9 93 2 Q68GP8 NOST Q68gp8 anabaena so
449 33 58.9 93 2 Q68GM6 NOST Q68gm6 anabaena sp
450 33 58.9 93 2 Q68GR2 NOST Q68gr2 anabaena pl
451 33 58.9 93 2 Q5BLG7 BRARE Q5blg7 brachydanio
452 33 58.9 96 2 Q5XEJ2 STRP6 Q5xej2 streptococc
453 33 58.9 97 2 Q9RAG1 9CIAN Q9rag1 planktothri
454 33 58.9 98 2 Q4YV72 PLABE Q4yv72 plasmodium
455 33 58.9 113 2 KVJ31 HUMAN KVJ31 homo sapien
456 33 58.9 115 1 Q6LD17 MOUSE Q6ld17 mus musculus
457 33 58.9 118 2 Q8GND8 VIBME Q8gnd8 vibrio mets
458 33 58.9 120 2 Q5A6T7 CANAL Q5a6t7 candida alb
459 33 58.9 122 2 Q8CWJ9 VIBVUL Q8cwj9 vibrio vuln
460 33 58.9 129 2 Q5E592 VIBF1 Q5e592 vibrio fisc
461 33 58.9 131 2 Q9VH51 DROME Q9vh51 drosophila
462 33 58.9 137 2 Q9CZU9 MOUSE Q9czu9 mus musculus
463 33 58.9 139 2 Q97PT3 STRPN Q97pt3 streptococc
464 33 58.9 142 2 Q5FGT5 EHRRG Q5fgt5 ehrlichia r
465 33 58.9 145 2 Q90BB8 9HIV1 Q90bb8 human immun
466 33 58.9 147 2 Q90BB9 9HIV1 Q90bb9 human immun
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468 33 58.9 148 2 Q5HBB7 EHRRW Q5hbb7 ehrlichia r
469 33 58.9 156 2

470 470 33 58.9 160 2 Q5FEX5 EHRRW Q5fex5 ehrlichia r
471 33 58.9 160 2 Q8CXJ9 STRR6 Q8cxj9 streptococc
472 33 58.9 172 2 Q5JGV8 PYRKO Q5jgv8 pyrococcus
473 33 58.9 178 2 Q4N2C1 THEPA Q4n2c1 theileria p
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475 33 58.9 185 2 Q7PXG2 ANOGEA Q7pxg2 anopheles g
476 33 58.9 189 2 Q569I7 HUMAN Q569i7 homo sapien
477 33 58.9 199 2 Q81U75 BACAN Q81u75 bacillus an
478 33 58.9 200 2 Q6P820 XENTR Q6p820 xenopus tro
479 33 58.9 201 2 Q9JVP5 NEIMA Q9jvp5 neisseria m
480 33 58.9 201 2 Q9KOM0 NEIME Q9kom0 neisseria m
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482 33 58.9 221 2 Q7V738 PROMM Q7v738 prochloroco
483 33 58.9 224 2 Q6BFP1 PARTE Q6bfp1 paramectum
484 33 58.9 226 2 Q5LMU2 SILPO Q5lmu2 silicibacte
485 33 58.9 228 2 Q98RM8 GUTH Q98rm8 guillardia
486 33 58.9 236 2 Q6PIH7 HUMAN Q6pih7 homo sapien
487 33 58.9 237 2 Q8Y3C7 RALSO Q8y3c7 ralstonia s
488 33 58.9 240 1 HLYX ACTPL HLYX ACTPL
489 33 58.9 240 2 Q9Y864 ASPPA Q9y864 aspergillus
490 33 58.9 248 2 Q87PG6 VIBPA Q87pg6 vibrio para
491 33 58.9 248 2 Q7MKU9 VIBVUL Q7mku9 vibrio vuln
492 33 58.9 248 2 Q6D535 ERWCT Q6d535 erwina car
493 33 58.9 250 1 ETRA SHEON ETRA SHEON
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506 33 58.9 250 2 Q6LR34 PHOPR Q6lr34 photobacter
507 33 58.9 250 2 Q66AB0 YERPS Q66ab0 yerinia ps
508 33 58.9 251 2 Q7N4Y2 PHOLL Q7n4y2 photorhabd
509 33 58.9 252 2 Q6HMP7 BACHK Q6hmp7 bacillus th
510 33 58.9 252 2 Q7VLK2 HAEDU Q7vlk2 haemophilus
511 33 58.9 255 2 FNR ACTAC FNR ACTAC
512 33 58.9 257 1 FNR HAEIN FNR HAEIN
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514 33 58.9 257 2 Q9L801 9PAST Q9l801 actinobacil
515 33 58.9 257 2 Q4QK9 HAEI8 Q4qk9 haemophilus
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517 33 58.9 260 2 Q6L224 PICTO Q6l224 picophili
518 33 58.9 264 2 Q5PHR1 SALPA Q5phr1 salmonella
519 33 58.9 266 2 Q65TM6 MANSM Q65tm6 manheimia
520 33 58.9 267 2 Q8ITX2 DROKT Q8itx2 drosophila
521 33 58.9 270 2 Q8G7A7 BIFLO Q8g7a7 bifidobacte
522 33 58.9 272 2 Q6XUQ2 9PSED Q6xuq2 pseudomonas
523 33 58.9 273 1 FNR PASMU FNR PASMU
524 33 58.9 273 2 Q9JJD1 MOUSE Q9jjd1 mus musculus
525 33 58.9 279 2 Q57NZ9 SALCH Q57nz9 salmonella
526 33 58.9 281 2 Q6QXG9 GVAS Q6qxg9 agrotis seg
527 33 58.9 282 2 Q6MMJ3 BDELVIBR Q6mmj3 bdellovibri
528 33 58.9 288 1 GIDB BDEBA GIDB BDEBA
529 33 58.9 294 2 Q9XMG3 EPITY Q9xm3 epichloe ty
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531 33 58.9 303 2 Q85G62 CYAME Q85g62 cyanidiosch
532 33 58.9 305 2 Q7SSG1 NEUCR Q7ssg1 neurospora
533 33 58.9 305 2 Q416R3 GIBZE Q4i6r3 gibberella
534 33 58.9 309 1 YCF30 ODOI YCF30 ODOI
535 33 58.9 312 2 Q97A52 THEVO Q97a52 thermoplas
536 33 58.9 317 1 TNF11 HUMAN TNF11 h tumor nec
537 33 58.9 317 2 Q5T9V4 HUMAN Q5t9v4 homo sapien
538 33 58.9 333 2 Q8UU7 LACPL Q8uu7 lactobacill
539 33 58.9 338 2 Q5LE45 BACFN Q5le45 bacteroides
540 33 58.9 338 2 Q9F753 BACFN Q9f753 bacteroides
541 33 58.9 340 2 Q64T59 BACFR Q64t59 bacteroides
542 33 58.9 353 2 Q69703 MYCTU Q69703 mycobacteri

543	33	58.9	353	2	Q7TWT5_MYCBO	Q7Tvt5 mycobacteri	616	33	58.9	521	2	Q86NW0_DROME	Q86nw0 drosophila
544	33	58.9	356	2	Q6JTA7_CAPAN	Q6jta7 capeuic an	617	33	58.9	522	2	Q93ET1_ERRRW	Q93et1 ehrlichia r
545	33	58.9	361	2	Q86NR2_DROME	Q86nr2 drosophila	618	33	58.9	522	2	Q5HBB5_ERRRW	Q5hbb5 ehrlichia r
546	33	58.9	363	2	Q628T4_CAEHR	Q628t4 caenorhabdi	619	33	58.9	526	2	Q5PGT3_ERRRG	Q5pgt3 ehrlichia r
547	33	58.9	363	2	Q25617_HELPPY	Q25617 helicobacte	620	33	58.9	526	2	Q5FEX3_ERRRW	Q5fex3 ehrlichia r
548	33	58.9	366	1	QURA_SFWY3	Q5850 synecocyst	621	33	58.9	528	2	Q72EB0_DRSVH	Q72eb0 desulfovibr
549	33	58.9	367	2	Q5GX83_XANOR	Q5gx83 xanthomonas	622	33	58.9	541	2	Q7Q60_GIALA	Q7q60 giardia lam
550	33	58.9	369	2	Q7PUT1_ANOGA	Q7put1 anopheles g	623	33	58.9	544	2	Q8CQK8_STAEP	Q8cqk8 staphylococ
551	33	58.9	370	1	PRIS_PICTO	Q51w5 picophilus	624	33	58.9	550	2	Q53EK0_BOMMO	Q53ek0 bomby mori
552	33	58.9	370	2	Q5XJR9_BRARE	Q5xjr9 brachydanio	625	33	58.9	557	1	INARI_HUMAN	pl17181 homo sapien
553	33	58.9	373	2	Q42467_TETFL	Q42467 tetraodon f	626	33	58.9	557	2	Q53GW9_HUMAN	Q53gw9 homo sapien
554	33	58.9	373	2	Q5UJ79_BRARE	Q5uj79 brachydanio	627	33	58.9	557	2	Q53H11_HUMAN	Q53h11 homo sapien
555	33	58.9	376	2	Q9ESU0_MOUSE	Q9esu0 mus musculu	628	33	58.9	560	1	INARI_BOVIN	Q04790 bos taurus
556	33	58.9	378	2	Q4KL10_RAT	Q4kl10 rattus norv	629	33	58.9	566	2	Q5F9I0_NEIG1	Q5f9i0 neisseria g
557	33	58.9	378	2	Q6DFM1_XENTR	Q6dfm1 xenopus tro	630	33	58.9	566	2	Q9L6I4_NEIGO	Q9l6i4 neisseria g
558	33	58.9	380	2	Q6GQ82_XENLA	Q6gq82 xenopus lae	631	33	58.9	566	2	Q9JV09_NEIMA	Q9jv09 neisseria m
559	33	58.9	382	2	Q4IJ99_GIBZE	Q4ije9 gibberella	632	33	58.9	566	2	Q9JZZ0_NEIMB	Q9jzz0 neisseria m
560	33	58.9	385	1	SNF5_HUMAN	Q12824 homo sapien	633	33	58.9	589	2	Q9C497_GLOLA	Q9c497 glomerella
561	33	58.9	385	1	SNF5_MOUSE	Q920h3 mus musculu	634	33	58.9	590	1	INARI_MOUSE	P33896 mus musculu
562	33	58.9	385	2	Q5BIN2_BOVIN	Q5bin2 bos taurus	635	33	58.9	590	2	Q8OUJ3_MOUSE	Q8ouj3 mus musculu
563	33	58.9	385	2	Q9ESU1_MOUSE	Q9esu1 mus musculu	636	33	58.9	593	2	Q8OUR8_MOUSE	Q8our8 mus musculu
564	33	58.9	385	2	Q6ZWP4_MOUSE	Q6zwp4 mus musculu	637	33	58.9	593	2	Q5O8J8_LACRE	Q5o8j8 lactobacill
565	33	58.9	387	2	Q5ZK40_CHICK	Q5zk40 gallus gall	638	33	58.9	599	2	Q94Z17_SCHCO	Q94zi7 schizophyll
566	33	58.9	387	2	Q6AMC1_DRSPPS	Q6amc1 desulfovibr	639	33	58.9	612	1	CO88_HUMAN	Q96mw5 homo sapien
567	33	58.9	388	2	Q7JAU5_DRSVH	Q7jaus desulfovibr	640	33	58.9	619	1	GIDA_CAMJF	Q9pna7 campylobact
568	33	58.9	392	2	Q97DC8_CLOAB	Q97dc8 clostridium	641	33	58.9	619	1	GIDA_CAMJF	Q5hts6 campylobact
569	33	58.9	394	2	Q9H836_HUMAN	Q9h836 homo sapien	642	33	58.9	621	2	Q55LN5_CRYNE	Q55ln5 cryptococcu
570	33	58.9	399	2	Q8L2G8_ERWCH	Q8l2g8 erwinia chr	643	33	58.9	621	2	Q5KD72_CRYNE	Q5kd72 cryptococcu
571	33	58.9	403	2	Q6K1X6_ORYSA	Q6k1x6 oryza sativ	644	33	58.9	639	2	Q5GMJ9_9BACT	Q5gmj9 uncultured
572	33	58.9	411	2	Q82BG8_STRAW	Q82bg8 streptomyce	645	33	58.9	647	2	Q4HUJ3_CAMLA	Q4huj3 campylobact
573	33	58.9	412	2	Q4RPN3_TETNG	Q4rpn3 tetraodon n	646	33	58.9	653	2	Q856A7_9CAUD	Q856a7 mycobacteri
574	33	58.9	416	2	Q5GT37_WOLTR	Q5gt37 wolbachia s	647	33	58.9	654	1	SAS6_MOUSE	Q8ouk7 mus musculu
575	33	58.9	420	1	CNNA_CHLVR	P51986 chlorohydra	648	33	58.9	657	2	Q4HJAB_CAMLA	Q4hjab campylobact
576	33	58.9	421	2	Q9UK19_CTEVA	Q9uk19 ctenodactyl	649	33	58.9	662	2	Q6CFJ7_YARLI	Q6cfj7 yarrowia li
577	33	58.9	422	2	Q55BW2_DICDI	Q55bw2 dictyosteli	650	33	58.9	695	1	YHRA_SCHPO	Q8vzk0 schizosacch
578	33	58.9	422	2	Q9VPU3_DROME	Q9vpj3 drosophila	651	33	58.9	705	2	Q9LVN9_ARATH	Q9lvn9 arabidopsis
579	33	58.9	424	2	Q4UAK3_THEAN	Q4uak4 theileria a	652	33	58.9	728	2	Q8W3L4_9PROT	Q8w3l4 alvinella p
580	33	58.9	424	2	Q6W0X7_RHISN	Q6w0x7 rhizobium s	653	33	58.9	761	2	Q6FMU0_CANGA	Q6fmu0 candida gla
581	33	58.9	424	2	Q6UAH0_AGRIS	Q6uah0 agrobacteri	654	33	58.9	775	2	Q9ZRX3_PETHY	Q9zrx3 petunia hyb
582	33	58.9	425	2	Q92Y69_RHIME	Q92y69 rhizobium m	655	33	58.9	792	1	OSTA_XYLPA	Q9yf41 xyella fas
583	33	58.9	428	2	Q4TLE0_TETNG	Q4tle0 tetraodon n	656	33	58.9	792	1	OSTA_XYLPA	Q87a19 xyella fas
584	33	58.9	438	2	Q49337_ARATH	Q49337 arabidopsis	657	33	58.9	793	2	Q87X95_PSESM	Q87x95 pseudomonas
585	33	58.9	441	2	Q5XILI_RAT	Q5xill1 rattus norv	658	33	58.9	796	2	Q4ZP96_PSESY	Q4zpp96 pseudomonas
586	33	58.9	444	2	Q5OWI0_ENTHI	Q5ow10 entamoeba h	659	33	58.9	805	2	Q60ND5_CAEBR	Q60nd5 caenorhabdi
587	33	58.9	444	2	Q4LYT4_9BURK	Q4lyt4 burkholderi	660	33	58.9	805	2	Q87651_AERHY	Q87651 aeromonas h
588	33	58.9	446	2	Q987I2_RHILO	Q987i2 rhizobium l	661	33	58.9	826	2	Q4K909_PSEHF	Q4k909 pseudomonas
589	33	58.9	449	1	GBRD_MOUSE	P22933 mus musculu	662	33	58.9	832	2	Q5X8P9_LEGPA	Q5x8p9 legionella
590	33	58.9	449	1	GBRD_RAT	P18506 rattus norv	663	33	58.9	835	2	Q9S2I5_STRCO	Q9s2i5 streptomyce
591	33	58.9	449	1	GBRD_MOUSE	Q14766 mus musculu	664	33	58.9	846	2	Q51MD0_MAGGR	Q51md0 magnaporthe
592	33	58.9	452	1	GBRD_HUMAN	O14764 homo sapien	665	33	58.9	853	2	Q8IMZ9_DROME	Q8imz9 drosophila
593	33	58.9	455	2	Q6AWX1_ARATH	Q6awx1 arabidopsis	666	33	58.9	867	2	Q6L3P6_SOLDE	Q6l3p6 solanum dem
594	33	58.9	463	2	Q8JHG2_BRARE	Q8jhg2 brachydanio	667	33	58.9	872	2	Q9VCW4_DROME	Q9vcw4 drosophila
595	33	58.9	463	2	Q8PC35_BRARE	Q8pc35 brachydanio	668	33	58.9	881	2	Q5ZIB8_CHICK	Q5zib8 gallus gall
596	33	58.9	464	2	Q4WIV7_ASFFU	Q4wiv7 aspergillus	669	33	58.9	881	2	Q8JED9_9HIV1	Q8jed9 human immun
597	33	58.9	465	2	Q9R8M7_PONPY	Q9r8m7 pongo pygma	670	33	58.9	882	2	Q54QY9_DICDI	Q54qy9 dictyosteli
598	33	58.9	470	2	Q9PRC1_UREPA	Q9prc1 ureaplasma	671	33	58.9	886	2	Q6LZP0_METMP	Q6lzp0 methanococ
599	33	58.9	476	2	Q8TF11_HUMAN	Q8tf11 homo sapien	672	33	58.9	886	2	Q5XWN5_SOLTU	Q5xwn5 solanum tub
600	33	58.9	477	2	Q6Z035_ORYSA	Q6z035 oryza sativ	673	33	58.9	895	2	Q5XWQ4_SOLTU	Q5xwq4 solanum tub
601	33	58.9	478	2	Q96W48_CANAL	Q96w48 candida alb	674	33	58.9	896	2	Q8XZ06_RALSO	Q8xz06 raletonia s
602	33	58.9	478	2	Q4RPN8_TETNG	Q4rpn8 tetraodon n	675	33	58.9	908	2	Q64D81_9ARCH	Q64d81 uncultured
603	33	58.9	480	2	Q5A209_CANAL	Q5a209 candida alb	676	33	58.9	928	2	Q8MR73_DROME	Q8mr73 drosophila
604	33	58.9	483	1	VATH_BOVIN	Q46563 bos taurus	677	33	58.9	930	2	Q9VTN6_DROME	Q9vtn6 drosophila
605	33	58.9	483	1	VATH_HUMAN	Q9u112 homo sapien	678	33	58.9	932	2	Q6K892_ORYSA	Q6k892 oryza sativ
606	33	58.9	483	1	VATH_PIG	Q9tvc1 eus scrofa	679	33	58.9	940	2	Q6H5U8_ORYSA	Q6h5u8 oryza sativ
607	33	58.9	483	2	Q8BEV3_MOUSE	Q8bve3 mus musculu	680	33	58.9	942	2	Q6L447_SOLDE	Q6l447 solanum dem
608	33	58.9	483	2	Q92IX8_MOUSE	Q92ix8 mus musculu	681	33	58.9	945	2	Q7XUL7_ORYSA	Q7xul7 oryza sativ
609	33	58.9	487	2	Q4KDC1_PSEFS	Q4kdc1 pseudomonas	682	33	58.9	947	2	Q7QHU2_ANOGA	Q7qhu2 anopheles g
610	33	58.9	487	2	Q82CH2_STRAW	Q82ch2 streptomyce	683	33	58.9	963	2	Q6L3P3_SOLDE	Q6l3p3 solanum dem
611	33	58.9	494	1	AMVR_DROPS	O18552 drosophila	684	33	58.9	974	2	Q4MW12_BACCE	Q4mw12 bacillus th
612	33	58.9	495	2	Q8I9R0_DROFC	O819r0 drosophila	685	33	58.9	974	2	Q6HMF0_BACHK	Q6hmf0 bacillus th
613	33	58.9	507	2	Q92TI4_RHIME	Q92ti4 rhizobium m	686	33	58.9	974	2	Q73CF5_BACCI	Q73cf5 bacillus ce
614	33	58.9	511	2	Q8MS19_DROPHILA	Q8ms19 drosophila	687	33	58.9	974	2	Q8I3W8_BACCR	Q8i3w8 bacillus ce
615	33	58.9	521	2	Q7S0A8_NEUCR	Q7s0a8 neurospora	688	33	58.9	974	2	Q63EZ1_BACCR	Q63ez1 bacillus ce

689	33	58.9	1011	2	Q82N43_STRAW	Q82n43 streptomyc	762	32	57.1	164	1	PHEA1_SYNPNW	Q08086 synechococc
690	33	58.9	1019	2	Q6BVH3_DEBHA	Q6bv3 debatyomyce	763	32	57.1	164	1	PHEA1_SYNPNW	Q02179 synechococc
691	33	58.9	1024	2	Q7VJW1_HELHP	Q7vj1 helicobacte	764	32	57.1	164	1	Q7U4Q1_SYNPNX	Q7u4q1 synechococc
692	33	58.9	1055	2	Q9Y2K8_HUMAN	Q9y2k8 homo sapien	765	32	57.1	167	1	CDN2A_MOUSE	P51480 mus musculus
693	33	58.9	1068	2	Q6L3W8_SOLDE	Q6l3w8 solanum dem	766	32	57.1	168	2	O89088_MOUSE	O89088 mus musculus
694	33	58.9	1076	2	Q5XWQ9_SOLITU	Q5xwq9 solanum tub	767	32	57.1	168	2	P97510_MOUSE	P97510 mus musculus
695	33	58.9	1101	2	Q5XWV1_SOLITU	Q5xwv1 solanum tub	768	32	57.1	171	2	Q9ZXC1_BPPH1	Q9zxc1 bacterioph
696	33	58.9	1102	2	Q57VN8_9TRYP	Q57vn8 trypanosoma	769	32	57.1	171	2	Q5N0X1_SYNPN6	Q5n0x1 synechococc
697	33	58.9	1102	2	Q87HL9_VIBPA	Q87hl9 vibrio para	770	32	57.1	172	2	Q68KU4_9BACT	Q68ku4 uncultured
698	33	58.9	1114	2	Q9ZR38_LYCES	Q9zr38 lycopersico	771	32	57.1	172	2	Q68KU5_9BACT	Q68ku5 uncultured
699	33	58.9	1114	2	Q6L3V3_SOLDE	Q6l3v3 solanum dem	772	32	57.1	176	2	Q38867_ARATH	Q38867 arabidopsis
700	33	58.9	1114	2	Q60D38_SOLITU	Q60d38 solanum tub	773	32	57.1	176	2	Q5D5F9_9RICK	Q5d5f9 wolbachia e
701	33	58.9	1140	1	Y376_MYCPN	P75605 mycoplasma	774	32	57.1	181	1	NIP7_YEAST	Q08962 saccharomyc
702	33	58.9	1164	2	Q9XIK6_ARATH	Q9xik6 arabidopsis	775	32	57.1	181	2	Q6BV36_DEBHA	O6bv36 debatyomyce
703	33	58.9	1172	2	Q5CLH4_CRYHO	Q5clh4 cryptospori	776	32	57.1	181	2	Q6CWQ7_KLULA	O6cwq7 kluyveromyc
704	33	58.9	1173	2	Q5CV20_CRYPV	Q5cv20 cryptospori	777	32	57.1	181	2	Q6FJU7_CANGA	Q6fjj7 candida gla
705	33	58.9	1202	2	Q9Lmq4_ORYZA	Q9lmq4 oryza sativ	778	32	57.1	181	2	Q755C7_ASHGO	Q755c7 ashbya goss
706	33	58.9	1231	2	Q543V3_MOUSE	Q543v3 mus musculu	779	32	57.1	182	2	Q8EBW8_SHEON	Q8ebw8 shewanella
707	33	58.9	1233	1	IRS1_MOUSE	P35569 mus musculu	780	32	57.1	184	2	Q8IXH0_PLAF7	Q8ikh0 plasmodium
708	33	58.9	1243	1	SMC4_MICAR	Q9eras microtus ar	781	32	57.1	185	2	Q876M3_ASPFU	Q876m3 aspergillus
709	33	58.9	1259	2	Q932J7_ENTPA	Q932j7 enterococcu	782	32	57.1	185	2	Q4WZG3_ASPFU	Q4wzg3 aspergillus
710	33	58.9	1293	2	Q4P384_USTMA	Q4p3e4 ustiliago ma	783	32	57.1	186	2	Q7Q529_GIALA	Q7q529 giardia lam
711	33	58.9	1315	2	Q68CZ1_HUMAN	Q68cz1 homo sapien	784	32	57.1	187	2	Q6NM52_ARATH	Q6nm52 arabidopsis
712	33	58.9	1348	2	Q60043_9THEO	Q60043 thermoanaer	785	32	57.1	187	2	Q4FUS4_9GNMM	Q4fus4 psychrobact
713	33	58.9	1458	2	Q08095_TRIGR	Q08095 tripeuistes	786	32	57.1	187	2	Q9E1W4_9ALPH	Q9e1w4 psychopithe
714	33	58.9	1491	2	Q4J601_AZOV1	Q4j601 azotobacter	787	32	57.1	193	2	Q8POV1_XANAC	Q8pov1 xanthomonas
715	33	58.9	1556	2	Q4Q626_LEIMA	Q4q626 leishmania	788	32	57.1	199	2	Q65VM8_MANSM	Q65vm8 mannheimia
716	33	58.9	1712	2	Q55GNI_DICTDI	Q5sgni dictyosteli	789	32	57.1	204	2	Q4XR33_PLACH	Q4xr33 plasmodium
717	33	58.9	1717	2	Q51GM3_ENTHI	Q51gm3 entamoeba h	790	32	57.1	209	1	RL1_HALUVO	P41199 halobacteri
718	33	58.9	2484	2	Q5CPZ7_CRYPV	Q5cpz7 cryptospori	791	32	57.1	211	1	RL1_HALUVO	P12738 haloarcula
719	33	58.9	3014	1	CELR1_HUMAN	Q9nyq6 homo sapien	792	32	57.1	213	2	Q4ZB11_9VIRU	Q4zb11 bacterioph
720	33	58.9	3014	2	Q5TH47_HUMAN	Q5th47 homo sapien	793	32	57.1	215	2	Q9V1L4_DROME	Q9v1l4 drosophila
721	33	58.9	3196	2	Q6AL05_DESPS	Q6alq5 desulfofale	794	32	57.1	219	1	TRMB_ANASP	O8yvz4 anabaena sp
722	33	58.9	3795	2	Q4Q754_LEIMA	Q4q754 leishmania	795	32	57.1	226	1	ASHPA_PASMU	O3l8j3 pasteurella
723	32.5	58.0	5276	2	Q7QJA9_ANOGA	Q7qja9 anopheles g	796	32	57.1	226	1	Q5U8S5_PASMU	Q5u8s5 pasteurella
724	32.5	58.0	409	1	KV3A_HUMAN	P01619 homo sapien	797	32	57.1	227	2	Q5TGS3_HUMAN	Q5tgs3 homo sapien
725	32.5	58.0	409	2	Q59500_PVRHO	Q59500 pyrococcus	798	32	57.1	234	2	Q41IS2_GIBZE	Q41is2 gibberella
726	32	57.1	75	2	Q23428_ARATH	Q23428 arabidopsis	799	32	57.1	235	2	Q6P2J1_HUMAN	O6p2j1 homo sapien
727	32	57.1	92	2	Q33108_MYCLE	Q33108 mycobacteri	800	32	57.1	236	2	Q6P1Q7_HUMAN	O6p1q7 homo sapien
728	32	57.1	93	2	Q68GN4_NOST	Q68gn4 anabaena ki	801	32	57.1	236	2	Q52L95_MOUSE	Q52l95 mus musculu
729	32	57.1	96	2	Q6NLX8_ARATH	Q6nlx8 arabidopsis	802	32	57.1	239	2	Q5WUM2_LEGFL	Q5wum2 legionella
730	32	57.1	96	2	Q4TJ02_TETNG	Q4tj02 tetradodon n	803	32	57.1	239	2	Q5X363_LEGPA	Q5x363 legionella
731	32	57.1	108	1	KV08_RABIT	P01689 oryctolagus	804	32	57.1	239	2	Q5ZTE1_LEGPH	Q5zte1 legione
732	32	57.1	108	1	KV1V_HUMAN	P04430 homo sapien	805	32	57.1	240	2	Q5RC99_PONPY	Q5rc99 pongo pygma
733	32	57.1	112	2	Q9QW44_MOUSE	Q9qwh4 mus musculu	806	32	57.1	243	2	Q6F6T6_ACIAD	O6f6t6 acinetobact
734	32	57.1	113	2	Q9QWH5_MOUSE	Q9qwh5 mus musculu	807	32	57.1	251	2	Q5LUD4_SILPO	O5lud4 silicibacte
735	32	57.1	113	2	Q9QWH6_MOUSE	Q9qwh6 mus musculu	808	32	57.1	258	2	Q4Q386_LEIMA	Q4q386 leishmania
736	32	57.1	113	2	Q9QWH7_MOUSE	Q9qwh7 mus musculu	809	32	57.1	260	2	Q7RFB1_PLAYO	Q7rfb1 plasmodium
737	32	57.1	113	2	Q9QWH8_MOUSE	Q9qwh8 mus musculu	810	32	57.1	261	2	Q41IL5_GIBZE	Q41il5 gibberella
738	32	57.1	113	2	Q921C2_MUASP	Q921c2 mus spretus	811	32	57.1	261	2	Q8A1S2_BACTN	Q8a1s2 bacteroides
739	32	57.1	121	2	Q5WJ97_BACSK	Q5wj97 bacillus cl	812	32	57.1	262	2	Q59S61_CANAL	Q59s61 candida alb
740	32	57.1	124	2	Q6PEA2_MOUSE	Q6pea2 mus musculu	813	32	57.1	263	2	Q77506_RABIT	Q77506 oryctolagus
741	32	57.1	124	2	Q6AVU5_XENLA	Q6avu5 xenopus lae	814	32	57.1	267	2	Q61IS2_CABER	Q61is2 caenorhabdi
742	32	57.1	124	2	Q6GQ35_XENLA	Q6gq35 xenopus lae	815	32	57.1	268	2	Q8EBE4_SHEON	Q8ebe4 shewanella
743	32	57.1	129	1	PROF4_HUMAN	Q8nh9r homo sapien	816	32	57.1	271	2	Q8ELA9_ARATH	Q8ela9 arabidopsis
744	32	57.1	129	2	Q53TL5_HUMAN	Q53tl5 homo sapien	817	32	57.1	271	2	Q8EDG4_SHEON	Q8edg4 shewanella
745	32	57.1	129	2	Q97PI5_STRFN	Q97pis streptococc	818	32	57.1	273	2	Q4NL08_9MICC	Q4nl08 arthrobacte
746	32	57.1	132	2	Q89TF9_BRAJA	Q89tf9 bradyrhizob	819	32	57.1	273	2	Q9QXU3_RAT	Q9qxu3 rattus norv
747	32	57.1	140	2	Q7RKJ9_PLAYO	Q7rkj9 plasmodium	820	32	57.1	274	2	Q6Y9R7_9TRYP	Q6y9r7 leishmania
748	32	57.1	144	2	Q4L6D8_STAHL	Q4l6d8 staphylococ	821	32	57.1	274	2	Q6Y9R8_LEIGU	Q6y9r8 leishmania
749	32	57.1	149	2	Q9W377_DROME	Q9w3t7 drosophila	822	32	57.1	274	2	Q6Y9R9_LEIBR	Q6y9r9 leishmania
750	32	57.1	152	2	Q31525_PSEAE	Q31525 pseudomonas	823	32	57.1	274	2	Q86L91_9TRYP	Q86l91 leishmania
751	32	57.1	153	1	PRN3_ADBE2	Q96623 bovine aden	824	32	57.1	281	2	Q4WGG4_ASPFU	Q4wgg4 aspergillus
752	32	57.1	154	2	Q720G5_LISMF	Q720g5 listeria mo	825	32	57.1	281	2	Q5LQH8_SILPO	O5lqhs silicibacte
753	32	57.1	154	2	Q7AP06_LISIN	Q7ap06 listeria in	826	32	57.1	283	1	EFTS_HAEDU	Q7l80 haemophilus
754	32	57.1	154	2	Q92CE7_LISMO	Q92ce7 listeria mo	827	32	57.1	284	2	Q6LP53_PHOPR	Q6lp53 photobacter
755	32	57.1	155	1	PLC_HALLA	P82596 halictis la	828	32	57.1	285	2	Q741B1_LACJO	Q741b1 lactobacill
756	32	57.1	155	2	Q9S328_PROMA	Q9s328 prochloroco	829	32	57.1	286	2	Q6W145_RHISN	Q6w145 rhizobium s
757	32	57.1	155	2	P72213_PROMA	P72213 prochloroco	830	32	57.1	287	2	Q57MD8_SALCH	Q57md8 salmonella
758	32	57.1	155	2	P78E57_MOUSE	P78e57 mus musculu	831	32	57.1	287	2	Q4HL90_CAMLA	Q4hl90 campylobact
759	32	57.1	157	1	X1070_METJA	Q8470 methanococc	832	32	57.1	287	2	Q5PE48_SALPA	Q5pe48 salmonella
760	32	57.1	159	2	Q9F555_ECOLI	Q9f555 escherichia	833	32	57.1	287	2	Q7N366_PHOLL	Q7n366 photorhabdu
761	32	57.1	162	1	PHCA2_FREDDI	P08040 fremyella d	834	32	57.1	287	2	Q8Z595_SALTI	Q8z595 salmonella

835	2	Q8ZKN6_SALTY	287	2	Q8ZKN6_salmonella	908	32	57.1	389	1	NEIL1_HUMAN	Q96fi4 homo sapien
836	2	Q6BWC1_DEBHA	288	2	Q6bwc1 debaryomyce	909	32	57.1	391	2	Q4HP14_CAMUP	Q4hp14 campylobact
837	2	Q7MB15_WOLSU	289	2	Q7mb15 wolinnella s	910	32	57.1	391	2	O25670_HELPU	O25670 helicobacte
838	2	Q93DC5_YEREN	290	2	Q93dc5 yersinia en	911	32	57.1	391	2	Q9ZM25_HELPU	Q9zm25 helicobacte
839	2	Q66CR3_YERPS	291	2	Q66cr3 yersinia ps	912	32	57.1	397	2	Q6XRC3_HUMAN	Q6xrc3 homo sapien
840	2	Q8ZG19_YERPE	292	2	Q8zg19 yersinia pe	913	32	57.1	401	2	Q84BS9_9BACT	Q84bs9 gram-negati
841	2	YEIE_ECOLI	293	1	YEIE_ECOLI	914	32	57.1	401	2	Q84BT3_9BACT	Q84bt3 gram-negati
842	2	Q9V4W8_DROME	294	2	Q9v4w8 drosophila	915	32	57.1	401	2	Q84BT4_9BACT	Q84bt4 gram-negati
843	2	Q83QW7_SHIFL	295	2	Q83qw7 shigella fl	916	32	57.1	401	2	Q84BS7_9PSED	Q84bs7 pseudomonas
844	2	Q5HQY9_STAEO	296	2	Q5hqy9 staphylococ	917	32	57.1	401	2	Q84BS8_9VIBR	Q84bs8 vibrio sp.
845	2	Q8NCP0_STAEP	297	2	Q8ncp0 staphylococ	918	32	57.1	401	2	Q84BT2_9GAMM	Q84bt2 photobacter
846	2	Q5NFP11_PRAAT	298	2	Q5nfp11 francisella	919	32	57.1	401	2	Q84BT5_9GAMM	Q84bt5 photobacter
847	2	Q6PC13_BRARE	302	2	Q6pc13 brachydanio	920	32	57.1	404	2	Q7SSFI1_NEUCR	Q7ssfi1 neurospora
848	2	Q6BS53_DEBHA	310	2	Q6bs53 debaryomyce	921	32	57.1	406	2	Q91920_XENLA	Q91920 xenopus lae
849	2	FMT_AGR15	311	1	FMT_AGR15	922	32	57.1	411	2	Q7VFN5_HELHP	Q7vfn5 helicobacte
850	2	Q6DN73_HUMAN	311	2	Q6dn73 homo sapien	923	32	57.1	412	2	Q6MM18_BDEBA	Q6mm18 bdellovibri
851	2	Q7NIZ1_GLOVI	311	2	Q7niz1 gloeobacter	924	32	57.1	413	2	Q4HZP5_GIBZE	Q4hzp5 gibberella
852	2	Q4WNK2_BACCE	312	2	Q4wnk2 bacillus ce	925	32	57.1	413	2	Q6ZNI1_HUMAN	Q6zni1 homo sapien
853	2	Q6HFF9_BACCH	312	2	Q6hff9 bacillus th	926	32	57.1	416	2	Q73G50_WOLPM	Q73g50 wolbachia p
854	2	Q81AD4_BACCR	312	2	Q81ad4 bacillus ce	927	32	57.1	417	2	Q4SSK9_TETNG	Q4ssk9 tetradion n
855	2	Q81Y53_BACAN	312	2	Q81y53 bacillus an	928	32	57.1	419	2	Q7MYT8_PHOLL	Q7myt8 photorhabd
856	2	Q63716_BACCZ	312	2	Q63716 bacillus ce	929	32	57.1	420	2	Q8H010_ORYSA	Q8h010 oryza sativ
857	2	Q6BVV9_DEBHA	317	2	Q6bv9 debaryomyce	930	32	57.1	420	2	Q5I3L9_ECOLI	Q5i3l9 escherichia
858	2	Q6BVV1_DEBHA	318	2	Q6bv1 debaryomyce	931	32	57.1	423	2	Q8F6T3_ACIAD	Q8f6t3 acinetobact
859	2	Q4XYB1_PLACH	320	2	Q4xyb1 plasmodium	932	32	57.1	427	2	Q650Y8_ORYSA	Q650y8 oryza sativ
860	2	Q6GLL8_XENLA	323	2	Q6gl18 xenopus lae	933	32	57.1	428	2	Q917A3_PSEAE	Q917a3 pseudomonas
861	2	Q4UWM6_XANCP	324	2	Q4uwm6 xanthomonas	934	32	57.1	429	2	Q4FVJ0_9GAMM	Q4fvj0 psychrobact
862	2	Q8P787_XANCP	324	2	Q8p787 xanthomonas	935	32	57.1	429	2	Q83D93_COXBU	Q83d93 coxiella bu
863	2	Q5V495_HALMA	325	2	Q5v495 haloarcula	936	32	57.1	431	2	Q5Z904_ORYSA	Q5z904 oryza sativ
864	2	MS12H_HUMAN	328	1	MS12H_HUMAN	937	32	57.1	434	1	SYS_RHILO	Q591c8 rhizobium l
865	2	Q6BS51_DEBHA	328	2	Q6bs51 debaryomyce	938	32	57.1	434	2	Q6DN72_HUMAN	Q6dn72 homo sapien
866	2	Q5F203_MOUSE	328	2	Q5f203 mus musculu	939	32	57.1	435	2	Q607H8_METCA	Q607h8 methylococc
867	2	Q18524_CAEEL	330	2	Q18524 caenorhabdi	940	32	57.1	436	2	Q4IKX7_GIBZE	Q4ikx7 gibberella
868	2	Q67PN2_SYWTH	330	2	Q67pn2 symbiobacte	941	32	57.1	437	2	Q7ZU71_BRARE	Q7zu71 brachydanio
869	2	Q58D99_BOVIN	332	2	Q58d99 bos taurus	942	32	57.1	438	2	Q6TGM3_BRARE	Q6tgm3 brachydanio
870	2	Q73H72_WOLPM	335	2	Q73h71 wolbachia p	943	32	57.1	439	2	Q70G45_RHOBA	Q70g45 rhodopirell
871	2	Q54407_9ACTO	337	2	Q54407 streptomyce	944	32	57.1	440	1	X1189_COXBU	Q39918 coxiella bu
872	2	Q87AN8_XYLFT	337	2	Q87an8 xyliella fas	945	32	57.1	440	2	Q6ALK0_HBLVI	Q6alk0 heliothis v
873	2	Q6MQ23_BDEBA	338	2	Q6mq23 bdellovibri	946	32	57.1	440	2	Q9U8D3_PLAFA	Q9u8d3 plasmodium
874	2	Q4TF85_TETNG	342	2	Q4tf85 tetradion n	947	32	57.1	440	2	Q4ZRL3_PSESY	Q4zrl3 pseudomonas
875	2	Q8GNP3_ECOLI	344	2	Q8gnp3 escherichia	948	32	57.1	440	2	Q74BH4_GROSL	Q74bh4 geobacter s
876	2	Q7FLN1_CHRVO	345	2	Q7fln1 chromobacte	949	32	57.1	440	2	Q87ZS7_PSESM	Q87zst7 pseudomonas
877	2	MS12H_MOUSE	346	1	MS12H_MOUSE	950	32	57.1	441	2	Q8K9V5_PSEFS	Q8k9v5 pseudomonas
878	2	Q5F202_MOUSE	346	2	Q5f202 mus musculu	951	32	57.1	441	2	Q88FT0_PSEPK	Q88ft0 pseudomonas
879	2	Q6B0H0_FUGRU	350	2	Q6boh0 fuqu rubrip	952	32	57.1	442	2	Q8IDF6_PLAPF7	Q8idf6 plasmodium
880	2	Q90YJ8_BRARE	354	2	Q90yj8 brachydanio	953	32	57.1	446	2	Q6LT01_PHOPR	Q6lt01 photobacter
881	2	Q90YL8_BRARE	354	2	Q90yl8 brachydanio	954	32	57.1	446	2	Q7VLV3_HAEDU	Q7vlv3 haemophilus
882	2	WNT8C_CHICK	357	1	WNT8C_CHICK	955	32	57.1	446	2	Q5R0A8_IDILO	Q5r0a8 idiomarina
883	2	Q564K5_CHICK	357	2	Q564k5 gallus gall	956	32	57.1	448	2	Q5E6B4_VIBF1	Q5e6e4 vibrio fibc
884	2	Q7UNT9_RHOBA	360	2	Q7unt9 rhodopirell	957	32	57.1	449	2	Q6MPI4_BDEBA	Q6mpi4 bdellovibri
885	2	Q8ZT98_PYRAE	363	2	Q8zt98 pyrobaculum	958	32	57.1	451	2	Q8KED2_CHLTE	Q8ked2 chlorobium
886	2	Q5ZKP3_CHICK	363	2	Q5zkp3 gallus gall	959	32	57.1	452	2	Q83050_9CLOS	Q83050 lettuce inf
887	2	Q4P019_USTMA	364	2	Q4p019 ustilago ma	960	32	57.1	452	2	Q91ZQ9_9CLOS	Q91zq9 lettuce inf
888	2	Q5RHMO_BRARE	364	2	Q5rhm0 brachydanio	961	32	57.1	452	2	Q91ZR5_9CLOS	Q91zr5 lettuce inf
889	2	Q9PEX8_XYLFA	365	2	Q9pex8 xyliella fas	962	32	57.1	455	2	Q5SME1_CRYNE	Q5sme1 cryptococcu
890	2	Q7MRK7_WOLSU	365	2	Q7mrk7 wolinnella s	963	32	57.1	455	2	Q5K8D1_CRYNE	Q5k8d1 cryptococcu
891	2	MT52_METJA	366	1	MT52_METJA	964	32	57.1	456	2	Q5M6S3_CAMJE	Q5m6s3 campylobact
892	2	Q7W3L5_BORPA	368	2	Q7w3l5 bordetella	965	32	57.1	457	2	Q803Y6_BRARE	Q803y6 brachydanio
893	2	Q7WEZ0_BORBR	368	2	Q7wez0 bordetella	966	32	57.1	460	2	Q8X739_ECO57	Q8x739 escherichia
894	2	Q8Y009_RALSO	369	2	Q8y009 ralysonia s	967	32	57.1	464	2	Q41ZB2_AZOVI	Q41zb2 azotobacter
895	2	Q6ASZ6_ORYSA	371	2	Q6asz6 oryza sativ	968	32	57.1	465	2	Q531A7_STRGR	Q531a7 streptomyce
896	2	Q7FSI1_9TRAC	371	2	Q7fsi1 isoetes his	969	32	57.1	467	2	Q6CGT9_YARLI	Q6cgt9 yarrowia li
897	2	Q621T2_CAEER	379	2	Q621t2 caenorhabdi	970	32	57.1	478	2	Q7MLL5_VIBVY	Q7ml15 vibrio vuln
898	2	Q6W1P4_RHLSN	380	2	Q6w1p4 rhizobium s	971	32	57.1	478	2	Q7M6B9_ADEB2	Q7m6e9 bovine aden
899	2	Q8DBV8_VIBVU	381	2	Q8dbv8 vibrio vuln	972	32	57.1	484	2	Q93TP9_YERPS	Q93tp9 yersinia ps
900	2	Q9KRH8_VIBCH	382	2	Q9krh8 vibrio chol	973	32	57.1	484	2	Q9ZIN8_PECOC	Q9zin8 pectobacter
901	2	Q5FLU0_LACAC	387	2	Q5flu0 lactobacill	974	32	57.1	484	2	Q93TP8_YERPE	Q93tp8 yersinia pe
902	2	Q4KLMO_RAT	387	2	Q4klm0 rattus norv	975	32	57.1	484	2	Q6D4B5_BRWCT	Q6d4e5 erwina car
903	2	NEIL1_MOUSE	388	1	NEIL1_MOUSE	976	32	57.1	484	2	Q7BFC7_YERPS	Q7bfc7 yersinia ps
904	2	Q9HG17_GANLU	388	2	Q9hg17 ganoderma l	977	32	57.1	486	1	PHOQ_ECOLI	P23837 escherichia
905	2	Q61H09_DROME	388	2	Q61h09 drosophila	978	32	57.1	486	2	Q6FTB9_CANGA	Q6ftb9 candida gla
906	2	Q4R0K4_STRCX	388	2	Q4r0k4 streptomyce	979	32	57.1	486	2	Q7AF16_ECO57	Q7af16 escherichia
907	2	Q74HZ7_LACJO	388	2	Q74hz7 lactobacill	980	32	57.1	486	2	Q8F1B8_ECOL6	Q8fib8 escherichia


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981 32 57.1 486 2 Q6D6Y2 ERWCT
982 32 57.1 486 2 Q83RR1_SHIFL
983 32 57.1 487 1 PHOQ_SALCH
984 32 57.1 487 1 PHOQ_SALPA
985 32 57.1 487 1 PHOQ_SALTI
986 32 57.1 487 1 PHOQ_SALTY
987 32 57.1 487 1 PHOQ_SALTY
988 32 57.1 490 2 Q6JUL9_SHIVL
989 32 57.1 491 2 Q8GC78_ERWCH
990 32 57.1 496 2 Q66ACL_YERPS
991 32 57.1 497 2 Q8CON0_MOUSE
992 32 57.1 502 2 Q8D0H8_YERPE
993 32 57.1 506 2 Q9HI92_THEAC
994 32 57.1 511 2 Q7N241_PHOLL
995 32 57.1 511 2 Q7RJ56_PLAYO
996 32 57.1 512 1 AGT2_RAT
997 32 57.1 512 2 Q642F1_RAT
998 32 57.1 513 2 Q6B384_9PROT
999 32 57.1 514 2 Q8FED9_ECOL6
1000 32 57.1 514 2 Q666K3_YERPS

Q6D6Y2 erwinia car
Q83rr1 shigella fl
Q57qc4 salmonella
Q8pmj0 salmonella
Q8z7h3 salmonella
P14147 salmonella
Q7n3b1 photorhabdu
Q6jul9 human immun
Q8gc78 erwinia chr
Q86acl yersinia ps
Q8con0 mus musculu
Q8d0h8 yersinia pe
Q9hi92 thermoplas
Q7n241 photorhabdu
Q7rj56 plasmodium
Q64565 r alanine--
Q642f1 rattus norv
Q6b384 uncultured
Q8fed9 escherichia
Q666k3 yersinia ps

ALIGNMENTS

RESULT 1
KV5K_MOUSE
ID _KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC PIR: A01927; KVMKAR.
DR HSP; P01594; 1JVS.
DR SMR; P01644; 1JVS.
DR Ensembl; ENSMUSG00000029991; Mus musculus.
DR InterPro; IPR007110; IG-Like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 80.4%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 3
KV5M_MOUSE
ID _KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC -----
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CC removed.
CC -----
CC PDB; 1A14; X-ray; L=5-102.
DR SMR; P01645; 1-108.
DR Ensembl; ENSMUSG00000029991; Mus musculus.
DR InterPro; IPR007110; IG-Like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 80.4%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 3
KV5M_MOUSE

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ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-V region HP 123B6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC
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CC
CC SMR; 1E2V; X-ray; Y=5-107.
DR PDB; P01647; 1-108.
DR Ensembl; ENSMUSG0000029991; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653E9FA2 CRC64;

Query Match 80.4%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.81; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 24 RASQDIGNYL 33

RESULT 5
KV5O_MOUSE STANDARD; PRT; 108 AA.
ID KV5O_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC HSSP; P01594; 1JVS.
DR Ensembl; ENSMUSG0000029991; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 80.4%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 24 RASQDIGNYL 33

RESULT 4
KV5N_MOUSE STANDARD; PRT; 108 AA.
ID KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;

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DR SMR; P01648; 1-108.
DR Ensembl; ENSMUSG00000029991; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;

Query Match 80.4%; Score 45; DB 1; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNVL 33

RESULT 6
Q723Y4 HUMAN
ID Q723Y4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Skeletal Muscle;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci E., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
KW SEQUENCE 236 AA; 25702 MW; 7BFBFE4ED23084BC6 CRC64;

Query Match 80.4%; Score 45; DB 2; Length 236;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 46 RASQDISNYL 55

RESULT 7
Q6FMX7 CANGA
ID Q6FMX7_CANGA PRELIMINARY; PRT; 283 AA.
AC Q6FMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P53237 Saccharomyces cerevisiae YGR057c.
GN OrderedLocuNames=CAGLOK0411g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Fairhead C., Confanioli F., de Daruvar A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR380957; CAG61378.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 283 AA; 31675 MW; 030B1059FF287CBF CRC64;

Query Match 78.6%; Score 44; DB 2; Length 283;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SQDIGNYL 11
Db 220 TQDIGNYL 228

RESULT 8
Q7D6F1 MYCTU
ID Q7D6F1 MYCTU PRELIMINARY; PRT; 2188 AA.
AC Q7D6F1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

DE Polyketide synthase.
GN OrderedLocusNames=MT3003;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_taxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAINS=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
EX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
DR EMBL: AE000516; AAK47330.1; -; Genomic_DNA.
DR SMR: Q7D6F1; 1571-1753.
DR TIGR: MT3003; -;
DR GO: GO:0048037; F: cofactor binding; IEA.
DR GO: GO:0016491; F: oxidoreductase activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0008270; F: zinc ion binding; IEA.
DR GO: GO:0006633; F: fatty acid biosynthesis; IEA.
DR GO: GO:0008152; F: metabolism; IEA.
DR InterPro: IPR001227; Ac transferase.
DR InterPro: IPR002198; ADH short.
DR InterPro: IPR002085; Adh zn family.
DR InterPro: IPR006163; Phosphateth_bind.
DR InterPro: IPR006162; Ppantne S.
DR Pfam: PF00698; Acyl_transf_1.
DR Pfam: PF00107; adh_short; 1.
DR Pfam: PF00109; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt_C; 1.
DR Pfam: PF00550; PP-binding; 1.
DR PROSITE: PS00075; ACP DOMAIN; 1.
DR PROSITE: PS00506; B_KETOACYL SYNTHASE; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; UNKNOWN 1.
SQ SEQUENCE 2188 AA; 230688 MW; 0CE650201E88ED1F CRC64;
Query Match 75.0%; Score 42; DB 2; Length 2188;
Best Local Similarity 72.7%; Pred. NO. 82;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 11
Db 854 RASVDVDNYLR 864
RESULT 9
Q6LBV5_HUMAN
ID Q6LBV5_HUMAN PRELIMINARY; PRT; 50 AA.
AC Q6LBV5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE DNA rearranged by a t(2;8) translocation leading to Burkitt's lymphoma
in the cell line JI (clone JIP) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87259967; PubMed=3110741;

RA Klobeck H.G., Combriato G., Zachau H.G.;
RT "N segment insertion and region directed somatic hypermutation in a
kappa gene of a t(2;8) chromosomal translocation.";
RL Nucleic Acids Res. 15:4877-4888 (1987).
DR EMBL: X05929; C8E82012.1; -; Genomic_DNA.
DR HSSP: P01607; IAR2.
DR SMR: Q6LBV5; 4-50.
DR NON_TER 1
FT NON_TER 50
SQ SEQUENCE 50 AA; 5486 MW; 3A74178720E0DA21 CRC64;
Query Match 73.2%; Score 41; DB 2; Length 50;
Best Local Similarity 80.0%; Pred. NO. 2.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db 27 QASQDISNYL 36
RESULT 10
TNF11_MOUSE
ID TNF11_MOUSE STANDARD; PRT; 316 AA.
AC O35235; O35306; Q9JJK8; Q9JJK9; Q9RIY0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
superfamily member 11, membrane form; Tumor necrosis factor ligand
superfamily member 11, soluble form].
GN Name=Tnfsf11; Synonyms=Oppl, Rankl, Trance;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Hydridoma;
RX MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlicki J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE" is a novel ligand of the tumor necrosis factor receptor family
that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Thymic lymphoma;
RX MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
RL Nature 390:175-179 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Bone marrow;
RX MEDLINE=98227663; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparello C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation.";
RL Cell 93:165-176 (1998).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RC TISSUE=Bone marrow stroma;
RX MEDLINE=9818248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tada E.,
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT to TRANCE/RANKL.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC STRAIN=129;
RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor.";
RL Gene 230:121-127(1999).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21150053; PubMed=11250921; DOI=10.1074/jbc.274.19.13613;
RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT Determination of three isoforms of the receptor activator of nuclear
RT factor-kappaB ligand and their differential expression in bone and
RT thymus.";
RL Endocrinology 142:1419-1426(2001).
RN [7]
RP PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX MEDLINE=99240759; PubMed=10241392; DOI=10.1074/jbc.274.19.13613;
RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA Schoendorff J., Tempst P., Choi Y., Blobel C.P.;
RT Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT converting enzyme-like protease in shedding of TRANCE, a TNF family
RT member involved in osteoclastogenesis and dendritic cell survival.";
RL J. Biol. Chem. 274:13613-13618(1999).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX MEDLINE=21464816; PubMed=11581298;
RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT of receptor-ligand specificity.";
RL J. Clin. Invest. 108:971-979(2001).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT Crystal structure of the extracellular domain of mouse RANK ligand at
RT 2.2-A resolution.";
RL J. Biol. Chem. 277:16631-16636(2002).
RN [10]
RP FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
RN TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcemia of malignancy.
CC [11]
RP SUBUNIT: Homotrimer.
CC [12]
RP SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC [13]
RP ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O35235-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O35235-2; Sequence=VSP_006449;
CC Name=3;
CC IsoId=O35235-3; Sequence=VSP_006448;
CC [14]
RP TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC but not in nonlymphoid tissues and is abundantly expressed in T
CC cells but not in B cells. A high level expression is also seen in
CC the trabecular bone and lung.
CC [15]
RP PTM: N-glycosylated.

CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing. The cleavage may be catalyzed by
CC ADAM17. A further shorter soluble form was observed.
CC -1- DISEASE: Deficiency in Tnfrsf11 results in failure to form lobulo-
CC alveolar mammary structures during pregnancy, resulting in death
CC of newborns. France-deficient mice show severe osteopetrosis, with
CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC profound growth retardation at several skeletal sites, including
CC the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC with thick, irregular growth plates and a relative increase in
CC hypertrophic chondrocytes.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF013170; AAC71061.1; -; mRNA.
CC EMBL; AF019048; AAB86812.1; -; mRNA.
CC EMBL; AF053713; AAC40113.1; -; mRNA.
CC EMBL; AB008426; BAA25425.1; -; mRNA.
CC EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
CC EMBL; AB032771; BAA97257.1; -; mRNA.
CC EMBL; AB032772; BAA97258.1; -; mRNA.
CC EMBL; AB036798; BAA97259.1; -; mRNA.
CC PDB; 1IQ2; X-ray; A/B/C=157-316.
CC PDB; 1JTG; X-ray; X/Y/Z=156-316.
CC Ensembl; ENSMUSG0000022015; Mus musculus.
CC MGI; MGI:1100089; Tnfrsf11.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:000515; F:protein binding; IPI.
CC GO; GO:0045453; P:bone resorption; IDA.
CC GO; GO:0007515; P:lymph gland development; TAS.
CC GO; GO:0009887; P:organogenesis; IMP.
CC GO; GO:0001503; P:ossification; IMP.
CC GO; GO:0045672; P:positive regulation of osteoclast different. .; IDA.
CC GO; GO:0051260; P:protein homooligomerization; IDA.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; FALSE_NEG.
CC PROSITE; PS00049; TNF_2; 1.
CC 3D-structure; Alternative splicing; Cytokine; Developmental protein;
CC Differential; Direct protein sequencing; Glycoprotein; Receptor;
CC Signal-anchor; Transmembrane.
CHAIN 1 316 Tumor necrosis factor ligand superfamily
member 11, membrane form.
CHAIN 139 316 Tumor necrosis factor ligand superfamily
member 11, soluble form.
TOPO_DOM 1 48 Cytoplasmic (Potential).
TRANSMEM 49 69 Signal-anchor for type II membrane
protein (Potential).
TOPO_DOM 70 316 Extracellular (Potential).
SITE 138 139 Cleavage.
CARBOHYD 197 197 N-linked (GlcNAc. .) (Potential).
CARBOHYD 262 262 N-linked (GlcNAc. .) (Potential).
VARSPPLIC 1 117 Missing (in isoform 3).
FTID=VSP_006448.
FTID=VSP_006449.
FTID=VSP_006449.
G -> D (in Ref. 2).
Missing (in Ref. 5).
CONFLICT 99 99
CONFLICT 141 143
STRAND 164 169
TURN 171 172
TURN 181 182
STRAND 186 187
TURN 191 192
STRAND 194 196

```
FT STRAND 198 201
FT TURN 202 203
FT STRAND 204 207

Query Match 73.2%; Score 41; DB 1; Length 316;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11
Db 3 RASRDYGVKYL 13

RESULT 11
Q75115 ASHGO
ID Q75115 ASHGO PRELIMINARY; PRT; 451 AA.
AC Q75115
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGL279Cp.
GN Name=AGL279C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=331169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed:15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
DR EMBL; AB016820; AAS54212.1; -; Genomic_DNA.
DR AGD; AGL279C; -.
DR GO; GO:0043087; P:regulation of GTPase activity; IEA.
DR InterPro; IPR001164; ArfGAP.
DR Pfam; PF01412; ArfGAP; 1.
DR PRINTS; PR00405; REVINTACTING.
DR SMART; SM00105; ArfGAP; 1.
DR PROSITE; PS0115; ARFGAP; 1.
KW Complete proteome.
SQ SEQUENCE 451 AA; 49372 MW; A9E21ECD34BD5FE9 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 451;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11
Db 436 RASQKIGNYL 446

RESULT 12
KVLY HUMAN
ID KVLY HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
```

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RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP PROTEIN SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT CONFLICT 30 31 TN -> SD (in Ref. 2).
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 8.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 24 RASQDITNYV 33

RESULT 13
KV5J_MOUSE
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ID KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76091934; PubMed=812696;
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
  immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01926; KWS73.
DR HSSP; P01594; LJV5.
DR Ensembl; ENSMUSG0000058965; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 10
Db ||| |||||
25 ASQSIGNYL 33

RESULT 14
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
```

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RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K00745; AAA38690.1; -; mRNA.
DR HSSP; P01594; LJV5.
DR SMR; P04946; 1-107.
DR Ensembl; ENSMUSG0000029991; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11870 MW; DB2C885920DC6DDD CRC64;

Query Match 71.4%; Score 40; DB 1; Length 108;
Best Local Similarity 88.9%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 10
Db ||| |||||
25 ASQDISNYL 33

RESULT 15
QSEFE6_HUMAN PRELIMINARY; PRT; 234 AA.
AC QSEFE6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 kappa light chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Belliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
  antibody T125.".
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW82027.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
```

FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light chain.
 SQ SEQUENCE 234 AA; 25698 MW; 866DCD1E4FD7D5EA CRC64;
 Query Match 71.4%; Score 40; DB 2; Length 234;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 44 RASQDIRNV 53

RESULT 16
 Q72473 HUMAN
 ID Q72473 HUMAN PRELIMINARY; PRT; 234 AA.
 AC Q72473;
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC056256; AAH56256.1; -; mRNA.
 DR HSSP; P01834; 1HEZ.
 DR SMR; Q72473; 22-234.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 71.4%; Score 40; DB 2; Length 234;
 Best Local Similarity 80.0%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 44 RASQSIGSVL 53

RESULT 17
 Q6GMXO HUMAN
 ID Q6GMXO HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q6GMXO;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC073775; AAH73775.1; -; mRNA.
 DR SMR; Q6GMXO; 23-236.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 71.4%; Score 40; DB 2; Length 236;
 Best Local Similarity 80.0%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 DB 46 RASQINNYL 55

```
RESULT 18
Q4ZD65_9VIRU
ID Q4ZD65_9VIRU PRELIMINARY; PRT; 2008 AA.
AC Q4ZD65;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ORF001.
OS Bacteriophage 2638A.
OC Viruses.
OX NCBI_TaxID=320836;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 Staphylococcus aureus
bacteriophages.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179 (2005).
DR EMBL; AY954954; AAX30989.1; -, Genomic DNA.
SQ SEQUENCE 2008 AA; 220152 MW; CD0C4E691227F005 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 2008;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 11
| | | | |
Db 966 AFQDLGNLYK 975

RESULT 19
Q7RQ61_PLAYO
ID Q7RQ61_PLAYO PRELIMINARY; PRT; 2033 AA.
AC Q7RQ61;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase family 2, putative.
GN Name=PY01242;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=17XNL;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.P., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABJ01000326; EAA20533.1; -, Genomic DNA.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thioesterase activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS50235; UCH_2_3; 1.
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KW Hydrolase.
SQ SEQUENCE 2033 AA; 240632 MW; B89BABC33AA07FDB CRC64;

Query Match 71.4%; Score 40; DB 2; Length 2033;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
| | | | |
Db 1568 QASEHIGNYIR 1578

RESULT 20
Q9UL81_HUMAN
ID Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; AAD56269.1; -, mRNA.
DR HSSP; P01607; 1BWV.
DR SMR; Q9UL81; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | |
Db 24 RASQISINYL 33

RESULT 21
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-1 region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light type from two human
```


RT lymphoid cell lines are closely related.";
 RL Nucleic Acids Res. 12:6995-7006(1984).

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.

DR PIR; A01883; K1HWK.

DR HSP; P01607; 1BWK.

DR SMR; P04431; 23-129.

DR Ensembl; ENSG00000163245; Homo sapiens.

DR GO; GO:000576; C:extracellular region; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 22

FT CHAIN 23 129 Ig kappa chain V-I region Walker.

FT REGION 23 45 Framework-1.

FT REGION 46 56 Complementarity-determining-1.

FT REGION 57 71 Framework-2.

FT REGION 72 78 Complementarity-determining-2.

FT REGION 79 110 Framework-3.

FT REGION 111 119 Complementarity-determining-3.

FT REGION 120 129 Framework-4.

FT DISULFID 45 110 By similarity.

FT NON TER 129 129

SQ SEQUENCE 129 AA; 14069 MW; F941FA07DA4FC2F9 CRC64;

Query Match

Best Local Similarity 69.6%; Score 39; DB 1; Length 129;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10

DB 46 RASQISNYL 55

RESULT 22

Q7N5S4 PHOLL

ID Q7N5S4_PHOLL PRELIMINARY; PRT; 443 AA.

AC Q7N5S4; 01-MAR-2004 (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Similar to nitrilotriacetate monoxygenase component A.

GN OrderedLocustNames=plu1866;

OS Photorhabdus luminescens (subsp. laumondii).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Photorhabdus.

OX NCBI_TaxID=141679;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RT01;

RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbr886;

RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,

RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-P.,

RA Dasse E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,

RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,

RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;

RT "The genome sequence of the entomopathogenic bacterium Photorhabdus

luminescens."

RL Nat. Biotechnol. 21:1307-1313(2003).

DR EMBL; BX571865; CAE14159.1; -; Genomic_DNA.

DR Photolist; plu1866; -.

DR GO; GO:0004497; F:monoxygenase activity; IEA.

DR InterPro; IPR011251; Luciferase_like.

KW Complete proteome; Monoxygenase.

SQ SEQUENCE 443 AA; 49686 MW; 3D62F53C73020D72 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 443;

Best Local Similarity 70.0%; Pred. No. 60;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10

DB 33 QAAQDIGHYL 42

RESULT 23

Q4INP3 GIBZE

ID Q4INP3_GIBZE PRELIMINARY; PRT; 937 AA.

AC Q4INP3;

DT 13-SEP-2005 (TRENBLrel. 31, Created)

DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=FG01165.1;

OS Gibberella zeae PH-1.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

OX NCBI_TaxID=229533;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PH-1;

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,

RA Boukhgaltier B., Butler J., Calvo S.E., Camarata J., Chang J.,

RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,

RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,

RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,

RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,

RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,

RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,

RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,

RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,

RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Lander E.;

RT "Fusarium graminearum genome sequence."

RL Submitted (FSB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AACM0100058; EAA68631.1; -; Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 937 AA; 102714 MW; A519055366ED2FE1 CRC64;

Query Match

Best Local Similarity 63.6%; Score 39; DB 2; Length 937;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11

DB 528 RRSEDIGSYFR 538

RESULT 24

Q5F0M1 9CYAN

ID Q5F0M1_9CYAN PRELIMINARY; PRT; 94 AA.

AC Q5F0M1;

DT 10-MAY-2005 (TRENBLrel. 30, Created)


```

10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Phycocyanin alpha subunit (Fragment).
GN Name=cpcA;
OS Lyngbya kuetzingiana PACC 5419.
OC Bacteria; Cyanobacteria; Oscillatoriales; Lyngbya.
OX NCBI_TaxID=264743;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PACC 5419;
RA Teneva I., Dzhanbazov B., Mladenov R., Schirmer K.;
RT "Molecular and phylogenetic characterization of Phormidium species
  (Cyanoprokaryota) using the cpcB-IGS-cpcA locus.";
RL J. Phycol. 41:188-194(2005).
DR EMBL; AY466121; AAS46997.1; -; Genomic_DNA.
DR SMR; Q5F0M1; 1-93.
DR GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR GO; GO:0030089; C:phycobilisome; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR001659; Phycobilisome.
DR InterPro; IPR012128; Phycocyanin.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Electron transport; Photosynthesis; Phycobilisome.
FT NON TER 94
SQ SEQUENCE 94 AA; 10175 MW; 186F82FB2C101A42 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 94;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
: : ||||| |||
Db 83 KCAQDIGYLR 93

RESULT 25
QSMOT4 STRT1 PRELIMINARY; PRT; 95 AA.
AC QSMOT4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=stc0571;
OS Streptococcus thermophilus (strain CNRZ 1066).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidis A., Goltzman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masny D., Hancy F., Burteau S., Boutry M., Delcour J.,
RA Goffeau A., Holts P.;
RT "Complete sequence and comparative genome analysis of the dairy
  bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV62167.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 95 AA; 11233 MW; 80A93518872584F0 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 95;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SODIGNYL 11
: : ||||| |||
Db 59 SNDIGNFLR 67

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RESULT 26
Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
  (Fragment).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
  Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
  Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
  Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
  associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
DR EMBL; AF035044; AAD56280.1; -; mRNA.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBBW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
: : ||||| |||
Db 24 RASQGISNYL 33

RESULT 27
Q5HTQ0_CAMJR PRELIMINARY; PRT; 236 AA.
AC Q5HTQ0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Conserved domain protein.
GN OrderedLocusNames=CJE1348;
OS Bacteriophage jejuni (strain RM1221).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=195099;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15660156; DOI=10.1371/journal.pbio.0030015;
  Fouts D.E., Mongodin B.F., Mandrell R.E., Miller W.G., Rasko D.A.,
  Ravel J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
  Dodson R.J., Durkin A.S., Madupu R., Sullivan S.A., Shetty J.U.,
  Ayodeji M.A., Shvartsbeyn A., Schatz M.C., Badger J.H., Fraser C.M.,
  Nelson K.E.;

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RT "Major structural differences and novel potential virulence mechanisms
 from the genomes of multiple Campylobacter species.";

RL PLOS Biol. 3:72-85(2005).
 DR EMBL; CP000025; AAW35668.1; -; Genomic_DNA.
 DR TIGR; CJE1348; -;
 KW Complete proteome.
 SQ SEQUENCE 236 AA; 26695 MW; A218E75F0E1EBF60 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 236;
 Best Local Similarity 77.8%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDIGNYLRL 11
 ||:|||||
 Db 216 SQEIGNYLR 224

RESULT 28

ID Q9PNB1_CAMJTE PRELIMINARY; PRT; 241 AA.
 AC Q9PNB1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein Cj1214c.
 OS OrderedLocustNames=Cj1214.3;
 GN Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCTC 11168;
 RX MEDLINE=2015012; PubMed=10688204; DOI=10.1038/35001088;
 RA Parkhill J., Wren B.W., Mungall K.L., Kelsey J.M., Churcher C.W.,
 RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtwell S.,
 RA Jais K., Kariyeh A.V., Moutre S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream A.V., Moule S., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrall B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL; AL139077; CAB73468.1; -; Genomic_DNA.
 DR PIR; H81327; H81327.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 241 AA; 27308 MW; CCBBC0CC19716C6B CRC64;

Query Match 67.9%; Score 38; DB 2; Length 241;
 Best Local Similarity 77.8%; Pred. No. 50;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQDIGNYLRL 11
 ||:|||||
 Db 221 SQEIGNYLR 229

RESULT 29

ID TNF11_RAT STANDARD; PRT; 318 AA.
 AC Q9ESE2; Q9IZ19;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 induced cytokine) (TNF) (Osteoprotegerin ligand) (OPGL) (Osteoclast
 differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
 superfamily member 11, membrane form; Tumor necrosis factor ligand
 superfamily member 11, soluble form].
 DE Name=TNFsf11; Synonyms=Oppl, Rankl, Trance;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Tibial bone;
 RX MEDLINE=20540945; PubMed=11092398;
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
 RA Zheng M.H.;
 RT "Cloning, sequence and functional characterization of the rat
 homologue of receptor activator of NF-kB ligand.";
 RL J. Bone Miner. Res. 15:2178-2186(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 266-318.
 RC STRAIN=Fischer 344;
 RX MEDLINE=21662371; PubMed=11804028;
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,
 RA Safadi P.P., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
 RA Marks S.C. Jr.;
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
 the TNFSF11 (TNF, RANKL, ODF, OPGL) gene.";
 RL Int. J. Dev. Biol. 45:853-859(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFSF11B/OPG and to
 TNFSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AF187319; AAG17031.1; -; mRNA.
 CC EMBL; AF425669; AAL23963.1; -; mRNA.
 DR HSSP; O35235; 1JTZ.
 DR SMR; Q9ESE2; 163-318.
 DR Ensembl; ENSRNOG00000009559; Rattus norvegicus.
 DR RGD; 620784; Tnfsl1.
 DR GO; GO:0045780; P:positive regulation of bone resorption; IMP.
 DR GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; FALSE_NEG.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Developmental protein; Differentiation; Glycoprotein;
 KW Receptor; Signal-anchor; Transmembrane.
 FT CHAIN 1 318
 FT Tumor necrosis factor ligand superfamily
 FT member 11, membrane form.
 FT Tumor necrosis factor ligand superfamily
 FT member 11, soluble form.
 FT Cytoplasmic (Potential).
 FT Signal-anchor for type II membrane
 FT protein (Potential).
 FT Extracellular (Potential).
 FT Cleavage (By similarity).
 FT SITE 140 141
 FT CARBOHYD 199 199
 FT CARBOHYD 264 264
 FT CONFLICT 317 317
 FT SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

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Query Match      67.9%; Score 38; DB 1; Length 318;
Best Local Similarity 63.6%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
   ||:| | |||
Db 3 RANRDYGYLR 13

RESULT 30
Q75D24 ASHGO PRELIMINARY; PRT; 348 AA.
AC Q75D24
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ABR198Cp.
GN Name=ABR198C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RA "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
DR EMBL; AB016815; AAS50971.1; -; Genomic_DNA.
DR AGD; ABR198C; -.
DR GO; GO:0008198; F:ferrous iron binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004183; XdioL_doise_3B.
DR Pfam; PF02900; LigB; 1.
KW Complete proteome.
SQ SEQUENCE 348 AA; 38616 MW; 7B18C472E272737B8 CRC64;

Query Match      67.9%; Score 38; DB 2; Length 348;
Best Local Similarity 54.5%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
   ||:| | |||
Db 56 RATQNLGYLR 66

RESULT 31
Q9BLX6 CIOIN PRELIMINARY; PRT; 409 AA.
AC Q9BLX6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Intermediate filament protein IF-P.
GN Name=if-f;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=whole animal.
RX MEDLINE=22061815; PubMed=12067066;
RA Wang J., Karabinos A., Zimek A., Meyer M., Riemer D., Hudson C.,
RA Lemaire P., Weber K.;
RA "Cytoplasmic intermediate filament protein expression in tunicate

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RT development; a specific marker for the test cells.";
RL Eur. J. Cell Biol. 81:302-311(2002).
DR EMBL; AJ298333; CAC24554.1; -; mRNA.
DR HSPSP; P03069; I1J2.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PRO1248; TYPB1KERATIN.
SQ SEQUENCE 409 AA; 47142 MW; 9958F3F73844AF2E CRC64;

Query Match      67.9%; Score 38; DB 2; Length 409;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 11
   ||||| | |
Db 311 AKQDIGNKYL 320

RESULT 32
Q6TH77 9APHY PRELIMINARY; PRT; 524 AA.
AC Q6TH77
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laccase [EC 1.10.3.2].
GN Name=lac3;
OS Trametes sp. C30.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=191221;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C30;
RA Klonowska A., Gaudin C., Asso M., Pournel A., Reglier M., Tron T.;
RT "LAC3, a new low redox potential laccase from Trametes sp. strain C30
RT obtained as a recombinant protein in yeast.";
RL Enzyme Microb. Technol. 36:34-41(2005).
DR EMBL; AY397783; AAR00925.1; -; mRNA.
DR HSPSP; Q9Y780; IA65.
DR SMK; Q6TH77; 24-515.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0008471; F:laccase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR01117; Cu-oxidase.
DR InterPro; IPR011706; Cu-oxidase_2.
DR InterPro; IPR011707; Cu-oxidase_3.
DR InterPro; IPR002355; Cu_ox_copper_BS.
DR InterPro; IPR002345; Lipocalin.
DR Pfam; PF00394; Cu-oxidase; 1.
DR Pfam; PF07731; Cu-oxidase_2; 1.
DR Pfam; PF07732; Cu-oxidase_3; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Copper; Metal-binding; Oxidoreductase; Repeat.
SQ SEQUENCE 524 AA; 56280 MW; 29B79B8921FEE39B CRC64;

Query Match      67.9%; Score 38; DB 2; Length 524;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQDIGNY 9
   ||||| |
Db 274 ADQDIGNY 281

RESULT 33
Q70KQ6 CIOIN PRELIMINARY; PRT; 733 AA.
ID Q70KQ6_CIOIN

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AC Q70K06;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Intermediate filament IF-Fb.
 GN Name=if-f;
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Clonidae; Ciona.
 OX NCBI_TaxID=7719;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole animal;
 RX PubMed=14729270; DOI=10.1016/j.gene.2003.10.019;
 RA Karabinos A., Zimek A., Weber K.;
 RT "The genome of the early chordate Ciona intestinalis encodes only five
 RT cytoplasmic intermediate filament (IF) proteins including a single
 RT type I and type II keratin and a unique IF-annexin fusion protein.";
 RL Gene 326:123-129 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole animal;
 RA Wang J.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ575294; CAB01321.1; -; mRNA.
 DR HSP; P17153; IALA.
 DR Ensembl; ENSCING0000006934; Ciona intestinalis.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR001464; Annexin.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR002957; Keratin_I.
 DR Pfam; PF00191; Annexin; 4.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR00196; ANNEXIN.
 DR PRINTS; PR01248; TYPEKERATIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 3.
 DR PROSITE; PS00223; ANNEXIN; 2.
 SQ SEQUENCE 733 AA; 84169 MW; 670836B6AB82B9E9 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 733;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQDIGNYL 11
 Db 311 AKQDIGRYLK 320

RESULT 34
 Q818Y2 ANOQA PRELIMINARY; PRT; 1009 AA.
 AC Q818Y2;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Laccase 1 (EC 1.10.3.2).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jiang H., Kanost M.R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AY135184; AAN17505.1; -; mRNA.
 DR HSP; Q9Y780; 1HTU.
 DR Ensembl; ENSANGG00000004251; Anopheles gambiae.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0008471; F:laccase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR011706; Cu-oxidase_2.
 DR InterPro; IPR011707; Cu-oxidase_3.
 DR InterPro; IPR002355; Cu ox copper_BS.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR Pfam; PF07731; Cu-oxidase_2; 1.
 DR Pfam; PF07732; Cu-oxidase_3; 1.
 DR Pfam; PF00093; VWC; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 1009 AA; 114164 MW; C64E277FB3E4FE3F CRC64;

Query Match 67.9%; Score 38; DB 2; Length 1009;
 Best Local Similarity 70.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
 Db 666 KANQPIGNYL 675

RESULT 35
 Q7PS90 ANOQA PRELIMINARY; PRT; 1009 AA.
 AC Q7PS90;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DE ENSANGP0000005549.
 GN ORFNames=ENSANGG00000004251;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBSJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- COFACTOR: Binds 4 copper ions per monomer (By similarity).
 DR EMBL; AAB01008844; EAA05994.3; -; Genomic DNA.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR011706; Cu-oxidase_2.
 DR InterPro; IPR011707; Cu-oxidase_3.
 DR InterPro; IPR002355; Cu ox copper_BS.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR Pfam; PF07731; Cu-oxidase_2; 1.
 DR Pfam; PF07732; Cu-oxidase_3; 1.
 DR Pfam; PF00093; VWC; 1.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
 KW Copper; Metal-binding; Oxidoreductase; Repeat.
 SQ SEQUENCE 1009 AA; 114165 MW; 8976EB5021877BE7 CRC64;

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Query Match 67.9%; Score 38; DB 2; Length 1009;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 666 KANQPIGNYL 675

RESULT 36
Q9F2E8_9CVAN PRELIMINARY; PRT; 101 AA.
ID Q9F2E8;
AC STRAIN=PC6313;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phycocyanin alpha subunit (Fragment).
GN Name=pcpA;
OS Spirulina sp. PCC 6313.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=129961;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22048976; PubMed=12054250; DOI=10.1099/ijb.0.01981-0;
RA Manen J.F., Falquet J.;
RT "The pcB-cpA locus as a tool for the genetic characterization of the
RL Int. J. Syst. Evol. Microbiol. 52:861-867(2002).
DR EMBL; AJ401188; CAC10077.1; -; Genomic_DNA.
DR HSSP; P50032; 1JBO.
DR SMR; P50032; 1-101.
DR GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR GO; GO:0030089; C:phycobilisome; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR01659; Phycobilisome.
DR InterPro; IPR012128; Phycocyanin.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD00340; Phycobilisome; 1.
DR Electron transport; Photosynthesis; Phycobilisome.
KW NON TER 101 101
FT SEQUENCE 101 AA; 10982 MW; F6BB5DF5229B9D4D CRC64;

Query Match 66.1%; Score 37; DB 2; Length 101;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
Db 83 KCARDIGHYL 93

RESULT 37
O50318 MICAE PRELIMINARY; PRT; 102 AA.
ID O50318 MICAE PRELIMINARY;
AC O50318;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phycocyanin alpha subunit (Fragment).
GN Name=pcA;
OS Microcystis aeruginosa EAAG175.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=324056;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EAAG175;
RA Niederberger J.G., Preisig H.R., Hanselmann K.;
RT "Genotypic diversity of strains of Microcystis aeruginosa
(R Cyanobacteria) based on RAPD and partial DNA-sequences of phycocyanin
genes."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AJ003181; CAA05952.1; -; Genomic_DNA.
DR HSSP; P50032; 1JBO.
DR SMR; O50318; 1-102.
DR GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR GO; GO:0030089; C:phycobilisome; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
DR InterPro; IPR01659; Phycobilisome.
DR InterPro; IPR012128; Phycocyanin.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD00340; Phycobilisome; 1.
DR Electron transport; Photosynthesis; Phycobilisome.
KW NON TER 102 102
FT SEQUENCE 102 AA; 10847 MW; 48F93BE9ED58CA3E CRC64;

Query Match 66.1%; Score 37; DB 2; Length 102;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
Db 83 KCARDIGHYL 93

RESULT 38
KVSP MOUSE
ID KVSP_MOUSE STANDARD; PRT; 108 AA.
AC P01649;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V regions (Anti-arsenate antibodies).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=77250895; PubMed=70482;
RA Capra J.D., Tung A.S., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. V. The complete amino acid sequence of the light chain
RT variable regions of anti-p-azophenylarsenate antibodies from A/J mice
RT bearing a cross-reactive idiotype."
RL J. Immunol. 119:993-999(1977).
CC -1- MISCELLANEOUS: The mixture sequenced contained at least two or
CC three different light chains. Peptides containing the following
CC substitutions were also isolated: Val-3, Ile-10, and Leu-12; Leu-
CC 22; Phe-36, Glu-42, and Ala-43; Thr-63 and Arg-68; Ser-76, Ser-77,
CC Val-78, Ala-80, and Asp-85; and Gln-100 and Arg-107.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01928; KVM5AA.
DR HSSP; P01594; 1JVV5.
DR SMR; P01649; 1-108.
DR Ensembl; ENSMUSG00000029991; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
RN REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT Complementarity-determining-1.
FT Complementarity-determining-2.
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FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12057 MW; AE2861E5AAC09DD2 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 108;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDLSQYL 33

RESULT 39
KV5F MOUSE STANDARD; PRT; 115 AA.
AC P01638;
DT 21-JUL-1986 (Rel. 01, Created)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region L6 precursor (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81220975; PubMed=6264318;
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RL coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01921; KVMSL6.
DR HSSP; P01607; 1BWW.
DR Ensembl; ENSMUSG0000061260; Mus musculus.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR007110; Ig-like.
DR PRINTS; PR00024; HOMEOBOX.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-V region L6.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 77 108 Framework-3.
FT DISULFID 109 >115 Complementarity-determining-3.
FT NON TER 115 115 By similarity.
SQ SEQUENCE 115 AA; 12986 MW; BA852C58F328E1C3 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 115;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 44 KASQDINSYL 53

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RESULT 40
KV5H MOUSE STANDARD; PRT; 117 AA.
AC P01641;
DT 21-JUL-1986 (Rel. 01, Created)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MOPC 173B precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81064681; PubMed=677049; DOI=10.1016/0092-8674(80)90442-0;
RA Max E.E., Seidman J.G., Miller H., Leder P.;
RT "Variation in the crossover point of kappa immunoglobulin gene V-J
RL recombination: evidence from a cryptic gene.";
RL Cell 21:793-799(1980).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; K00880; AAA39031.1; -; Genomic_DNA.
DR PIR; A01924; KVM3JB.
DR HSSP; P01607; 1BWW.
DR SMR; P01641; 23-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 117 Ig kappa chain V-V region MOPC 173B.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Complementarity-determining-3.
FT REGION 111 >117 By similarity.
FT DISULFID 45 110
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12955 MW; 24B3D4B9AC2E4D6C CRC64;

Query Match 66.1%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 46 RASQDIHGYL 55

RESULT 41
Q6RX70 SPIPL
ID Q6RX70 SPIPL PRELIMINARY; PRT; 125 AA.
AC Q6RX70;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Phycocyanin alpha subunit (Fragment).
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
NCBI_TaxID=1156;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sajja U.B., Gopalaswamy G., Raghu R.;

```

Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY487164; AAS58443.1; -; Genomic_DNA.
 DR HSSP; Q9AM02; 1KTP.
 DR SMR; Q6RX70; 1-121.
 DR GO; GO:0009503; C-light-harvesting complex (sensu Viridiplantae); IEA.
 DR GO; GO:0030089; C-phycobilisome; IEA.
 DR GO; GO:0006118; P-electron transport; IEA.
 DR GO; GO:0015979; P-photosynthesis; IEA.
 DR InterPro; IPR001659; Phycobillosome.
 DR InterPro; IPR012128; Phycocyanin.
 DR Pfam; PF00502; Phycobilisome; 1.
 DR ProDom; PD000340; Phycobilisome; 1.
 KW Electron transport; Photosynthesis; Phycobillosome.
 FT NON TER 125
 SQ SEQUENCE 125 AA; 13559 MW; OFDDA8234CB5898F CRC64;

Query Match 66.1%; Score 37; DB 2; Length 125;
 Best Local Similarity 54.5%; Pred.No. 40;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11 : : ||||| : ||
 Db 83 KCARDIGHYLR 93

RESULT 42
 KVSE MOUSE STANDARD; PRT; 128 AA.
 ID _KVSE_MOUSE
 AC P01637; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-V region T1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=81052342; PubMed=6776411;
 RA Altenburger W., Steinmetz M., Zachau H.G.;
 RT "Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma.";
 RL Nature 287:603-607(1980).

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DR EMBL; V00772; CA244150.1; -; Genomic_DNA.
 DR PIR; A01920; KVMST1.
 DR HSSP; P80362; 1WTL.
 DR SMR; P01637; 21-128.
 DR Ensembl; ENSMUSG0000061260; Mus musculus.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR PRINTS; PR00024; HOMEBOX.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 128 Ig kappa chain V-V region T1.
 FT REGION 21 43 Framework-1.
 FT REGION 44 54 Complementarity-determining-1.
 FT REGION 55 69 Framework-2.
 FT REGION 70 76 Complementarity-determining-2.
 FT REGION 77 108 Framework-3.
 FT REGION 109 117 Complementarity-determining-3.
 FT REGION 118 127 Framework-4.

FT DISULFID 43 108 By similarity.
 FT NON_TER 128
 SQ SEQUENCE 128 AA; 14386 MW; AFA5563D31BB7E05 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 128;
 Best Local Similarity 70.0%; Pred.No. 41;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10 : ||||| : ||
 Db 44 KASQDINSYL 53

RESULT 43
 KVSG MOUSE STANDARD; PRT; 130 AA.
 ID KVSG_MOUSE
 AC P01639; P01640;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-V region MOPC 41 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=79221900; PubMed=111146;
 RA Seidman J.G., Max E.E., Leder P.;
 RT "A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.";
 RL Nature 280:370-375(1979).
 RN [2]
 RP PROTEIN SEQUENCE OF 1-33.
 RX MEDLINE=77148916; PubMed=403522;
 RA Burstein Y., Schechter I.;
 RT "Amino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda1-type and kappa-type light chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
 RN [3]
 RP PROTEIN SEQUENCE OF 23-130.
 RX MEDLINE=67056897; PubMed=4162931;
 RA Gray W.R., Dreyer W.J., Hood L.E.;
 RT "Mechanism of antibody synthesis: size differences between mouse kappa chains";
 RL Science 155:465-467(1967).
 CC -!- MISCELLANEOUS: This precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polyosomes.
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

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DR PIR; A93211; KVMSM4.
 DR HSSP; P01594; 1JV5.
 DR SMR; P01639; 23-130.
 DR Ensembl; ENSMUSG0000062548; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 130 Ig kappa chain V-V region MOPC 41.
 FT REGION 23 45 Framework-1.
 FT REGION 46 56 Complementarity-determining-1.
 FT REGION 57 71 Framework-2.


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FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 119 Complementarity-determining-3.
FT REGION 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT VARIANT 1 2 Missing (in 25% of the molecules).
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; 58FE0FE71D5F1BEC CRC64;

Query Match 66.1%; Score 37; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 46 RASQDIGSSL 55

RESULT 44
PHRA_SYNYP STANDARD; PRT; 161 AA.
AC Q02182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE R-phycocyanin II alpha chain.
GN Name=rpcA;
OS Synechococcus sp. (strain WH8020).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32052;
RN [1]
RP MEDLINE=93144698; PubMed=8425055;
RA de Lorimier R., Wilbanks S.M., Glazer A.N.;
RT "Genes of the R-phycocyanin II locus of marine Synechococcus spp., and
RT comparison of protein-chromophore interactions in phycocyanins
RT Plant Mol. Biol. 21:225-237(1993).
CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC -!- from the phycobiliprotein complex.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- PTM: Contains one covalently linked bilin chromophore.
CC -!- SIMILARITY: Belongs to the phycobiliprotein family.
CC
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CC removed.
CC
CC EMBL; M95288; AAA27346.1; -; Genomic_DNA.
CC HSP; P72509; 1HAY.
CC SMR; Q02182; 1-161.
CC InterPro; IPR001659; Phycobilisome.
CC InterPro; IPR012128; Phycocyanin.
CC InterPro; IPR006246; Phycocyanin_a.
CC Pfam; PF00502; Phycobilisome; 1.
CC PIRSF; PIRSF000081; Phycocyanin; 1.
CC ProDom; PD000340; Phycobilisome; 1.
CC TIGRFAMs; TIGR01338; phycocyc alpha; 1.
CC Bile pigment; Chromophore; Electron transport; Photosynthesis;
CC Phycobilisome; Transport.
CC INIT_MET 0 0 By similarity.
CC BINDING 83 83 Phycocerythrobilin chromophore.
CC SEQUENCE 161 AA; 17238 MW; 43B49A4A71730DF9 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 161;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11
Db 82 KCSRDIGYTLR 92

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RESULT 45
PHCA_CYACA STANDARD; PRT; 162 AA.
ID PHCA_CYACA
AC O19910;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-phycocyanin alpha chain.
GN Name=cpca;
OS Cyanidium caldarium.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;
OC Cyanidium.
OX NCBI_TaxID=2771;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
RT genome."
RL J. Mol. Evol. 51:382-390(2000).
CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC -!- from the phycobiliprotein complex.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- PTM: Contains one covalently linked bilin chromophore.
CC -!- SIMILARITY: Belongs to the phycobiliprotein family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF022186; AAB82679.1; -; Genomic_DNA.
CC PIR; T11978; T11978.
CC HSP; P00306; 1PHN.
CC SMR; O19910; 1-162.
CC InterPro; IPR001659; Phycobilisome.
CC InterPro; IPR012128; Phycocyanin.
CC InterPro; IPR006246; Phycocyanin_a.
CC Pfam; PF00502; Phycobilisome; 1.
CC PIRSF; PIRSF000081; Phycocyanin; 1.
CC ProDom; PD000340; Phycobilisome; 1.
CC TIGRFAMs; TIGR01338; phycocyc alpha; 1.
CC Bile pigment; Chloroplast; Chromophore; Electron transport;
CC Photosynthesis; Phycobilisome; Transport.
CC BINDING 84 84 Phycocyanobilin chromophore (By
CC similarity).
CC SEQUENCE 162 AA; 17245 MW; 01D3DDCB35720E73 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 162;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 11
Db 83 KCSRDIGYTLR 93

RESULT 46
PHCA_MASLA STANDARD; PRT; 162 AA.
ID PHCA_MASLA
AC P00307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-phycocyanin alpha chain.
GN Name=cpca;
OS Mastigocladus laminosus (Fischerella sp.).
OC Bacteria; Cyanobacteria; Stigonematales; Mastigocladus.

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OX NCBI_TaxID=83541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kufer W., Hoegner A., Eberlein M., Mayer K., Buchner A.,
RT Gottschalk L.;
RT "Structure and molecular evolution of the gene cluster encoding
RT proteins of the rod substructure of the phycobilisome from the
RT cyanobacterium Mastigocladus laminosus.";
RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE.
RX MEDLINE=79087164; PubMed=103794;
RA Frank G., Sidler W., Widmer H., Zuber H.;
RT "The complete amino acid sequence of both subunits of C-phycocyanin
RT from the cyanobacterium Mastigocladus laminosus.";
RL Hoppe-Seyler's Z. Physiol. Chem. 359:1491-1507(1978).
CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- PTM: Contains one covalently linked bilin chromophore.
CC -!- SIMILARITY: Belongs to the phycobiliprotein family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M75999; AAC64650.1; -; Genomic_DNA.
DR PIR; A00315; CFMWA.
DR HSSP; P00306; 1PHN.
DR SWE; P00307; 1-162.
DR InterPro; IPR001659; Phycobilisome.
DR InterPro; IPR012128; Phycocyanin.
DR InterPro; IPR006246; Phycocyanin.a.
DR Pfam; PF00502; Phycobilisome; 1.
DR PIRSF; PIRSF000081; Phycocyanin; 1.
DR ProDom; PD000340; Phycobilisome; 1.
DR TIGRPFAMs; TIGR01338; phycocy_alpha; 1.
KW Bile pigment; Chromophore; Direct protein sequencing;
KW Electron transport; Photosynthesis; Phycobilisome; Transport.
FT INIT MET 0
FT BINDING 66 84 Phycocyanobilin chromophore.
FT CONFLICT 66 67 TT->LI (in Ref. 2).
SQ SEQUENCE 162 AA; 17392 MW; B19F9856A51E4AD CRC64;

Query Match 66.1%; Score 37; DB 1; Length 162;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
Db 83 KCARDIGHYLR 93

RESULT 47
PHCA SYNY1 STANDARD; PRT; 162 AA.
ID PHCA SYNY1
AC P20776;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-phycocyanin alpha chain.
GN Name=cpcA;
OS Synechocystis sp. (strain PCC 6701).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1144;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90170839; PubMed=2106506;
RA Anderson L.K., Grossman A.R.;
RT "Genes for phycocyanin subunits in Synechocystis sp. strain PCC 6701
RT and assembly mutant UV16.";
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RL J. Bacteriol. 172:1289-1296(1990).
CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein
CC from the phycobiliprotein complex.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- PTM: Contains one covalently linked bilin chromophore.
CC -!- SIMILARITY: Belongs to the phycobiliprotein family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M33820; AAA27282.1; -; Genomic_DNA.
DR PIR; B35126; B35126.
DR HSSP; P07122; ICPC.
DR SWE; P20776; 2-162.
DR InterPro; IPR001659; Phycobilisome.
DR InterPro; IPR012128; Phycocyanin.
DR InterPro; IPR006246; Phycocyanin.a.
DR Pfam; PF00502; Phycobilisome; 1.
DR PIRSF; PIRSF000081; Phycocyanin; 1.
DR ProDom; PD000340; Phycobilisome; 1.
DR TIGRPFAMs; TIGR01338; phycocy_alpha; 1.
KW Bile pigment; Chromophore; Electron transport; Photosynthesis;
KW Phycobilisome; Transport.
FT INIT MET 0
FT BINDING 84 84 Phycocyanobilin chromophore.
SQ SEQUENCE 162 AA; 17321 MW; 9AA227420F20AA19 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 162;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
Db 83 KCSRDIGYLR 93

RESULT 48
Q82RA8 STRAW PRELIMINARY; PRT; 162 AA.
ID Q82RA8 STRAW PRELIMINARY;
AC Q82RA8;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative anti-sigma factor antagonist.
GN OrderedLocusNames=SAV235;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RA avermitilis: deducing the ability of producing secondary
RA metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RA MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RA microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; BA000030; BAC67944.1; -; Genomic_DNA.
```

DR InterPro; IPR003658; Antisig_antgnet.
 DR InterPro; IPR002645; STAS.
 DR Pfam; PF01740; STAS; 1.
 DR ProDom; PD005210; Antisig_antgnet; 1.
 DR TIGRFAMs; TIGR00377; antisig; 1.
 DR PROSITE; PS0801; STAS; 1.
 KW Complete proteome.
 SQ SEQUENCE 162 AA; 17601 MW; A4720E5346D7C48 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 162;
 Best Local Similarity 63.6%; Pred. No. 52;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASQDIGNYLR 11
 ||: || | : ||
 DB 119 RAAQDAGGWL 129

RESULT 49

Q8PVD9_METMA PRELIMINARY; PRT; 195 AA.
 AC Q8PVD9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein MM2026.
 GN OrderedLocustNames=MM2026;
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Goel / GoI / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=12125824;
 RA Deppe-meier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wietzer A., Baeumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 transfer between Bacteria and Archaea."
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
 DR EMBL; AE013442; AAM31722.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 195 AA; 21559 MW; 58C68B5990E2FB56 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 195;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SODIGNYLR 11
 : : ||| : ||
 DB 176 NEDIGNFLR 184

RESULT 50

Q7PVR5_ANOGA PRELIMINARY; PRT; 201 AA.
 AC Q7PVR5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000016703 (Fragment).
 GN ORFNames=ENSANG0000014214;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;
 RL "Anopheles gambiae re-annotation."
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008984; EAA14722.2; -; Genomic_DNA.
 DR InterPro; IPR011893; CXXU_selWTH.
 DR TIGRFAMs; TIGR02174; CXXU_selWTH; 1.
 FT NON_TER 1
 SQ SEQUENCE 201 AA; 22847 MW; F318F74660C191B7 CRC64;

Query Match 66.1%; Score 37; DB 2; Length 201;
 Best Local Similarity 85.7%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SODIGNY 9
 ||| : |||
 DB 37 SODVGNV 43

Search completed: May 11, 2006, 16:36:46
 Job time : 131.705 secs

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GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:37 ; Search time 25.4262 Seconds
(without alignments)
35.767 Million cell updates/sec

Title: US-10-808-538-4
Perfect score: 56
Sequence: 1 RASQDIGNYLRL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	11	2	US-09-155-106-4
2	56	100.0	108	2	US-09-155-106-22
3	56	100.0	108	2	US-09-155-106-23
4	56	100.0	108	2	US-09-155-106-24
5	56	100.0	108	2	US-09-155-106-28
6	56	100.0	108	2	US-09-155-106-30
7	45	80.4	11	1	US-08-480-434-76
8	45	80.4	11	1	US-08-053-451B-76
9	45	80.4	11	2	US-08-649-100-11
10	45	80.4	11	2	US-08-649-100-27
11	45	80.4	31	2	US-08-525-539A-5
12	45	80.4	107	1	US-08-458-516-8
13	45	80.4	107	1	US-08-458-516-9
14	45	80.4	107	1	US-08-480-434-74
15	45	80.4	107	1	US-08-053-451B-74
16	45	80.4	107	1	US-08-053-451B-176
17	45	80.4	108	2	US-09-065-059-3
18	45	80.4	108	2	US-09-232-290-21
19	45	80.4	108	2	US-08-913-555-3
20	45	80.4	108	2	US-08-913-555-21
21	45	80.4	109	1	US-07-942-245-10
22	45	80.4	109	1	US-07-934-373C-47
23	45	80.4	109	2	US-08-437-642B-47
24	45	80.4	127	1	US-08-458-516-5
25	45	80.4	127	1	US-08-137-117D-37
26	45	80.4	127	1	US-08-436-717-37
27	45	80.4	127	1	US-08-574-699A-2
28	45	80.4	127	2	US-08-649-100-17
29	45	80.4	127	2	US-08-649-100-33
30	45	80.4	131	1	US-08-236-520-2
31	45	80.4	131	4	PCT-US95-05362-2
32	45	80.4	212	2	US-10-011-125A-5
33	45	80.4	214	1	US-08-425-763-1
34	45	80.4	214	1	US-08-458-516-12
35	45	80.4	214	1	US-07-934-373C-24
36	45	80.4	214	1	US-07-934-373C-39
37	45	80.4	214	1	US-07-934-373C-40
38	45	80.4	214	1	US-08-788-800-11
39	45	80.4	214	2	US-08-437-642B-24
40	45	80.4	214	2	US-08-437-642B-39
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44	45	80.4	214	2	US-09-097-171A-2
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47	45	80.4	214	2	US-08-146-206C-24
48	45	80.4	214	2	US-09-705-686-24
49	45	80.4	214	2	US-09-940-166A-2
50	45	80.4	214	2	US-09-705-392A-24
51	45	80.4	214	2	US-09-705-398-24
52	45	80.4	214	4	PCT-US93-07832-24
53	45	80.4	214	4	PCT-US93-07832-39
54	45	80.4	214	4	PCT-US93-07832-40
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56	45	80.4	233	2	US-08-437-642B-25
57	45	80.4	233	2	US-08-146-206C-25
58	45	80.4	233	2	US-09-705-686-25
59	45	80.4	233	2	US-09-705-392A-25
60	45	80.4	233	2	US-09-705-398-25
61	45	80.4	233	4	PCT-US93-07832-25
62	45	80.4	237	2	US-09-097-309-6
63	45	80.4	237	2	US-09-097-171A-10
64	45	80.4	237	2	US-09-422-712B-2
65	45	80.4	237	2	US-09-607-756-2
66	45	80.4	237	2	US-09-460-587-6
67	45	80.4	237	2	US-09-940-166A-6
68	45	80.4	273	1	US-08-403-853-18
69	44	78.6	236	1	US-08-157-101A-5
70	43	76.8	104	1	US-08-276-852-112
71	43	76.8	104	1	US-08-899-575-112
72	43	76.8	104	1	US-08-899-575-112
73	43	76.8	104	1	PCT-US95-08743-112
74	43	76.8	107	1	US-07-934-373C-16
75	43	76.8	107	1	US-07-934-373C-17
76	43	76.8	107	2	US-08-437-642B-16
77	43	76.8	107	2	US-08-437-642B-17
78	43	76.8	107	2	US-08-146-206C-16
79	43	76.8	107	2	US-08-146-206C-17
80	43	76.8	107	2	US-09-705-686-16
81	43	76.8	107	2	US-09-705-686-17
82	43	76.8	107	2	US-09-705-392A-16
83	43	76.8	107	2	US-09-705-392A-17
84	43	76.8	107	2	US-09-705-398-16
85	43	76.8	107	2	US-09-705-398-17
86	43	76.8	107	4	PCT-US93-07832-16
87	43	76.8	107	4	PCT-US93-07832-17
88	43	76.8	211	2	US-09-170-769A-8
89	43	76.8	247	2	US-10-620-049-21
90	43	76.8	247	2	US-10-620-049-23
91	43	76.8	247	2	US-10-620-049-25
92	43	76.8	274	2	US-08-813-659-30
93	43	76.8	274	2	US-09-549-067A-30
94	43	76.8	302	1	US-08-121-054C-18
95	43	76.8	302	1	US-08-121-054C-30
96	43	76.8	302	2	US-08-539-436-18
97	43	76.8	302	2	US-08-539-436-30
98	43	76.8	302	2	US-08-813-659-18
99	43	76.8	302	2	US-09-813-659-32
100	43	76.8	302	2	US-09-549-067A-18

101	43	76.8	302	2	US-09-549-0678A-32	Sequence 32, Appl	174	40	71.4	110	2	US-09-440-781-94	Sequence 94, Appl
102	42	75.0	107	2	US-08-483-749A-26	Sequence 26, Appl	175	40	71.4	110	2	US-08-908-469-103	Sequence 103, App
103	42	75.0	108	2	US-09-232-290-16	Sequence 16, Appl	176	40	71.4	110	2	US-08-908-469-105	Sequence 105, App
104	42	75.0	112	2	US-09-627-218B-1	Sequence 1, Appl	177	40	71.4	110	2	US-08-908-469-107	Sequence 107, App
105	42	75.0	127	2	US-08-348-548-4	Sequence 4, Appl	178	40	71.4	110	2	US-08-908-469-117	Sequence 117, App
106	42	75.0	127	4	PCT-US95-15716-4	Sequence 4, Appl	179	40	71.4	111	1	US-08-137-117D-67	Sequence 67, Appl
107	42	75.0	243	1	US-08-133-804-6	Sequence 6, Appl	180	40	71.4	111	1	US-08-436-717-67	Sequence 67, Appl
108	42	75.0	243	1	US-08-461-838-6	Sequence 6, Appl	181	40	71.4	126	1	US-08-137-117D-71	Sequence 71, Appl
109	42	75.0	243	1	US-08-461-386-6	Sequence 6, Appl	182	40	71.4	126	1	US-08-436-717-71	Sequence 71, Appl
110	42	75.0	243	1	US-08-356-786-4	Sequence 4, Appl	183	40	71.4	127	1	US-08-137-117D-29	Sequence 29, Appl
111	42	75.0	355	2	US-08-875-811-41	Sequence 41, Appl	184	40	71.4	127	1	US-08-436-717-29	Sequence 29, Appl
112	42	75.0	355	2	US-08-875-811-49	Sequence 49, Appl	185	40	71.4	128	2	US-09-225-322B-10	Sequence 10, Appl
113	42	75.0	355	2	US-08-875-811-64	Sequence 64, Appl	186	40	71.4	128	2	US-09-225-322B-19	Sequence 19, Appl
114	42	75.0	358	2	US-08-875-811-45	Sequence 45, Appl	187	40	71.4	128	2	US-09-764-304-10	Sequence 10, Appl
115	42	75.0	358	2	US-08-875-811-51	Sequence 51, Appl	188	40	71.4	128	2	US-09-764-304-19	Sequence 19, Appl
116	42	75.0	360	2	US-08-875-811-47	Sequence 47, Appl	189	40	71.4	237	2	US-08-908-469-100	Sequence 100, App
117	42	75.0	379	2	US-08-875-811-43	Sequence 43, Appl	190	40	71.4	240	1	US-08-488-113B-147	Sequence 147, App
118	42	75.0	534	1	US-08-356-786-10	Sequence 10, Appl	191	40	71.4	240	1	US-08-488-113B-148	Sequence 148, App
119	41	73.2	11	1	US-07-942-245-496	Sequence 496, App	192	40	71.4	240	1	US-08-477-484B-147	Sequence 147, App
120	41	73.2	30	2	US-08-525-539A-7	Sequence 7, Appl	193	40	71.4	240	1	US-08-477-484B-148	Sequence 148, App
121	41	73.2	76	2	US-08-851-362D-20	Sequence 20, Appl	194	40	71.4	240	1	US-08-646-360-147	Sequence 147, App
122	41	73.2	95	2	US-10-194-975-56	Sequence 56, Appl	195	40	71.4	240	1	US-08-646-360-148	Sequence 148, App
123	41	73.2	95	2	US-10-194-975-57	Sequence 57, Appl	196	40	71.4	240	2	US-08-839-765-147	Sequence 147, App
124	41	73.2	95	2	US-10-330-613A-59	Sequence 59, Appl	197	40	71.4	240	2	US-08-839-765-148	Sequence 148, App
125	41	73.2	105	2	US-08-851-362D-24	Sequence 24, Appl	198	40	71.4	240	2	US-09-136-389-147	Sequence 147, App
126	41	73.2	105	2	US-08-851-362D-28	Sequence 28, Appl	199	40	71.4	240	2	US-09-136-389-148	Sequence 148, App
127	41	73.2	105	2	US-08-851-362D-34	Sequence 34, Appl	200	40	71.4	240	2	US-09-610-838-147	Sequence 147, App
128	41	73.2	105	2	US-08-851-362D-38	Sequence 38, Appl	201	40	71.4	240	2	US-09-610-838-148	Sequence 148, App
129	41	73.2	107	2	US-09-232-290-29	Sequence 29, Appl	202	40	71.4	240	2	US-09-711-485-147	Sequence 147, App
130	41	73.2	107	2	US-10-330-613A-26	Sequence 26, Appl	203	40	71.4	240	2	US-09-711-485-148	Sequence 148, App
131	41	73.2	109	1	US-07-942-245-11	Sequence 11, Appl	204	40	71.4	491	2	US-10-011-125A-2	Sequence 2, Appl
132	41	73.2	234	2	US-09-800-729-150	Sequence 150, App	205	39	69.6	88	2	US-09-905-243-36	Sequence 36, Appl
133	41	73.2	316	1	US-08-842-842-7	Sequence 7, Appl	206	39	69.6	102	2	US-09-726-219A-173	Sequence 173, App
134	41	73.2	316	2	US-08-989-362-2	Sequence 2, Appl	207	39	69.6	102	2	US-09-136-522-173	Sequence 173, App
135	41	73.2	316	2	US-09-052-521C-2	Sequence 2, Appl	208	39	69.6	107	1	US-08-276-852-107	Sequence 107, App
136	41	73.2	316	2	US-09-671-658A-2	Sequence 2, Appl	209	39	69.6	107	1	US-08-899-575-107	Sequence 107, App
137	41	73.2	316	2	US-09-396-937-4	Sequence 4, Appl	210	39	69.6	107	1	US-08-899-575-107	Sequence 107, App
138	41	73.2	316	2	US-09-396-937-6	Sequence 6, Appl	211	39	69.6	107	1	US-07-934-373C-18	Sequence 18, Appl
139	41	73.2	316	2	US-09-957-944-8	Sequence 8, Appl	212	39	69.6	107	1	US-08-652-558-36	Sequence 36, Appl
140	40	71.4	11	1	US-08-137-117D-117	Sequence 117, App	213	39	69.6	107	1	US-08-378-339-14	Sequence 14, Appl
141	40	71.4	11	1	US-08-436-717-117	Sequence 117, App	214	39	69.6	107	2	US-08-437-642B-18	Sequence 18, Appl
142	40	71.4	11	2	US-08-908-469-4	Sequence 4, Appl	215	39	69.6	107	2	US-09-240-274-173	Sequence 173, App
143	40	71.4	51	1	US-08-472-788A-73	Sequence 73, Appl	216	39	69.6	107	2	US-09-240-274-179	Sequence 179, App
144	40	71.4	51	1	US-08-472-788A-74	Sequence 74, Appl	217	39	69.6	107	2	US-09-240-274-179	Sequence 18, Appl
145	40	71.4	51	1	US-08-082-842A-73	Sequence 73, Appl	218	39	69.6	107	2	US-08-146-206C-18	Sequence 18, Appl
146	40	71.4	51	1	US-08-082-842A-74	Sequence 74, Appl	219	39	69.6	107	2	US-09-648-067A-14	Sequence 14, Appl
147	40	71.4	84	2	US-09-471-276-816	Sequence 816, App	220	39	69.6	107	2	US-09-705-686-18	Sequence 18, Appl
148	40	71.4	107	1	US-08-425-336-125	Sequence 125, App	221	39	69.6	107	2	US-09-705-392A-18	Sequence 18, Appl
149	40	71.4	107	1	US-08-276-852-103	Sequence 103, App	222	39	69.6	107	2	US-09-705-398-18	Sequence 18, Appl
150	40	71.4	107	1	US-08-488-113B-125	Sequence 125, App	223	39	69.6	107	2	US-09-848-798-173	Sequence 173, App
151	40	71.4	107	1	US-08-477-484B-125	Sequence 125, App	224	39	69.6	107	2	US-09-602-812A-5	Sequence 5, Appl
152	40	71.4	107	1	US-08-107-669D-27	Sequence 27, Appl	225	39	69.6	107	4	PCT-US93-07832-18	Sequence 18, Appl
153	40	71.4	107	1	US-08-107-669D-65	Sequence 65, Appl	226	39	69.6	108	1	PCT-US95-08743-107	Sequence 107, App
154	40	71.4	107	1	US-08-472-788A-27	Sequence 27, Appl	227	39	69.6	108	1	US-08-276-852-102	Sequence 102, App
155	40	71.4	107	1	US-08-472-788A-87	Sequence 87, Appl	228	39	69.6	108	1	US-08-899-575-102	Sequence 102, App
156	40	71.4	107	1	US-08-899-575-103	Sequence 103, App	229	39	69.6	108	1	US-08-899-575-102	Sequence 102, App
157	40	71.4	107	1	US-08-899-575-103	Sequence 103, App	230	39	69.6	108	1	US-08-378-939-30	Sequence 30, Appl
158	40	71.4	107	1	US-08-477-531B-27	Sequence 27, Appl	231	39	69.6	108	2	US-08-974-899-3	Sequence 3, Appl
159	40	71.4	107	1	US-08-477-531B-65	Sequence 65, Appl	232	39	69.6	108	2	US-09-025-769B-14	Sequence 14, Appl
160	40	71.4	107	1	US-08-646-360-125	Sequence 125, App	233	39	69.6	108	2	US-09-490-070A-14	Sequence 14, Appl
161	40	71.4	107	1	US-08-082-842A-27	Sequence 27, Appl	234	39	69.6	108	2	US-09-795-798-3	Sequence 3, Appl
162	40	71.4	107	1	US-08-082-842A-87	Sequence 87, Appl	235	39	69.6	108	2	US-09-490-153-14	Sequence 14, Appl
163	40	71.4	107	2	US-08-839-765-125	Sequence 125, App	236	39	69.6	108	2	US-09-490-324-14	Sequence 14, Appl
164	40	71.4	107	2	US-09-136-389-125	Sequence 125, App	237	39	69.6	108	2	US-08-908-469-12	Sequence 12, Appl
165	40	71.4	107	2	US-09-610-838-125	Sequence 125, App	238	39	69.6	108	4	PCT-US93-08743-102	Sequence 102, App
166	40	71.4	107	2	US-09-711-485-125	Sequence 125, App	239	39	69.6	109	1	US-07-934-373C-3	Sequence 3, Appl
167	40	71.4	107	2	US-08-908-469-13	Sequence 13, Appl	240	39	69.6	109	2	US-08-437-642B-3	Sequence 3, Appl
168	40	71.4	107	2	US-08-908-469-15	Sequence 15, Appl	241	39	69.6	109	2	US-08-146-206C-3	Sequence 3, Appl
169	40	71.4	107	4	PCT-US95-08743-103	Sequence 103, App	242	39	69.6	109	2	US-09-705-686-3	Sequence 3, Appl
170	40	71.4	108	2	US-08-908-469-8	Sequence 8, Appl	243	39	69.6	109	2	US-09-705-392A-3	Sequence 3, Appl
171	40	71.4	108	2	US-08-908-469-10	Sequence 10, Appl	244	39	69.6	109	2	US-09-705-398-3	Sequence 3, Appl
172	40	71.4	108	2	US-08-908-469-126	Sequence 126, App	245	39	69.6	109	2	US-10-330-613A-10	Sequence 10, Appl
173	40	71.4	109	2	US-09-386-658A-4	Sequence 4, Appl	246	39	69.6	109	4	PCT-US93-07832-3	Sequence 3, Appl

247	38	67.9	88	2	US-09-905-243-29	Sequence 29, Appl	320	37	66.1	109	2	US-10-435-602-74	Sequence 74, Appl
248	38	67.9	95	2	US-09-627-896B-27	Sequence 27, Appl	321	36	64.3	11	1	US-07-942-225-497	Sequence 497, Appl
249	38	67.9	95	2	US-10-194-975-58	Sequence 58, Appl	322	36	64.3	11	1	US-08-599-246-7	Sequence 7, Appl
250	38	67.9	95	2	US-10-194-975-61	Sequence 61, Appl	323	36	64.3	11	2	US-09-125-098-7	Sequence 7, Appl
251	38	67.9	95	2	US-09-339-566A-42	Sequence 42, Appl	324	36	64.3	11	2	US-09-540-018-7	Sequence 7, Appl
252	38	67.9	95	2	US-10-330-613A-63	Sequence 63, Appl	325	36	64.3	11	2	US-09-192-854-178	Sequence 178, Appl
253	38	67.9	102	2	US-09-199-149-10	Sequence 10, Appl	326	36	64.3	11	2	US-08-511-939-316	Sequence 316, Appl
254	38	67.9	102	2	US-09-199-149-29	Sequence 29, Appl	327	36	64.3	31	2	US-08-525-539A-3	Sequence 3, Appl
255	38	67.9	105	1	US-08-276-852-89	Sequence 89, Appl	328	36	64.3	88	2	US-09-905-243-62	Sequence 62, Appl
256	38	67.9	105	1	US-08-899-575-89	Sequence 89, Appl	329	36	64.3	107	1	US-08-276-852-108	Sequence 108, Appl
257	38	67.9	105	2	US-08-899-575-89	Sequence 89, Appl	330	36	64.3	107	1	US-08-436-463-20	Sequence 20, Appl
258	38	67.9	105	2	US-09-199-149-31	Sequence 31, Appl	331	36	64.3	107	1	US-08-107-689D-1	Sequence 1, Appl
259	38	67.9	105	4	PCT-US95-08743-89	Sequence 89, Appl	332	36	64.3	107	1	US-08-472-788A-1	Sequence 1, Appl
260	38	67.9	106	1	US-08-276-852-83	Sequence 83, Appl	333	36	64.3	107	1	US-08-899-575-108	Sequence 108, Appl
261	38	67.9	106	1	US-08-276-852-85	Sequence 85, Appl	334	36	64.3	107	1	US-08-899-575-108	Sequence 108, Appl
262	38	67.9	106	1	US-08-899-575-83	Sequence 83, Appl	335	36	64.3	107	1	US-08-477-531B-1	Sequence 1, Appl
263	38	67.9	106	1	US-08-899-575-85	Sequence 85, Appl	336	36	64.3	107	1	US-08-290-532E-20	Sequence 20, Appl
264	38	67.9	106	1	US-08-899-575-83	Sequence 83, Appl	337	36	64.3	107	1	US-08-290-532E-21	Sequence 21, Appl
265	38	67.9	106	1	US-08-899-575-85	Sequence 85, Appl	338	36	64.3	107	1	US-08-082-842A-1	Sequence 1, Appl
266	38	67.9	106	4	PCT-US95-08743-83	Sequence 83, Appl	339	36	64.3	107	2	US-08-483-749A-28	Sequence 28, Appl
267	38	67.9	106	4	PCT-US95-08743-85	Sequence 85, Appl	340	36	64.3	107	2	US-08-599-226-9	Sequence 9, Appl
268	38	67.9	107	1	US-08-276-852-82	Sequence 82, Appl	341	36	64.3	107	2	US-08-599-226-9	Sequence 9, Appl
269	38	67.9	107	1	US-08-276-852-84	Sequence 84, Appl	342	36	64.3	107	2	US-09-125-098-1	Sequence 1, Appl
270	38	67.9	107	1	US-08-899-575-82	Sequence 82, Appl	343	36	64.3	107	2	US-03-125-098-9	Sequence 9, Appl
271	38	67.9	107	1	US-08-899-575-84	Sequence 84, Appl	344	36	64.3	107	2	US-09-540-018-1	Sequence 1, Appl
272	38	67.9	107	1	US-08-899-575-82	Sequence 82, Appl	345	36	64.3	107	2	US-09-540-018-9	Sequence 9, Appl
273	38	67.9	107	1	US-08-899-575-84	Sequence 84, Appl	346	36	64.3	107	2	US-10-268-883-6	Sequence 6, Appl
274	38	67.9	107	2	US-09-240-274-169	Sequence 169, Appl	347	36	64.3	107	2	US-10-330-613A-30	Sequence 30, Appl
275	38	67.9	107	2	US-09-848-798-169	Sequence 169, Appl	348	36	64.3	107	4	PCT-US95-08743-108	Sequence 108, Appl
276	38	67.9	107	4	PCT-US95-08743-82	Sequence 82, Appl	349	36	64.3	107	4	PCT-US95-10053-17	Sequence 17, Appl
277	38	67.9	107	4	PCT-US95-08743-84	Sequence 84, Appl	350	36	64.3	107	4	PCT-US95-10053-18	Sequence 18, Appl
278	38	67.9	108	1	US-08-276-852-109	Sequence 109, Appl	351	36	64.3	107	4	PCT-US96-09448-20	Sequence 20, Appl
279	38	67.9	108	1	US-08-899-575-109	Sequence 109, Appl	352	36	64.3	107	4	PCT-US96-09448-21	Sequence 21, Appl
280	38	67.9	108	1	US-08-899-575-109	Sequence 109, Appl	353	36	64.3	108	1	US-08-378-939-26	Sequence 26, Appl
281	38	67.9	108	2	US-09-199-149-7	Sequence 7, Appl	354	36	64.3	108	2	US-09-232-290-27	Sequence 27, Appl
282	38	67.9	108	2	US-09-199-149-14	Sequence 14, Appl	355	36	64.3	109	1	US-07-942-245-4	Sequence 4, Appl
283	38	67.9	108	2	US-09-905-243-73	Sequence 73, Appl	356	36	64.3	109	1	US-08-300-386A-69	Sequence 69, Appl
284	38	67.9	108	4	PCT-US95-08743-109	Sequence 109, Appl	357	36	64.3	109	2	US-08-931-6245-69	Sequence 69, Appl
285	38	67.9	110	1	US-08-300-386A-70	Sequence 70, Appl	358	36	64.3	109	4	PCT-US95-11235-69	Sequence 69, Appl
286	38	67.9	110	2	US-08-931-645-70	Sequence 70, Appl	359	36	64.3	127	2	US-10-268-883-5	Sequence 5, Appl
287	38	67.9	110	4	PCT-US95-11235-70	Sequence 70, Appl	360	36	64.3	129	1	US-08-860-174A-5	Sequence 5, Appl
288	38	67.9	112	2	US-08-487-761-13	Sequence 13, Appl	361	36	64.3	142	1	US-08-579-940-2	Sequence 2, Appl
289	38	67.9	112	2	US-10-148-737A-2	Sequence 2, Appl	362	36	64.3	142	2	US-08-838-692-4	Sequence 4, Appl
290	38	67.9	235	2	US-08-812-586-16	Sequence 16, Appl	363	36	64.3	150	2	US-09-472-087-24	Sequence 24, Appl
291	38	67.9	235	2	US-09-535-832A-17	Sequence 17, Appl	364	36	64.3	150	2	US-09-472-087-98	Sequence 98, Appl
292	38	67.9	24	1	US-08-140-137A-28	Sequence 28, Appl	365	36	64.3	258	1	US-08-860-174A-13	Sequence 13, Appl
293	37	66.1	92	1	US-08-273-146-45	Sequence 45, Appl	366	35	62.5	11	1	US-07-942-245-494	Sequence 494, Appl
294	37	66.1	92	1	US-08-273-146-47	Sequence 47, Appl	367	35	62.5	11	1	US-08-480-434-66	Sequence 66, Appl
295	37	66.1	92	1	US-08-273-146-53	Sequence 53, Appl	368	35	62.5	11	1	US-08-480-434-75	Sequence 75, Appl
296	37	66.1	95	2	US-10-194-975-93	Sequence 93, Appl	369	35	62.5	11	1	US-08-053-451B-66	Sequence 66, Appl
297	37	66.1	100	2	US-09-899-896-8	Sequence 8, Appl	370	35	62.5	11	1	US-08-053-451B-75	Sequence 75, Appl
298	37	66.1	107	1	US-08-425-336-123	Sequence 123, Appl	371	35	62.5	11	2	US-09-798-058-8	Sequence 8, Appl
299	37	66.1	107	1	US-08-488-113B-123	Sequence 123, Appl	372	35	62.5	88	2	US-09-905-243-31	Sequence 31, Appl
300	37	66.1	107	1	US-08-477-484B-123	Sequence 123, Appl	373	35	62.5	88	2	US-09-905-243-33	Sequence 33, Appl
301	37	66.1	107	1	US-08-107-669D-26	Sequence 26, Appl	374	35	62.5	106	2	US-08-635-109-8	Sequence 8, Appl
302	37	66.1	107	1	US-08-472-788A-26	Sequence 26, Appl	375	35	62.5	106	2	US-08-844-215-11	Sequence 11, Appl
303	37	66.1	107	1	US-08-472-788A-26	Sequence 26, Appl	376	35	62.5	107	1	US-08-480-434-73	Sequence 73, Appl
304	37	66.1	107	1	US-08-477-531B-26	Sequence 26, Appl	377	35	62.5	107	1	US-08-480-434-73	Sequence 73, Appl
305	37	66.1	107	1	US-08-646-360-123	Sequence 123, Appl	378	35	62.5	107	1	US-08-053-451B-73	Sequence 73, Appl
306	37	66.1	107	1	US-08-082-842A-26	Sequence 26, Appl	379	35	62.5	107	1	US-08-053-451B-174	Sequence 174, Appl
307	37	66.1	107	1	US-08-888-366-14	Sequence 14, Appl	380	35	62.5	108	2	US-09-240-274-41	Sequence 41, Appl
308	37	66.1	107	1	US-08-888-366-20	Sequence 20, Appl	381	35	62.5	108	2	US-09-848-798-41	Sequence 41, Appl
309	37	66.1	107	1	US-08-888-366-26	Sequence 26, Appl	382	35	62.5	108	2	US-10-268-883-12	Sequence 12, Appl
310	37	66.1	107	2	US-09-136-389-123	Sequence 123, Appl	383	35	62.5	109	2	US-07-942-245-1	Sequence 1, Appl
311	37	66.1	107	2	US-09-610-838-123	Sequence 123, Appl	384	35	62.5	109	2	US-09-798-058-4	Sequence 4, Appl
312	37	66.1	107	2	US-09-711-485-123	Sequence 123, Appl	385	35	62.5	129	2	US-08-943-136-2	Sequence 2, Appl
313	37	66.1	107	2	US-08-766-350B-47	Sequence 47, Appl	386	35	62.5	129	2	US-08-973-518-2	Sequence 2, Appl
314	37	66.1	108	2	US-08-726-219A-267	Sequence 267, Appl	387	35	62.5	130	2	US-09-019-441A-6	Sequence 6, Appl
315	37	66.1	108	2	US-09-196-522-267	Sequence 267, Appl	388	35	62.5	131	1	US-10-268-883-11	Sequence 11, Appl
316	37	66.1	109	1	US-08-713-939A-74	Sequence 74, Appl	389	35	62.5	138	1	US-08-480-434-63	Sequence 63, Appl
317	37	66.1	109	2	US-09-036-579-74	Sequence 74, Appl	390	35	62.5	138	1	US-08-053-451B-63	Sequence 63, Appl
318	37	66.1	109	2	US-09-550-374-74	Sequence 74, Appl	391	35	62.5	144	2	US-08-713-273A-4	Sequence 4, Appl
319	37	66.1	109	2	US-09-943-906-74	Sequence 74, Appl	392	35	62.5	148	2	US-09-318-786-25	Sequence 25, Appl
										185	2	US-09-605-703B-2692	Sequence 2692, Ap

393	35	62.5	259	2	US-09-419-788-29	Sequence 29, Appl	466	34	60.7	107	2	US-09-240-274-38	Sequence 38, Appl
394	35	62.5	287	2	US-09-318-786-37	Sequence 37, Appl	467	34	60.7	107	2	US-09-240-274-39	Sequence 39, Appl
395	35	62.5	440	1	US-08-459-100A-2	Sequence 2, Appli	468	34	60.7	107	2	US-09-240-274-40	Sequence 40, Appl
396	35	62.5	440	4	PCT-US94-09589-2	Sequence 2, Appli	469	34	60.7	107	2	US-09-240-274-156	Sequence 156, App
397	35	62.5	1138	2	US-09-590-101A-8	Sequence 10, Appli	470	34	60.7	107	2	US-09-240-274-158	Sequence 158, App
398	35	62.5	1151	2	US-09-590-101A-10	Sequence 10, Appl	471	34	60.7	107	2	US-09-240-274-168	Sequence 168, App
399	35	62.5	1457	2	US-09-436-874-2	Sequence 2, Appli	472	34	60.7	107	2	US-09-240-274-175	Sequence 175, App
400	35	62.5	1457	2	US-09-713-273A-18	Sequence 18, Appl	473	34	60.7	107	2	US-09-240-274-176	Sequence 176, App
401	35	62.5	1469	2	US-09-713-273A-16	Sequence 16, Appl	474	34	60.7	107	2	US-09-247-352-8	Sequence 8, Appli
402	35	62.5	1493	2	US-09-713-273A-20	Sequence 20, Appl	475	34	60.7	107	2	US-09-247-352-12	Sequence 12, Appl
403	34.5	61.6	12	2	US-09-563-222C-38	Sequence 38, Appl	476	34	60.7	107	2	US-09-438-954-3	Sequence 3, Appli
404	34.5	61.6	108	1	US-08-202-047-24	Sequence 24, Appl	477	34	60.7	107	2	US-09-434-870-1	Sequence 1, Appli
405	34.5	61.6	108	2	US-08-964-690-24	Sequence 24, Appl	478	34	60.7	107	2	US-09-848-798-33	Sequence 33, Appl
406	34.5	61.6	109	1	US-08-561-521-42	Sequence 42, Appl	479	34	60.7	107	2	US-09-848-798-37	Sequence 37, Appl
407	34.5	61.6	109	2	US-09-357-710A-21	Sequence 21, Appl	480	34	60.7	107	2	US-09-848-798-38	Sequence 38, Appl
408	34.5	61.6	109	2	US-09-357-707-21	Sequence 21, Appl	481	34	60.7	107	2	US-09-848-798-39	Sequence 39, Appl
409	34.5	61.6	109	2	US-09-357-708-21	Sequence 21, Appl	482	34	60.7	107	2	US-09-848-798-40	Sequence 40, Appl
410	34.5	61.6	109	4	PCT-US95-01219-42	Sequence 42, Appl	483	34	60.7	107	2	US-09-848-798-156	Sequence 156, App
411	34	60.7	11	2	US-09-192-854-6	Sequence 6, Appli	484	34	60.7	107	2	US-09-848-798-158	Sequence 158, App
412	34	60.7	11	2	US-09-802-083-10	Sequence 10, Appl	485	34	60.7	107	2	US-09-848-798-168	Sequence 168, App
413	34	60.7	11	2	US-09-511-939-10	Sequence 10, Appl	486	34	60.7	107	2	US-09-848-798-175	Sequence 175, App
414	34	60.7	11	2	US-09-511-939-16	Sequence 16, Appl	487	34	60.7	107	2	US-09-848-798-176	Sequence 176, App
415	34	60.7	11	2	US-09-511-939-22	Sequence 22, Appl	488	34	60.7	107	4	PCT-US95-08743-105	Sequence 105, App
416	34	60.7	11	2	US-09-511-939-28	Sequence 28, Appl	489	34	60.7	108	1	US-08-379-057-29	Sequence 29, Appl
417	34	60.7	11	2	US-09-511-939-34	Sequence 34, Appl	490	34	60.7	108	2	US-08-983-607-29	Sequence 29, Appl
418	34	60.7	11	2	US-09-511-939-40	Sequence 40, Appl	491	34	60.7	108	2	US-08-983-607-37	Sequence 37, Appl
419	34	60.7	11	2	US-09-511-939-46	Sequence 46, Appl	492	34	60.7	108	2	US-09-240-274-32	Sequence 32, Appl
420	34	60.7	11	2	US-09-511-939-52	Sequence 52, Appl	493	34	60.7	108	2	US-09-240-274-43	Sequence 43, Appl
421	34	60.7	11	2	US-09-511-939-64	Sequence 64, Appl	494	34	60.7	108	2	US-09-240-274-163	Sequence 163, App
422	34	60.7	11	2	US-09-511-939-100	Sequence 100, App	495	34	60.7	108	2	US-09-240-274-167	Sequence 167, App
423	34	60.7	11	2	US-09-511-939-106	Sequence 106, App	496	34	60.7	108	2	US-09-247-352-1	Sequence 1, Appli
424	34	60.7	11	2	US-09-511-939-112	Sequence 112, App	497	34	60.7	108	2	US-09-466-635-1	Sequence 1, Appli
425	34	60.7	11	2	US-09-511-939-118	Sequence 118, App	498	34	60.7	108	2	US-09-848-798-32	Sequence 32, Appl
426	34	60.7	11	2	US-09-511-939-124	Sequence 124, App	499	34	60.7	108	2	US-09-848-798-43	Sequence 43, Appl
427	34	60.7	11	2	US-09-511-939-136	Sequence 136, App	500	34	60.7	108	2	US-09-848-798-163	Sequence 163, App
428	34	60.7	11	2	US-09-511-939-154	Sequence 154, App	501	34	60.7	108	2	US-09-848-798-167	Sequence 167, App
429	34	60.7	11	2	US-09-511-939-160	Sequence 160, App	502	34	60.7	108	2	US-09-157-370-3	Sequence 3, Appli
430	34	60.7	11	2	US-09-511-939-166	Sequence 166, App	503	34	60.7	109	2	US-09-802-083-4	Sequence 4, Appli
431	34	60.7	11	2	US-09-511-939-172	Sequence 172, App	504	34	60.7	109	2	US-08-339-582-4	Sequence 4, Appli
432	34	60.7	11	2	US-09-511-939-178	Sequence 178, App	505	34	60.7	128	1	US-08-339-582-4	Sequence 23, Appl
433	34	60.7	11	2	US-09-511-939-202	Sequence 202, App	506	34	60.7	134	2	US-09-472-087-23	Sequence 97, Appl
434	34	60.7	11	2	US-09-511-939-208	Sequence 208, App	507	34	60.7	134	2	US-09-472-087-97	Sequence 24, Appl
435	34	60.7	11	2	US-09-511-939-226	Sequence 226, App	508	34	60.7	137	2	US-09-582-337-24	Sequence 22, Appl
436	34	60.7	11	2	US-09-511-939-232	Sequence 232, App	509	34	60.7	139	2	US-09-472-087-22	Sequence 22, Appl
437	34	60.7	11	2	US-09-511-939-244	Sequence 244, App	510	34	60.7	139	2	US-09-472-087-96	Sequence 96, Appl
438	34	60.7	11	2	US-09-511-939-250	Sequence 250, App	511	34	60.7	145	2	US-09-096-244-2	Sequence 2, Appli
439	34	60.7	11	2	US-09-511-939-256	Sequence 256, App	512	34	60.7	145	2	US-08-766-350B-2	Sequence 2, Appli
440	34	60.7	11	2	US-09-511-939-280	Sequence 280, App	513	34	60.7	145	2	US-08-766-350B-58	Sequence 58, Appl
441	34	60.7	11	2	US-09-511-939-292	Sequence 292, App	514	34	60.7	172	2	US-09-583-110-4903	Sequence 4903, Ap
442	34	60.7	11	2	US-09-511-939-304	Sequence 304, App	515	34	60.7	172	2	US-09-107-433-4439	Sequence 4439, Ap
443	34	60.7	76	2	US-08-851-362D-21	Sequence 21, Appl	516	34	60.7	214	2	US-09-247-352-4	Sequence 4, Appli
444	34	60.7	95	2	US-09-472-087-94	Sequence 94, Appl	517	34	60.7	214	2	US-09-466-635-4	Sequence 4, Appli
445	34	60.7	95	2	US-10-194-975-54	Sequence 54, Appl	518	34	60.7	224	2	US-09-456-090A-48	Sequence 48, Appl
446	34	60.7	95	2	US-10-194-975-55	Sequence 55, Appl	519	34	60.7	224	2	US-09-453-234-48	Sequence 48, Appl
447	34	60.7	95	2	US-10-330-613A-43	Sequence 43, Appl	520	34	60.7	224	2	US-09-192-854-2	Sequence 2, Appli
448	34	60.7	96	1	US-08-737-560A-9	Sequence 9, Appli	521	34	60.7	240	2	US-09-511-939-2	Sequence 2, Appli
449	34	60.7	103	2	US-09-240-274-42	Sequence 42, Appl	522	34	60.7	240	2	US-09-489-039A-13653	Sequence 13653, A
450	34	60.7	103	2	US-09-848-798-42	Sequence 42, Appl	523	34	60.7	342	2	US-09-646-028-16	Sequence 16, Appl
451	34	60.7	105	2	US-08-851-362D-36	Sequence 36, Appl	524	34	60.7	359	2	US-09-646-028-13	Sequence 13, Appl
452	34	60.7	106	1	US-08-276-852-101	Sequence 101, App	525	34	60.7	361	2	US-09-646-028-15	Sequence 15, Appl
453	34	60.7	106	1	US-08-899-575-101	Sequence 101, App	526	34	60.7	374	2	US-09-248-796A-18285	Sequence 18285, A
454	34	60.7	106	1	US-08-899-575-101	Sequence 101, App	527	34	60.7	679	2	US-09-107-532A-5429	Sequence 5429, Ap
455	34	60.7	106	1	US-08-899-575-101	Sequence 101, App	528	34	60.7	795	2	US-09-192-854-56	Sequence 56, Appl
456	34	60.7	107	1	US-08-276-852-104	Sequence 104, App	529	33	58.9	11	2	US-09-511-939-88	Sequence 88, Appl
457	34	60.7	107	1	US-08-276-852-105	Sequence 105, App	530	33	58.9	11	2	US-08-142-551B-114	Sequence 114, App
458	34	60.7	107	1	US-08-899-575-104	Sequence 104, App	531	33	58.9	35	1	US-08-478-039-87	Sequence 87, Appl
459	34	60.7	107	1	US-08-899-575-105	Sequence 105, App	532	33	58.9	49	1	US-08-476-349A-87	Sequence 87, Appl
460	34	60.7	107	1	US-08-899-575-104	Sequence 104, App	533	33	58.9	49	1	US-09-252-991A-22225	Sequence 22225, A
461	34	60.7	107	1	US-08-899-575-105	Sequence 105, App	534	33	58.9	89	2	US-08-713-939A-72	Sequence 72, Appl
462	34	60.7	107	1	US-08-888-366-22	Sequence 22, Appl	535	33	58.9	95	1	US-09-036-579-72	Sequence 72, Appl
463	34	60.7	107	1	US-08-851-362D-32	Sequence 32, Appl	536	33	58.9	95	2	US-09-550-374-72	Sequence 72, Appl
464	34	60.7	107	2	US-09-240-274-33	Sequence 33, Appl	537	33	58.9	95	2	US-09-943-906-72	Sequence 72, Appl
465	34	60.7	107	2	US-09-240-274-37	Sequence 37, Appl	538	33	58.9	95	2		

539	33	58.9	95	2	US-10-435-602-72	Sequence 72, Appl	612	33	58.9	255	2	US-09-489-039A-13931	Sequence 13931, A
540	33	58.9	95	2	US-10-194-975-60	Sequence 60, Appl	613	33	58.9	264	2	US-09-543-681A-4818	Sequence 4818, Ap
541	33	58.9	95	2	US-10-194-975-67	Sequence 67, Appl	614	33	58.9	317	2	US-08-996-139-13	Sequence 13, Appl
542	33	58.9	95	2	US-10-194-975-69	Sequence 69, Appl	615	33	58.9	317	2	US-08-995-659-13	Sequence 13, Appl
543	33	58.9	95	2	US-10-194-975-86	Sequence 86, Appl	616	33	58.9	317	2	US-09-215-649A-13	Sequence 13, Appl
544	33	58.9	100	2	US-09-899-896-4	Sequence 4, Appl	617	33	58.9	317	2	US-09-052-521C-4	Sequence 4, Appl
545	33	58.9	104	1	US-08-276-852-106	Sequence 106, App	618	33	58.9	317	2	US-09-577-800-13	Sequence 13, Appl
546	33	58.9	104	1	US-08-899-575-106	Sequence 106, App	619	33	58.9	317	2	US-09-577-800-13	Sequence 13, Appl
547	33	58.9	104	1	US-08-899-575-106	Sequence 106, App	620	33	58.9	317	2	US-09-466-496-13	Sequence 13, Appl
548	33	58.9	104	4	PCT-US95-08743-106	Sequence 106, App	621	33	58.9	317	2	US-09-871-856-13	Sequence 13, Appl
549	33	58.9	107	1	US-08-107-669D-14	Sequence 14, Appl	622	33	58.9	317	2	US-09-871-291-13	Sequence 13, Appl
550	33	58.9	107	1	US-08-472-788A-14	Sequence 14, Appl	623	33	58.9	317	2	US-09-396-937-2	Sequence 2, Appl
551	33	58.9	107	1	US-08-472-788A-14	Sequence 14, Appl	624	33	58.9	317	2	US-09-877-650-13	Sequence 13, Appl
552	33	58.9	107	1	US-08-652-558-2	Sequence 2, Appl	625	33	58.9	317	2	US-09-865-363-13	Sequence 13, Appl
553	33	58.9	107	1	US-08-652-558-35	Sequence 35, Appl	626	33	58.9	317	2	US-09-688-459-13	Sequence 13, Appl
554	33	58.9	107	1	US-08-824-842A-14	Sequence 14, Appl	627	33	58.9	317	2	US-09-957-944-6	Sequence 6, Appl
555	33	58.9	107	1	US-09-254-189-1	Sequence 1, Appl	628	33	58.9	327	2	US-09-513-505-14	Sequence 14, Appl
556	33	58.9	107	2	US-09-240-274-44	Sequence 44, Appl	629	33	58.9	385	1	US-08-516-801-2	Sequence 2, Appl
557	33	58.9	107	2	US-09-240-274-162	Sequence 162, App	630	33	58.9	385	2	US-08-248-355-2	Sequence 2, Appl
558	33	58.9	107	2	US-09-438-954-1	Sequence 1, Appl	631	33	58.9	385	2	US-09-167-206-16	Sequence 16, Appl
559	33	58.9	107	2	US-09-438-954-38	Sequence 38, Appl	632	33	58.9	385	4	PCT-US95-06683-2	Sequence 2, Appl
560	33	58.9	107	2	US-09-438-954-40	Sequence 40, Appl	633	33	58.9	399	2	US-09-949-016-10810	Sequence 10810, A
561	33	58.9	107	2	US-09-434-870-2	Sequence 2, Appl	634	33	58.9	452	2	US-08-809-802-12	Sequence 12, Appl
562	33	58.9	107	2	US-09-848-798-44	Sequence 44, Appl	635	33	58.9	455	2	US-09-906-408A-8	Sequence 8, Appl
563	33	58.9	107	2	US-09-848-798-162	Sequence 162, App	636	33	58.9	496	1	US-08-328-256-12	Sequence 12, Appl
564	33	58.9	108	1	US-08-378-939-16	Sequence 16, Appl	637	33	58.9	507	2	US-09-248-796A-19164	Sequence 19164, A
565	33	58.9	108	1	US-08-378-939-20	Sequence 20, Appl	638	33	58.9	544	2	US-09-710-279-38	Sequence 38, Appl
566	33	58.9	108	1	US-08-378-939-24	Sequence 24, Appl	639	33	58.9	557	1	US-08-328-256-10	Sequence 10, Appl
567	33	58.9	108	1	US-08-737-560A-11	Sequence 11, Appl	640	33	58.9	557	1	US-08-471-454-2	Sequence 2, Appl
568	33	58.9	108	2	US-09-240-274-181	Sequence 181, App	641	33	58.9	557	1	US-08-466-974-2	Sequence 2, Appl
569	33	58.9	108	2	US-09-157-370-4	Sequence 4, Appl	642	33	58.9	557	1	US-08-471-453-2	Sequence 2, Appl
570	33	58.9	108	2	US-09-848-798-181	Sequence 181, App	643	33	58.9	557	1	US-08-307-588-4	Sequence 4, Appl
571	33	58.9	109	1	US-08-713-939A-73	Sequence 73, Appl	644	33	58.9	557	2	US-07-971-834-4	Sequence 4, Appl
572	33	58.9	109	2	US-09-036-579-73	Sequence 73, Appl	645	33	58.9	557	2	US-09-240-675-4	Sequence 4, Appl
573	33	58.9	109	2	US-09-025-769B-28	Sequence 28, Appl	646	33	58.9	557	2	US-09-949-016-5972	Sequence 5972, Ap
574	33	58.9	109	2	US-09-025-769B-43	Sequence 43, Appl	647	33	58.9	575	2	US-09-949-016-8640	Sequence 8640, Ap
575	33	58.9	109	2	US-09-550-374-73	Sequence 73, Appl	648	33	58.9	616	1	US-08-749-882A-2	Sequence 2, Appl
576	33	58.9	109	2	US-09-943-906-73	Sequence 73, Appl	649	33	58.9	616	1	US-08-539-134-2	Sequence 2, Appl
577	33	58.9	109	2	US-09-490-070A-28	Sequence 28, Appl	650	33	58.9	616	1	US-08-991-531-2	Sequence 2, Appl
578	33	58.9	109	2	US-09-490-070A-43	Sequence 43, Appl	651	33	58.9	616	1	US-09-032-315-9	Sequence 9, Appl
579	33	58.9	109	2	US-09-490-153-28	Sequence 28, Appl	652	33	58.9	616	1	US-08-993-318A-9	Sequence 9, Appl
580	33	58.9	109	2	US-09-490-153-43	Sequence 43, Appl	653	33	58.9	616	2	US-09-028-887-2	Sequence 2, Appl
581	33	58.9	109	2	US-09-490-324-28	Sequence 28, Appl	654	33	58.9	616	2	US-09-399-886-9	Sequence 9, Appl
582	33	58.9	109	2	US-09-490-324-43	Sequence 43, Appl	655	33	58.9	616	2	US-09-396-260-9	Sequence 9, Appl
583	33	58.9	109	2	US-10-435-602-73	Sequence 73, Appl	656	33	58.9	616	2	US-09-518-901-2	Sequence 2, Appl
584	33	58.9	113	2	US-10-114-716A-48	Sequence 48, Appl	657	33	58.9	616	2	US-09-576-281-9	Sequence 9, Appl
585	33	58.9	115	1	US-08-053-131-179	Sequence 179, App	658	33	58.9	616	4	PCT-US95-06816-2	Sequence 2, Appl
586	33	58.9	115	1	US-08-096-762-179	Sequence 179, App	659	33	58.9	1114	2	US-08-811-583-2	Sequence 3, Appl
587	33	58.9	115	2	US-09-042-353-42	Sequence 42, Appl	660	33	58.9	1188	2	US-10-011-146-3	Sequence 3, Appl
588	33	58.9	115	2	US-08-758-417A-307	Sequence 307, App	661	33	58.9	1234	4	PCT-US95-13041-15	Sequence 15, Appl
589	33	58.9	139	2	US-09-472-087-16	Sequence 16, Appl	662	33	58.9	1282	2	US-09-134-000C-5785	Sequence 5785, Ap
590	33	58.9	139	2	US-09-472-087-90	Sequence 90, Appl	663	33	58.9	11	1	US-08-182-067-4	Sequence 4, Appl
591	33	58.9	142	2	US-09-472-087-91	Sequence 91, Appl	664	33	58.9	11	1	US-08-465-313-4	Sequence 4, Appl
592	33	58.9	146	2	US-09-472-087-21	Sequence 21, Appl	665	33	58.9	11	1	US-09-809-739-2	Sequence 2, Appl
593	33	58.9	146	2	US-09-472-087-93	Sequence 93, Appl	666	33	58.9	11	2	US-09-378-967-4	Sequence 4, Appl
594	33	58.9	152	2	US-09-472-087-18	Sequence 18, Appl	667	33	58.9	11	2	US-09-192-854-153	Sequence 153, App
595	33	58.9	152	2	US-09-472-087-95	Sequence 95, Appl	668	33	58.9	11	2	US-09-511-939-268	Sequence 268, App
596	33	58.9	162	2	US-09-583-110-3375	Sequence 3375, Ap	669	33	58.9	11	2	US-08-581-918A-39	Sequence 39, Appl
597	33	58.9	164	2	US-09-107-433-4840	Sequence 4840, Ap	670	33	58.9	85	2	US-08-346-147B-39	Sequence 39, Appl
598	33	58.9	215	1	US-08-737-129A-8	Sequence 8, Appl	671	33	58.9	85	2	US-08-497-214D-39	Sequence 39, Appl
599	33	58.9	218	2	US-09-328-352-4680	Sequence 4680, Ap	672	33	58.9	88	2	US-09-905-243-32	Sequence 32, Appl
600	33	58.9	224	2	US-09-456-090A-46	Sequence 46, Appl	673	33	58.9	95	2	US-10-194-975-87	Sequence 87, Appl
601	33	58.9	224	2	US-09-456-090A-82	Sequence 82, Appl	674	33	58.9	105	2	US-08-851-362D-30	Sequence 30, Appl
602	33	58.9	224	2	US-09-456-090A-84	Sequence 84, Appl	675	33	58.9	105	2	US-08-635-109-6	Sequence 6, Appl
603	33	58.9	224	2	US-09-456-090A-88	Sequence 88, Appl	676	33	58.9	105	2	US-08-844-215-9	Sequence 9, Appl
604	33	58.9	224	2	US-09-456-090A-90	Sequence 90, Appl	677	33	58.9	107	1	US-08-300-386A-66	Sequence 66, Appl
605	33	58.9	224	2	US-09-453-234-46	Sequence 46, Appl	678	33	58.9	107	1	US-08-931-645-66	Sequence 66, Appl
606	33	58.9	224	2	US-09-453-234-82	Sequence 82, Appl	679	33	58.9	107	4	PCT-US95-11235-66	Sequence 16, Appl
607	33	58.9	224	2	US-09-453-234-84	Sequence 84, Appl	680	33	58.9	108	1	US-08-378-939-18	Sequence 18, Appl
608	33	58.9	224	2	US-09-453-234-88	Sequence 88, Appl	681	33	58.9	114	1	US-08-561-521-43	Sequence 43, Appl
609	33	58.9	224	2	US-09-453-234-90	Sequence 90, Appl	682	33	58.9	114	4	PCT-US95-01219-43	Sequence 43, Appl
610	33	58.9	234	2	US-09-472-087-17	Sequence 17, Appl	683	33	58.9	115	1	US-08-053-131-181	Sequence 181, App
611	33	58.9	234	2	US-09-472-087-69	Sequence 69, Appl	684	33	58.9				

685	32	57.1	115	1	US-08-096-762-181	Sequence 181, App	758	31	55.4	11	2	US-09-647-468-136	Sequence 136, App
686	32	57.1	115	2	US-09-042-353-44	Sequence 44, Appl	759	31	55.4	11	2	US-09-192-854-170	Sequence 170, App
687	32	57.1	115	3	US-08-758-417A-309	Sequence 309, App	760	31	55.4	11	2	US-09-511-939-298	Sequence 298, App
688	32	57.1	125	1	US-08-534-975-5	Sequence 5, Appl	761	31	55.4	13	2	US-09-339-922A-82	Sequence 82, Appl
689	32	57.1	125	1	US-08-039-198B-12	Sequence 12, Appl	762	31	55.4	13	2	US-09-016-061-82	Sequence 82, Appl
690	32	57.1	125	1	US-08-954-470-5	Sequence 5, Appl	763	31	55.4	30	2	US-08-525-539A-9	Sequence 9, Appl
691	32	57.1	125	1	US-08-306-511A-6	Sequence 6, Appl	764	31	55.4	56	1	US-08-162-102C-40	Sequence 40, Appl
692	32	57.1	125	1	US-08-893-274-6	Sequence 6, Appl	765	31	55.4	85	1	US-08-303-569B-8	Sequence 8, Appl
693	32	57.1	125	1	US-08-182-067-2	Sequence 2, Appl	766	31	55.4	85	2	US-09-795-515-8	Sequence 8, Appl
694	32	57.1	125	1	US-08-465-313-2	Sequence 2, Appl	767	31	55.4	88	2	US-09-805-243-30	Sequence 30, Appl
695	32	57.1	125	1	US-08-581-918A-6	Sequence 6, Appl	768	31	55.4	90	2	US-09-199-149-15	Sequence 15, Appl
696	32	57.1	125	1	US-09-129-855A-5	Sequence 5, Appl	769	31	55.4	95	2	US-10-194-975-91	Sequence 91, Appl
697	32	57.1	125	2	US-09-247-154-5	Sequence 5, Appl	770	31	55.4	95	2	US-10-194-975-92	Sequence 92, Appl
698	32	57.1	125	2	US-08-346-147B-6	Sequence 6, Appl	771	31	55.4	96	2	US-09-472-087-99	Sequence 99, Appl
699	32	57.1	125	2	US-08-822-936-6	Sequence 6, Appl	772	31	55.4	98	2	US-09-534-717-669	Sequence 669, App
700	32	57.1	125	2	US-08-497-214D-6	Sequence 6, Appl	773	31	55.4	99	2	US-09-899-896-6	Sequence 6, Appl
701	32	57.1	125	2	US-09-480-718-5	Sequence 5, Appl	774	31	55.4	99	2	US-09-899-896-10	Sequence 10, Appl
702	32	57.1	125	2	US-09-610-833-5	Sequence 5, Appl	775	31	55.4	103	2	US-09-460-384-35	Sequence 35, Appl
703	32	57.1	125	2	US-09-016-750C-6	Sequence 6, Appl	776	31	55.4	106	2	US-09-740-002-22	Sequence 22, Appl
704	32	57.1	125	2	US-09-129-855A-5	Sequence 5, Appl	777	31	55.4	107	1	US-07-634-278-50	Sequence 50, Appl
705	32	57.1	125	2	US-09-809-739-1	Sequence 1, Appl	778	31	55.4	107	1	US-07-634-278-51	Sequence 51, Appl
706	32	57.1	125	2	US-09-378-967-2	Sequence 2, Appl	779	31	55.4	107	1	US-08-477-728-50	Sequence 50, Appl
707	32	57.1	125	4	PCT-US95-04636-6	Sequence 6, Appl	780	31	55.4	107	1	US-08-477-728-51	Sequence 51, Appl
708	32	57.1	127	2	US-09-809-739-10	Sequence 10, Appl	781	31	55.4	107	1	US-08-474-040-50	Sequence 50, Appl
709	32	57.1	129	2	US-09-583-110-3242	Sequence 3242, Ap	782	31	55.4	107	1	US-08-474-040-51	Sequence 51, Appl
710	32	57.1	129	2	US-09-107-433-3947	Sequence 3947, Ap	783	31	55.4	107	1	US-08-487-200-50	Sequence 50, Appl
711	32	57.1	129	2	US-09-769-787-137	Sequence 137, App	784	31	55.4	107	1	US-08-487-200-51	Sequence 51, Appl
712	32	57.1	157	2	US-09-252-991A-19807	Sequence 19807, A	785	31	55.4	107	1	US-08-488-113B-149	Sequence 149, App
713	32	57.1	167	1	US-08-627-610-6	Sequence 6, Appl	786	31	55.4	107	1	US-08-477-669B-13	Sequence 13, Appl
714	32	57.1	168	1	US-08-508-735-46	Sequence 46, Appl	787	31	55.4	107	1	US-08-107-669D-13	Sequence 13, Appl
715	32	57.1	168	2	US-09-201-139-46	Sequence 46, Appl	788	31	55.4	107	1	US-08-472-788A-13	Sequence 13, Appl
716	32	57.1	181	2	US-09-538-092-792	Sequence 792, App	789	31	55.4	107	1	US-08-477-531B-13	Sequence 13, Appl
717	32	57.1	184	2	US-09-248-796A-15913	Sequence 15913, A	790	31	55.4	107	1	US-08-646-360-149	Sequence 149, App
718	32	57.1	224	2	US-09-456-090A-36	Sequence 36, Appl	791	31	55.4	107	1	US-08-561-521-6	Sequence 6, Appl
719	32	57.1	224	2	US-09-453-234-36	Sequence 36, Appl	792	31	55.4	107	1	US-08-561-521-8	Sequence 8, Appl
720	32	57.1	241	1	US-08-235-838-11	Sequence 11, Appl	793	31	55.4	107	1	US-08-652-558-34	Sequence 34, Appl
721	32	57.1	241	1	US-08-465-473B-11	Sequence 11, Appl	794	31	55.4	107	1	US-08-652-558-47	Sequence 47, Appl
722	32	57.1	243	2	US-09-248-796A-16273	Sequence 16273, A	795	31	55.4	107	1	US-08-082-842A-13	Sequence 13, Appl
723	32	57.1	248	2	US-09-710-279-464	Sequence 464, App	796	31	55.4	107	1	US-08-318-157B-6	Sequence 6, Appl
724	32	57.1	318	2	US-09-489-039A-8369	Sequence 8369, App	797	31	55.4	107	2	US-08-933-983-75	Sequence 75, Appl
725	32	57.1	334	2	US-09-270-767-38437	Sequence 38437, A	798	31	55.4	107	2	US-08-933-983-76	Sequence 76, Appl
726	32	57.1	334	2	US-09-270-767-53654	Sequence 53654, A	799	31	55.4	107	2	US-08-933-983-77	Sequence 77, Appl
727	32	57.1	388	2	US-09-252-991A-21907	Sequence 21907, A	800	31	55.4	107	2	US-08-839-765-149	Sequence 149, App
728	32	57.1	435	2	US-09-328-352-5037	Sequence 5037, Ap	801	31	55.4	107	2	US-09-136-389-149	Sequence 149, App
729	32	57.1	452	2	US-08-531-468-22	Sequence 22, Appl	802	31	55.4	107	2	US-08-484-537-50	Sequence 50, Appl
730	32	57.1	452	4	PCT-US94-06430-22	Sequence 22, Appl	803	31	55.4	107	2	US-08-484-537-51	Sequence 51, Appl
731	32	57.1	462	2	US-09-543-681A-5241	Sequence 5241, Ap	804	31	55.4	107	2	US-09-240-274-36	Sequence 36, Appl
732	32	57.1	508	2	US-09-489-039A-7887	Sequence 7887, Ap	805	31	55.4	107	2	US-09-240-274-172	Sequence 172, App
733	32	57.1	512	2	US-09-015-296-3	Sequence 3, Appl	806	31	55.4	107	2	US-09-240-274-174	Sequence 174, App
734	32	57.1	528	2	US-09-593-722-3	Sequence 3, Appl	807	31	55.4	107	2	US-09-025-203-15	Sequence 15, Appl
735	32	57.1	528	2	US-09-489-039A-13841	Sequence 13841, A	808	31	55.4	107	2	US-09-610-838-149	Sequence 149, App
736	32	57.1	533	2	US-09-248-796A-17526	Sequence 17526, A	809	31	55.4	107	2	US-09-711-485-149	Sequence 149, App
737	32	57.1	587	2	US-10-104-047-3783	Sequence 3783, Ap	810	31	55.4	107	2	US-09-253-794-6	Sequence 6, Appl
738	32	57.1	637	1	US-08-235-838-16	Sequence 16, Appl	811	31	55.4	107	2	US-09-647-468-93	Sequence 93, Appl
739	32	57.1	637	1	US-08-465-473B-16	Sequence 16, Appl	812	31	55.4	107	2	US-09-647-468-99	Sequence 99, Appl
740	32	57.1	687	2	US-09-489-039A-9290	Sequence 9290, Ap	813	31	55.4	107	2	US-09-647-468-101	Sequence 101, App
741	32	57.1	704	2	US-09-328-352-5537	Sequence 5537, Ap	814	31	55.4	107	2	US-09-647-468-107	Sequence 107, App
742	32	57.1	814	1	US-08-233-788A-42	Sequence 42, Appl	815	31	55.4	107	2	US-09-647-468-109	Sequence 109, App
743	32	57.1	902	1	US-08-701-846-2	Sequence 2, Appl	816	31	55.4	107	2	US-09-647-468-148	Sequence 148, App
744	32	57.1	913	1	US-08-487-890A-5	Sequence 5, Appl	817	31	55.4	107	2	US-09-999-021-15	Sequence 15, Appl
745	32	57.1	913	1	US-08-478-435-5	Sequence 5, Appl	818	31	55.4	107	2	US-09-999-025-15	Sequence 15, Appl
746	32	57.1	913	1	US-08-337-483-5	Sequence 5, Appl	819	31	55.4	107	2	US-10-040-997-15	Sequence 15, Appl
747	32	57.1	913	1	US-08-478-373-5	Sequence 5, Appl	820	31	55.4	107	2	US-09-999-040-15	Sequence 15, Appl
748	32	57.1	913	2	US-08-474-671-5	Sequence 5, Appl	821	31	55.4	107	2	US-09-998-817-15	Sequence 15, Appl
749	32	57.1	913	2	US-08-483-577A-5	Sequence 5, Appl	822	31	55.4	107	2	US-09-848-798-36	Sequence 36, Appl
750	32	57.1	913	2	US-08-897-438-5	Sequence 5, Appl	823	31	55.4	107	2	US-09-848-798-172	Sequence 172, App
751	32	57.1	913	2	US-08-637-654-5	Sequence 5, Appl	824	31	55.4	107	4	PCT-US94-07659-8	Sequence 8, Appl
752	32	57.1	913	2	US-08-649-518-5	Sequence 5, Appl	825	31	55.4	107	4	PCT-US95-01219-6	Sequence 6, Appl
753	31.5	56.2	551	2	US-09-248-796A-23413	Sequence 23413, A	826	31	55.4	107	4	PCT-US95-01219-8	Sequence 8, Appl
754	31	55.4	11	1	US-07-942-245-495	Sequence 495, App	827	31	55.4	108	1	US-08-162-102C-25	Sequence 25, Appl
755	31	55.4	11	1	US-08-034-253-16	Sequence 16, Appl	828	31	55.4	108	1	US-08-070-116A-7	Sequence 7, Appl
756	31	55.4	111	2	US-09-339-922A-110	Sequence 110, App	829	31	55.4	108	1	US-08-116-247-9	Sequence 9, Appl
757	31	55.4	111	2	US-09-649-063-16	Sequence 16, Appl	830	31	55.4	108	1		

831	31	55.4	108	1	US-08-602-725-29	Sequence 29, Appl	904	31	55.4	237	2	US-10-194-975-109	Sequence 109, App
832	31	55.4	108	2	US-09-240-274-31	Sequence 31, Appl	905	31	55.4	239	1	US-08-860-174A-2	Sequence 2, Appli
833	31	55.4	108	2	US-09-240-274-161	Sequence 161, App	906	31	55.4	241	2	US-09-554-765-13	Sequence 13, Appl
834	31	55.4	108	2	US-09-240-274-177	Sequence 177, App	907	31	55.4	243	1	US-08-230-843-4	Sequence 4, Appli
835	31	55.4	108	2	US-08-557-050-7	Sequence 7, Appli	908	31	55.4	243	1	US-08-636-936-4	Sequence 4, Appli
836	31	55.4	108	2	US-10-092-246-17	Sequence 17, Appl	909	31	55.4	243	1	US-09-649-063-23	Sequence 23, Appl
837	31	55.4	108	2	US-08-407-620A-32	Sequence 32, Appl	910	31	55.4	248	2	US-09-270-767-33633	Sequence 33633, A
838	31	55.4	108	2	US-09-649-063-12	Sequence 12, Appl	911	31	55.4	252	2	US-09-270-767-48850	Sequence 48850, A
839	31	55.4	108	2	US-08-454-899G-100	Sequence 100, App	912	31	55.4	252	2	US-09-248-796A-15819	Sequence 15819, A
840	31	55.4	108	2	US-08-920-100B-25	Sequence 25, Appl	913	31	55.4	262	2	US-09-726-219A-183	Sequence 183, App
841	31	55.4	108	2	US-09-348-224-9	Sequence 9, Appli	914	31	55.4	272	2	US-09-196-522-183	Sequence 183, App
842	31	55.4	108	2	US-09-726-219A-266	Sequence 266, App	915	31	55.4	274	2	US-09-248-796A-20766	Sequence 20766, A
843	31	55.4	108	2	US-10-096-246A-17	Sequence 17, Appl	916	31	55.4	280	2	US-09-248-796A-20765	Sequence 20765, A
844	31	55.4	108	2	US-09-848-798-31	Sequence 31, Appl	917	31	55.4	296	2	US-09-903-814A-10	Sequence 10, Appl
845	31	55.4	108	2	US-09-848-798-161	Sequence 161, App	918	31	55.4	296	2	US-10-723-061-10	Sequence 10, Appl
846	31	55.4	108	2	US-09-848-798-177	Sequence 177, App	919	31	55.4	297	2	US-09-252-991A-29778	Sequence 29778, A
847	31	55.4	108	2	US-10-194-975-94	Sequence 94, Appl	920	31	55.4	303	2	US-09-543-681A-7924	Sequence 7924, Ap
848	31	55.4	108	2	US-09-196-522-266	Sequence 266, App	921	31	55.4	306	2	US-09-252-991A-17153	Sequence 17153, A
849	31	55.4	108	4	PCT-US93-08786-25	Sequence 25, Appl	922	31	55.4	310	2	US-09-632-947B-8	Sequence 8, Appli
850	31	55.4	109	1	US-07-942-245-2	Sequence 2, Appli	923	31	55.4	340	2	US-09-543-681A-5778	Sequence 5778, Ap
851	31	55.4	109	2	US-08-875-674A-2	Sequence 2, Appli	924	31	55.4	341	1	US-08-190-802A-45	Sequence 45, Appl
852	31	55.4	109	2	US-08-875-674A-4	Sequence 4, Appli	925	31	55.4	341	2	US-08-477-346-45	Sequence 45, Appl
853	31	55.4	109	2	US-09-802-083-3	Sequence 3, Appli	926	31	55.4	341	2	US-08-473-089-45	Sequence 45, Appl
854	31	55.4	110	2	US-09-440-781-95	Sequence 95, Appl	927	31	55.4	341	2	US-08-487-072A-45	Sequence 45, Appl
855	31	55.4	110	2	US-08-908-469-109	Sequence 109, App	928	31	55.4	395	2	US-09-489-039A-12338	Sequence 12338, A
856	31	55.4	110	2	US-08-908-469-111	Sequence 111, App	929	31	55.4	410	2	US-09-205-448-1	Sequence 1, Appli
857	31	55.4	110	2	US-08-908-469-113	Sequence 113, App	930	31	55.4	413	2	US-09-248-796A-19337	Sequence 19337, A
858	31	55.4	110	2	US-08-908-469-115	Sequence 115, App	931	31	55.4	420	2	US-09-252-991A-31994	Sequence 31994, A
859	31	55.4	113	1	US-08-353-372A-38	Sequence 38, Appl	932	31	55.4	424	2	US-09-489-039A-8695	Sequence 8695, Ap
860	31	55.4	113	2	US-08-057-430A-28	Sequence 28, Appl	933	31	55.4	438	1	US-07-923-095-2	Sequence 2, Appli
861	31	55.4	113	2	US-09-902-540-15055	Sequence 15055, A	934	31	55.4	438	1	US-08-223-511-2	Sequence 2, Appli
862	31	55.4	121	2	US-08-579-378A-7	Sequence 7, Appli	935	31	55.4	438	1	US-08-314-979-2	Sequence 2, Appli
863	31	55.4	121	4	PCT-US93-11612-7	Sequence 7, Appli	936	31	55.4	438	1	US-08-436-716-2	Sequence 2, Appli
864	31	55.4	121	4	PCT-US93-11612-8	Sequence 8, Appli	937	31	55.4	450	2	US-09-907-794A-320	Sequence 320, App
865	31	55.4	121	4	PCT-US93-11612-8	Sequence 8, Appli	938	31	55.4	450	2	US-09-905-125A-320	Sequence 320, App
866	31	55.4	126	2	US-08-454-895G-17	Sequence 17, Appl	939	31	55.4	450	2	US-09-902-775A-320	Sequence 320, App
867	31	55.4	127	2	US-08-933-983-5	Sequence 5, Appli	940	31	55.4	450	2	US-09-906-700-320	Sequence 320, App
868	31	55.4	127	2	US-08-933-983-7	Sequence 7, Appli	941	31	55.4	450	2	US-09-904-620A-320	Sequence 320, App
869	31	55.4	127	2	US-08-933-983-9	Sequence 9, Appli	942	31	55.4	450	2	US-09-903-603A-320	Sequence 320, App
870	31	55.4	127	2	US-08-933-983-17	Sequence 17, Appl	943	31	55.4	450	2	US-09-909-064-320	Sequence 320, App
871	31	55.4	127	2	US-08-407-620A-34	Sequence 34, Appl	944	31	55.4	450	2	US-09-905-381A-320	Sequence 320, App
872	31	55.4	127	2	US-09-647-468-162	Sequence 162, App	945	31	55.4	450	2	US-09-906-618-320	Sequence 320, App
873	31	55.4	127	2	US-09-647-468-179	Sequence 179, App	946	31	55.4	450	2	US-09-906-646-320	Sequence 320, App
874	31	55.4	127	2	US-09-647-468-180	Sequence 180, App	947	31	55.4	450	2	US-09-904-462-320	Sequence 320, App
875	31	55.4	127	2	US-09-647-468-181	Sequence 181, App	948	31	55.4	450	2	US-09-902-736A-320	Sequence 320, App
876	31	55.4	127	2	US-09-647-468-182	Sequence 182, App	949	31	55.4	450	2	US-09-906-722A-320	Sequence 320, App
877	31	55.4	127	2	US-09-647-468-183	Sequence 183, App	950	31	55.4	451	2	US-09-489-039A-12072	Sequence 12072, A
878	31	55.4	128	1	US-08-024-253-4	Sequence 4, Appli	951	31	55.4	456	2	US-09-949-016-10421	Sequence 10421, A
879	31	55.4	140	2	US-08-579-378A-4	Sequence 4, Appli	952	31	55.4	459	2	US-09-543-681A-5116	Sequence 5116, Ap
880	31	55.4	140	2	US-08-579-378A-12	Sequence 12, Appl	953	31	55.4	465	2	US-09-248-796A-17155	Sequence 17155, A
881	31	55.4	140	4	PCT-US93-11612-4	Sequence 4, Appli	954	31	55.4	466	2	US-09-605-703B-2816	Sequence 2816, Ap
882	31	55.4	140	4	PCT-US93-11612-12	Sequence 12, Appl	955	31	55.4	477	1	US-08-432-016-3	Sequence 3, Appli
883	31	55.4	155	2	US-09-472-087-112	Sequence 20, Appl	956	31	55.4	477	1	US-08-684-594-3	Sequence 3, Appli
884	31	55.4	155	2	US-09-472-087-112	Sequence 112, App	957	31	55.4	480	2	US-09-248-796A-18693	Sequence 18693, A
885	31	55.4	162	2	US-08-992-176-9	Sequence 9, Appli	958	31	55.4	490	2	US-09-543-681A-7938	Sequence 7938, Ap
886	31	55.4	173	2	US-09-270-767-35799	Sequence 35799, A	959	31	55.4	494	2	US-10-280-579A-175	Sequence 175, App
887	31	55.4	173	2	US-09-270-767-51016	Sequence 51016, A	960	31	55.4	499	1	US-08-993-315-3	Sequence 3, Appli
888	31	55.4	174	2	US-09-328-352-6589	Sequence 6589, Ap	961	31	55.4	499	1	US-09-399-886-3	Sequence 3, Appli
889	31	55.4	190	2	US-08-881-094-20	Sequence 20, Appl	962	31	55.4	499	2	US-09-396-280-3	Sequence 3, Appli
890	31	55.4	194	2	US-09-270-767-37651	Sequence 37651, A	963	31	55.4	499	2	US-09-376-280-3	Sequence 3, Appli
891	31	55.4	194	2	US-09-270-767-52868	Sequence 52868, A	964	31	55.4	499	2	US-09-881-165-2	Sequence 2, Appli
892	31	55.4	209	2	US-10-380-105-4	Sequence 4, Appli	965	31	55.4	499	2	US-09-786-960-2	Sequence 2, Appli
893	31	55.4	219	2	US-09-248-796A-28006	Sequence 28006, A	966	31	55.4	499	2	US-09-786-960-2	Sequence 2, Appli
894	31	55.4	233	1	US-08-792-824-6	Sequence 6, Appli	967	31	55.4	511	1	US-08-462-484-8	Sequence 8, Appli
895	31	55.4	234	2	US-09-740-002-26	Sequence 26, Appl	968	31	55.4	511	1	US-08-441-147-8	Sequence 8, Appli
896	31	55.4	234	2	US-09-770-916-4	Sequence 4, Appli	969	31	55.4	511	4	PCT-US95-07536-8	Sequence 8, Appli
897	31	55.4	234	4	PCT-US94-07659-4	Sequence 4, Appli	970	31	55.4	517	1	US-09-252-991A-2249	Sequence 2249, A
898	31	55.4	235	2	US-09-800-729-152	Sequence 152, App	971	31	55.4	519	1	US-08-462-484-4	Sequence 4, Appli
899	31	55.4	236	1	US-08-792-824-3	Sequence 3, Appli	972	31	55.4	519	4	PCT-US95-07536-4	Sequence 4, Appli
900	31	55.4	236	1	US-08-792-824-9	Sequence 9, Appli	973	31	55.4	519	4	PCT-US95-07536-4	Sequence 4, Appli
901	31	55.4	236	1	US-08-792-824-12	Sequence 12, Appl	974	31	55.4	532	2	US-09-252-991A-25769	Sequence 25769, A
902	31	55.4	236	2	US-09-726-219A-188	Sequence 188, App	975	31	55.4	543	2	US-09-270-767-41677	Sequence 41677, A
903	31	55.4	236	2	US-09-196-522-188	Sequence 188, App	976	31	55.4	600	2	US-09-540-236-2965	Sequence 2965, Ap

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977 31 55.4 629 2 US-09-252-991A-17988 Sequence 17988, A
978 31 55.4 702 2 US-09-252-991A-31609 Sequence 31609, A
979 31 55.4 757 2 US-09-949-016-6963 Sequence 6963, Ap
980 31 55.4 758 2 US-09-949-016-8087 Sequence 8087, Ap
981 31 55.4 833 2 US-09-252-991A-31565 Sequence 31565, A
982 31 55.4 852 2 US-09-489-039A-13531 Sequence 13531, A
983 31 55.4 880 2 US-09-538-092-577 Sequence 577, App
984 31 55.4 913 2 US-09-252-991A-22127 Sequence 22127, A
985 31 55.4 1047 2 US-09-543-681A-6186 Sequence 6186, Ap
986 31 55.4 1179 2 US-09-540-236-3532 Sequence 3532, Ap
987 31 55.4 1208 2 US-09-463-702A-2 Sequence 2, Appli
988 31 55.4 1208 2 US-09-699-135-2 Sequence 2, Appli
989 31 55.4 1480 2 US-09-191-647-7 Sequence 7, Appli
990 31 55.4 1480 2 US-09-540-245A-7 Sequence 7, Appli
991 31 55.4 1480 2 US-09-540-153-7 Sequence 7, Appli
992 31 55.4 1480 2 US-09-182-024A-5 Sequence 5, Appli
993 31 55.4 1480 2 US-10-289-776-7 Sequence 7, Appli
994 31 55.4 1480 4 PCT-US91-09055-2 Sequence 2, Appli
995 31 55.4 1504 2 US-10-037-417-98 Sequence 98, Appli
996 30 5 54.5 92 2 US-10-330-613A-60 Sequence 60, Appli
997 30 53.6 11 1 US-08-318-157B-20 Sequence 20, Appli
998 30 53.6 11 2 US-09-339-922A-108 Sequence 108, App
999 30 53.6 11 2 US-08-407-620A-4 Sequence 4, Appli
1000 30 53.6 11 2 US-09-253-794-20 Sequence 20, Appli
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ALIGNMENTS

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RESULT 1
US-09-155-106-4
; Sequence 4, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-4
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Query Match 100.0%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RASQDIGNYL 11
|
Db 1 RASQDIGNYL 11
```

```
RESULT 2
US-09-155-106-22
; Sequence 22, Application US/09155106
```

```
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22
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Query Match 100.0%; Score 56; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RASQDIGNYL 11
|
Db 24 RASQDIGNYL 34
```

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RESULT 3
US-09-155-106-23
; Sequence 23, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23
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```
Query Match 100.0%; Score 56; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 RASQDIGNYL 11
      |||||
Db      24 RASQDIGNYL 34

RESULT 4
US-09-155-106-24
; Sequence 24, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-24

Query Match      100.0%; Score 56; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 11
      |||||
Db      24 RASQDIGNYL 34

RESULT 5
US-09-155-106-28
; Sequence 28, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-28

Query Match      100.0%; Score 56; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 11
      |||||
Db      24 RASQDIGNYL 34

RESULT 6
US-09-155-106-30
; Sequence 30, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-30

Query Match      100.0%; Score 56; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 11
      |||||
Db      24 RASQDIGNYL 34

RESULT 7
US-08-480-434-76
; Sequence 76, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-76

Query Match 80.4%; Score 45; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 1 RASQDISNYL 10

RESULT 8
US-08-053-451B-76
Sequence 76, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-76

Query Match 80.4%; Score 45; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 1 RASQDISNYL 10

RESULT 9
US-08-649-100-11
Sequence 11, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-11

Query Match 80.4%; Score 45; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 1 RASQDISNYL 10

RESULT 10
US-08-649-100-27
Sequence 27, Application US/08649100

```

; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, RAMON
; APPLICANT: MATSUE, SHOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-27

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```

Query Match      80.4%; Score 45; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 RASQDIGNYL 10
Db      1 RASQDISNYL 10

```

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RESULT 11
US-08-525-539A-5
; Sequence 5, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-5

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```

Query Match      80.4%; Score 45; DB 2; Length 31;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 RASQDIGNYL 10
Db      11 RASQDISNYL 20

```

```

RESULT 12
US-08-458-516-8
; Sequence 8, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-458-516-8

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDINNYL 33

RESULT 13

US-08-458-516-9
; Sequence 9, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/458,516

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/059,159

; FILING DATE: 03-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30, 223

; REFERENCE/DOCKET NUMBER: 11823-37-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-458-516-9

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDINNYL 33

RESULT 14

US-08-480-434-74
; Sequence 74, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:

; APPLICANT: Charles C. Ditlow, et al.

; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,

; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF

; NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,434

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Albert P. Halluin

; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 7606-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 854-3660

; TELEFAX: (415) 854-3694

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: N

; ANTI-SENSE: N

US-08-480-434-74

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 15

US-08-053-451B-74
; Sequence 74, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:

; APPLICANT: Chen, Francis W.

; APPLICANT: Ditlow, Charles C.

; APPLICANT: Calenoff, Emanuel

; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC

; NUMBER OF SEQUENCES: 176

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,451B

; FILING DATE: 26-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-74

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 16
US-08-053-451B-176
Sequence 176, Application US/08053451B
Patent No. 595584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Ditlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-053-451B-176

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33
RESULT 17
US-09-065-059-3
Sequence 3, Application US/09065059
Patent No. 6068841
GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 18
US-09-232-290-21
Sequence 21, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: FLUCKTHUN, ANDREAS
APPLICANT: NISBA, LARS
APPLICANT: HONEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230

;; EARLIER FILING DATE: 1996-05-23
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Murine
US-09-232-290-21

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 19

US-08-913-555-3
; Sequence 3, Application US/08913555
; Patent No. 6946255
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,555
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50356-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-913-555-3

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 20

US-08-913-555-21

; Sequence 21, Application US/08913555
; Patent No. 6946255
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,555
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50356-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-913-555-21

Query Match 80.4%; Score 45; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDISNYL 33

RESULT 21

US-07-942-245-10
; Sequence 10, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-10

Query Match 80.4%; Score 45; DB 1; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 22
US-07-934-373C-47
Sequence 47, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-47

Query Match 80.4%; Score 45; DB 1; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNLY 33

RESULT 23
US-08-437-642B-47
Sequence 47, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-47

Query Match 80.4%; Score 45; DB 2; Length 109;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNLY 33

RESULT 24
US-08-458-516-5
Sequence 5, Application US/08458516
Patent No. 577085

;; GENERAL INFORMATION:
;; APPLICANT: Tso, J. Yun
;; TITLE OF INVENTION: Humanized Antibodies Reactive with
;; TITLE OF INVENTION: GPIIB/IIIA
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-458-516-5

Query Match 80.4%; Score 45; DB 1; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 44 RASQDINNLY 53

RESULT 25
US-08-137-117D-37
; Sequence 37, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117D
;; FILING DATE: 20-DEC-1993
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-137-117D-37

Query Match 80.4%; Score 45; DB 1; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 44 RASQDISNYL 53

RESULT 26
US-08-436-717-37
; Sequence 37, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-436-717-37

Query Match 80.4%; Score 45; DB 1; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 27
US-08-574-699A-2
; Sequence 2, Application US/08574699A
; Patent No. 5985278
; GENERAL INFORMATION:
; APPLICANT: MITJANS, Francesc
; APPLICANT: PIULATS, Jaume
; APPLICANT: ROSELL, Elisabet
; APPLICANT: ADAN, Jaume
; APPLICANT: GOODMAN, Simon
; APPLICANT: HAHN, Diane
; TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
; TITLE OF INVENTION: Antibody
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd.
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,699A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94120165.9
; FILING DATE: 20-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1743
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-574-699A-2

Query Match 80.4%; Score 45; DB 1; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 28
US-08-649-100-17
; Sequence 17, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-PAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-649-100-17

Query Match 80.4%; Score 45; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 29
US-08-649-100-33
; Sequence 33, Application US/08649100
; Patent No. 6114507

GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-33

Query Match 80.4%; Score 45; DB 2; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 30
US-08-236-520-2
Sequence 2, Application US/08236520
Patent No. 5591629
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-236-520-2

Query Match 80.4%; Score 45; DB 1; Length 131;
Best Local Similarity 90.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDISNYL 10
|||||
Db 44 RASQDISNYL 53

RESULT 31
PCT-US95-05262-2
Sequence 2, Application PC/TUS9505262
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05262-2

Query Match 80.4%; Score 45; DB 4; Length 131;
Best Local Similarity 90.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 44 RASQDISNYL 53

RESULT 32
US-10-011-125A-5
; Sequence 5, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-5

Query Match 80.4%; Score 45; DB 2; Length 212;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNYL 33

RESULT 33
US-08-425-763-1
; Sequence 1, Application US/08425763
; Patent No. 5641870
; GENERAL INFORMATION:
; APPLICANT: Rinderknecht, Ernst H.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY PURIFICATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,763
; FILING DATE: 20-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-425-763-1

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNYL 33

RESULT 34
US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-12

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNYL 33

RESULT 35
US-07-934-373C-24
; Sequence 24, Application US/07934373C
; Patent No. 5821337

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-24

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
Db 24 RASQDINNYL 33

RESULT 36
US-07-934-373C-39
Sequence 39, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-39

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNYL 33

RESULT 37
US-07-934-373C-40
Sequence 40, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
US-07-934-373C-40

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNVL 33

RESULT 38

US-08-788-800-11
Sequence 11, Application US/08788800

Patent No. 5914112

GENERAL INFORMATION:

APPLICANT: Bednar, Martin M.

APPLICANT: Thomas, G. Roger

APPLICANT: Gross, Cordell E.

TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/788,800

FILING DATE: 22-Jan-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0987r1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-788-800-11

Query Match 80.4%; Score 45; DB 1; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNVL 33

RESULT 39

US-08-437-642B-24

Sequence 24, Application US/08437642B

Patent No. 6054297

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,642B

FILING DATE: 09-May-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 214 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-437-642B-24

Query Match 80.4%; Score 45; DB 2; Length 214;

Best Local Similarity 90.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10

Db 24 RASQDINNVL 33

RESULT 40

US-08-437-642B-39

Sequence 39, Application US/08437642B

Patent No. 6054297

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,642B

FILING DATE: 09-May-1995

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-39

Query Match 80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNLYL 33

RESULT 41
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-40

Query Match 80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNLYL 33

RESULT 42
US-08-811-757-1
; Sequence 1, Application US/08811757
; Patent No. 6066719
; GENERAL INFORMATION:
; APPLICANT: Rinderknecht, Ernst H.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY PURIFICATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,757
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/425,763
; FILING DATE: 20-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-811-757-1

Query Match 80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNLYL 33

RESULT 43
US-09-097-309-2
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-2

Query Match 80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 24 RASQDINNLY 33

RESULT 44
US-09-097-171A-2
; Sequence 2, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonari
; APPLICANT: Shahrakh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match 80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 24 RASQDINNLY 33

RESULT 45
US-09-249-230-1
; Sequence 1, Application US/09249230
; Patent No. 6214984
; GENERAL INFORMATION:
; APPLICANT: Rinderknecht, Ernst H.
; Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY PURIFICATION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,230
; FILING DATE: 11-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,757
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-249-230-1

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
      |||||
Db      24 RASQDINNLY 33

RESULT 46
US-09-460-587-2
; Sequence 2, Application US/09460587
; Patent No. 6322997
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,587
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-460-587-2

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
      |||||
Db      24 RASQDINNLY 33

RESULT 47
US-08-146-206C-24
; Sequence 24, Application US/08146206C
; Patent No. 6407213
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; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-24

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
      |||||
Db      24 RASQDINNLY 33

RESULT 48
US-09-705-686-24
; Sequence 24, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-No. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-705-686-24

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 49
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; Narindray, Daljit S.
; Zapata, Gerard A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940,166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-940-166A-2

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 50
US-09-705-392A-24
; Sequence 24, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-NO. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-705-392A-24

Query Match      80.4%; Score 45; DB 2; Length 214;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

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OM protein - protein search, using sw model

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55.408 Million cell updates/sec

Title: US-10-808-538-4

Perfect score: 56

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_Main:

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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	56	100.0	11	5	US-10-808-538-4	Sequence 4, Appli
3	56	100.0	108	3	US-09-155-106-22	Sequence 22, Appli
4	56	100.0	108	3	US-09-155-106-23	Sequence 23, Appli
5	56	100.0	108	3	US-09-155-106-24	Sequence 24, Appli
6	56	100.0	108	3	US-09-155-106-28	Sequence 28, Appli
7	56	100.0	108	3	US-09-155-106-30	Sequence 30, Appli
8	56	100.0	108	5	US-10-808-538-22	Sequence 22, Appli
9	56	100.0	108	5	US-10-808-538-23	Sequence 23, Appli
10	56	100.0	108	5	US-10-808-538-24	Sequence 24, Appli
11	56	100.0	108	5	US-10-808-538-28	Sequence 28, Appli
12	56	100.0	108	5	US-10-808-538-30	Sequence 30, Appli
13	47	83.9	106	4	US-10-466-242-20	Sequence 20, Appli
14	45	80.4	11	4	US-10-140-555-8	Sequence 8, Appli
15	45	80.4	11	4	US-10-279-633-47	Sequence 47, Appli
16	45	80.4	11	5	US-10-473-977-18	Sequence 18, Appli
17	45	80.4	11	5	US-10-783-311-152	Sequence 152, Appli
18	45	80.4	11	5	US-10-725-962-102	Sequence 102, Appli
19	45	80.4	31	3	US-09-956-206A-5	Sequence 5, Appli
20	45	80.4	31	5	US-10-965-616-5	Sequence 5, Appli
21	45	80.4	107	3	US-09-892-613C-10	Sequence 10, Appli
22	45	80.4	107	4	US-10-011-931-4	Sequence 4, Appli
23	45	80.4	107	4	US-10-411-037-51	Sequence 51, Appli
24	45	80.4	107	4	US-10-411-037-52	Sequence 52, Appli
25	45	80.4	107	4	US-10-411-026-51	Sequence 51, Appli
26	45	80.4	107	4	US-10-411-026-52	Sequence 52, Appli
27	45	80.4	107	4	US-10-251-085B-145	Sequence 145, Appli

101	43	76.8	247	5	US-10-620-049-21	Sequence 21, Appl	174	41	73.2	95	4	US-10-379-392-74	Sequence 74, Appl
102	43	76.8	247	5	US-10-620-049-23	Sequence 23, Appl	175	41	73.2	103	4	US-10-078-958-26	Sequence 26, Appl
103	43	76.8	247	5	US-10-620-049-25	Sequence 25, Appl	176	41	73.2	104	4	US-10-078-958-28	Sequence 28, Appl
104	43	76.8	274	3	US-09-813-659-30	Sequence 30, Appl	177	41	73.2	104	4	US-10-078-958-29	Sequence 29, Appl
105	43	76.8	274	3	US-10-283-610A-30	Sequence 30, Appl	178	41	73.2	105	3	US-09-187-693-40	Sequence 40, Appl
106	43	76.8	302	3	US-09-813-659-18	Sequence 18, Appl	179	41	73.2	105	3	US-09-187-693-44	Sequence 44, Appl
107	43	76.8	302	3	US-09-813-659-32	Sequence 32, Appl	180	41	73.2	105	3	US-09-187-693-50	Sequence 50, Appl
108	43	76.8	302	3	US-10-283-610A-18	Sequence 18, Appl	181	41	73.2	105	3	US-09-187-693-54	Sequence 54, Appl
109	43	76.8	302	4	US-10-283-610A-32	Sequence 32, Appl	182	41	73.2	105	3	US-10-078-958-12	Sequence 12, Appl
110	43	76.8	504	4	US-10-207-655-348	Sequence 348, App	183	41	73.2	105	6	US-11-021-795-40	Sequence 40, Appl
111	43	76.8	504	5	US-10-627-556-113	Sequence 113, App	184	41	73.2	105	6	US-11-021-795-44	Sequence 44, Appl
112	43	76.8	555	4	US-10-107-991B-3	Sequence 3, Appl	185	41	73.2	105	6	US-11-021-795-50	Sequence 50, Appl
113	43	76.8	555	5	US-10-627-556-444	Sequence 444, App	186	41	73.2	105	6	US-11-021-795-54	Sequence 54, Appl
114	43	76.8	555	5	US-10-627-556-512	Sequence 512, App	187	41	73.2	106	5	US-10-727-155-130	Sequence 130, App
115	43	76.8	601	3	US-09-480-236-1	Sequence 1, Appl	188	41	73.2	107	4	US-10-330-613-26	Sequence 26, Appl
116	43	76.8	637	4	US-10-286-085A-16	Sequence 16, Appl	189	41	73.2	107	4	US-10-330-530-26	Sequence 26, Appl
117	43	76.8	638	4	US-10-286-085A-21	Sequence 21, Appl	190	41	73.2	107	4	US-10-310-674A-34	Sequence 34, Appl
118	43	76.8	642	4	US-10-286-085A-38	Sequence 38, Appl	191	41	73.2	107	4	US-10-460-595-7	Sequence 7, Appl
119	43	76.8	642	5	US-10-496-179-6	Sequence 6, Appl	192	41	73.2	107	4	US-10-389-679-10	Sequence 10, Appl
120	43	76.8	643	4	US-10-296-085A-69	Sequence 69, Appl	193	41	73.2	107	4	US-10-660-357-26	Sequence 26, Appl
121	43	76.8	643	5	US-10-496-179-1	Sequence 1, Appl	194	41	73.2	107	5	US-10-727-155-318	Sequence 318, App
122	43	76.8	652	4	US-10-286-085A-120	Sequence 120, App	195	41	73.2	107	6	US-11-031-485-132	Sequence 132, App
123	43	76.8	656	4	US-10-286-085A-39	Sequence 39, Appl	196	41	73.2	111	4	US-10-203-754A-17	Sequence 17, Appl
124	43	76.8	657	4	US-10-286-085A-68	Sequence 68, Appl	197	41	73.2	112	4	US-10-364-743-51	Sequence 51, Appl
125	43	76.8	895	4	US-10-286-085A-19	Sequence 19, Appl	198	41	73.2	112	5	US-10-452-593-51	Sequence 51, Appl
126	43	76.8	895	4	US-10-286-085A-20	Sequence 20, Appl	199	41	73.2	113	4	US-10-364-743-49	Sequence 49, Appl
127	43	76.8	895	4	US-10-286-085A-27	Sequence 27, Appl	200	41	73.2	113	5	US-10-452-593-49	Sequence 49, Appl
128	43	76.8	895	5	US-10-436-179-4	Sequence 4, Appl	201	41	73.2	120	5	US-10-450-763-42267	Sequence 42267, A
129	43	76.8	896	4	US-10-286-085A-17	Sequence 17, Appl	202	41	73.2	129	5	US-10-893-576-30	Sequence 30, Appl
130	43	76.8	896	4	US-10-286-085A-18	Sequence 18, Appl	203	41	73.2	129	5	US-10-893-576-30	Sequence 30, Appl
131	43	76.8	896	4	US-10-286-085A-26	Sequence 26, Appl	204	41	73.2	164	5	US-10-364-743-21	Sequence 21, Appl
132	43	76.8	896	5	US-10-496-179-2	Sequence 2, Appl	205	41	73.2	164	5	US-10-452-593-21	Sequence 21, Appl
133	43	76.8	896	5	US-10-496-179-3	Sequence 3, Appl	206	41	73.2	214	5	US-10-644-277-64	Sequence 64, Appl
134	43	76.8	896	5	US-10-496-179-7	Sequence 7, Appl	207	41	73.2	234	3	US-09-800-729-150	Sequence 150, App
135	43	76.8	899	4	US-10-286-085A-28	Sequence 28, Appl	208	41	73.2	236	6	US-11-131-648-20	Sequence 20, App
136	43	76.8	899	5	US-10-496-179-5	Sequence 5, Appl	209	41	73.2	236	6	US-11-131-648-20	Sequence 20, App
137	42	75.0	11	4	US-10-279-633-57	Sequence 57, Appl	210	41	73.2	236	6	US-11-031-485-48	Sequence 48, Appl
138	42	75.0	11	4	US-10-436-782-34	Sequence 34, Appl	211	41	73.2	243	4	US-10-689-921-2	Sequence 2, Appl
139	42	75.0	11	4	US-10-436-783-2	Sequence 2, Appl	212	41	73.2	286	4	US-10-406-830-8	Sequence 8, Appl
140	42	75.0	11	5	US-10-994-129-2	Sequence 2, Appl	213	41	73.2	316	3	US-09-957-944-8	Sequence 8, Appl
141	42	75.0	11	6	US-11-004-795A-34	Sequence 34, Appl	214	41	73.2	316	3	US-09-079-569-7	Sequence 7, Appl
142	42	75.0	11	6	US-11-004-794A-34	Sequence 34, Appl	215	41	73.2	316	3	US-09-873-829-4	Sequence 4, Appl
143	42	75.0	11	6	US-11-036-098-2	Sequence 2, Appl	216	41	73.2	316	3	US-09-933-915A-16	Sequence 16, Appl
144	42	75.0	107	4	US-10-436-782-33	Sequence 33, Appl	217	41	73.2	316	4	US-10-017-910-4	Sequence 4, Appl
145	42	75.0	107	4	US-10-436-783-1	Sequence 1, Appl	218	41	73.2	316	4	US-10-105-057-2	Sequence 2, Appl
146	42	75.0	107	5	US-10-994-129-1	Sequence 1, Appl	219	41	73.2	316	4	US-10-272-411-19	Sequence 19, Appl
147	42	75.0	107	6	US-11-004-795A-33	Sequence 33, Appl	220	41	73.2	316	4	US-10-272-328A-19	Sequence 19, Appl
148	42	75.0	107	6	US-11-004-794A-33	Sequence 33, Appl	221	41	73.2	316	4	US-10-326-052-2	Sequence 2, Appl
149	42	75.0	107	6	US-11-036-098-16	Sequence 16, Appl	222	41	73.2	316	4	US-10-167-182-1	Sequence 1, Appl
150	42	75.0	109	4	US-10-078-757B-55	Sequence 55, Appl	223	41	73.2	316	4	US-10-460-623-1	Sequence 1, Appl
151	42	75.0	112	4	US-10-355-780-1	Sequence 1, Appl	224	41	73.2	316	4	US-10-664-801-4	Sequence 4, Appl
152	42	75.0	243	3	US-09-887-853-6	Sequence 6, Appl	225	41	73.2	316	4	US-10-664-801-6	Sequence 6, Appl
153	42	75.0	243	5	US-10-683-547-6	Sequence 6, Appl	226	41	73.2	316	4	US-10-799-345-10	Sequence 10, Appl
154	42	75.0	267	3	US-09-766-543-10	Sequence 10, Appl	227	41	73.2	316	5	US-10-825-898-2	Sequence 2, Appl
155	42	75.0	276	3	US-09-766-543-12	Sequence 12, Appl	228	41	73.2	316	5	US-10-854-300-1	Sequence 1, Appl
156	42	75.0	532	6	US-11-036-098-18	Sequence 18, Appl	229	41	73.2	316	6	US-11-099-059-8	Sequence 8, Appl
157	41	73.2	11	4	US-10-203-754A-4	Sequence 4, Appl	230	41	73.2	316	6	US-11-135-521-1	Sequence 1, Appl
158	41	73.2	11	5	US-10-726-332-179	Sequence 179, App	231	41	73.2	479	5	US-10-485-466-29	Sequence 29, Appl
159	41	73.2	11	5	US-10-893-576-63	Sequence 63, Appl	232	41	73.2	502	4	US-10-679-620-88	Sequence 88, Appl
160	41	73.2	30	3	US-09-956-206A-7	Sequence 7, Appl	233	41	73.2	502	6	US-11-132-143-88	Sequence 88, Appl
161	41	73.2	30	5	US-10-965-616-7	Sequence 7, Appl	234	41	73.2	551	5	US-10-485-466-31	Sequence 31, Appl
162	41	73.2	75	4	US-10-078-958-25	Sequence 25, Appl	235	40	71.4	11	3	US-09-056-160B-4	Sequence 4, Appl
163	41	73.2	76	3	US-09-187-693-36	Sequence 36, Appl	236	40	71.4	11	4	US-10-091-300-57	Sequence 57, Appl
164	41	73.2	76	4	US-10-078-958-10	Sequence 10, Appl	237	40	71.4	11	4	US-10-234-671-4	Sequence 4, Appl
165	41	73.2	76	6	US-11-021-795-36	Sequence 36, Appl	238	40	71.4	11	4	US-10-396-578-71	Sequence 71, Appl
166	41	73.2	90	3	US-09-864-761-34739	Sequence 34739, A	239	40	71.4	11	5	US-10-745-775-12	Sequence 12, Appl
167	41	73.2	95	4	US-10-194-975-56	Sequence 56, Appl	240	40	71.4	11	5	US-10-482-630-109	Sequence 109, App
168	41	73.2	95	4	US-10-194-975-57	Sequence 57, Appl	241	40	71.4	11	5	US-10-974-591-4	Sequence 4, Appl
169	41	73.2	95	4	US-10-308-817-3	Sequence 3, Appl	242	40	71.4	11	6	US-10-506-997-57	Sequence 57, Appl
170	41	73.2	95	4	US-10-308-817-4	Sequence 4, Appl	243	40	71.4	11	6	US-11-074-803-71	Sequence 71, Appl
171	41	73.2	95	4	US-10-453-698-3	Sequence 3, Appl	244	40	71.4	51	4	US-10-340-189-73	Sequence 73, Appl
172	41	73.2	95	4	US-10-453-698-4	Sequence 4, Appl	245	40	71.4	51	4	US-10-340-189-74	Sequence 74, Appl
173	41	73.2	95	4	US-10-379-392-73	Sequence 73, Appl	246	40	71.4	84	5	US-10-926-683-816	Sequence 816, App

247	40	71.4	103	4	US-10-379-392-100	Sequence 100, App	320	40	71.4	110	5	US-10-974-591-8	Sequence 8, Appli
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252	40	71.4	106	6	US-11-004-054-16	Sequence 16, Appli	325	40	71.4	111	5	US-10-726-332-20	Sequence 20, Appli
253	40	71.4	107	3	US-09-056-1608-13	Sequence 13, Appli	326	40	71.4	111	5	US-10-726-332-222	Sequence 222, App
254	40	71.4	107	3	US-09-056-1608-15	Sequence 15, Appli	327	40	71.4	118	3	US-09-811-737-4	Sequence 4, Appli
255	40	71.4	107	4	US-10-091-300-37	Sequence 37, Appli	328	40	71.4	118	3	US-09-811-737-11	Sequence 11, Appli
256	40	71.4	107	4	US-10-127-890-125	Sequence 125, App	329	40	71.4	126	5	US-10-837-904-64	Sequence 64, Appli
257	40	71.4	107	4	US-10-016-986-103	Sequence 103, App	330	40	71.4	126	5	US-10-837-904-68	Sequence 68, Appli
258	40	71.4	107	4	US-10-234-671-13	Sequence 13, Appli	331	40	71.4	127	5	US-10-837-904-29	Sequence 29, Appli
259	40	71.4	107	4	US-10-234-671-15	Sequence 15, Appli	332	40	71.4	128	3	US-09-764-304-10	Sequence 10, Appli
260	40	71.4	107	4	US-10-340-189-27	Sequence 27, Appli	333	40	71.4	128	3	US-09-764-304-19	Sequence 19, Appli
261	40	71.4	107	4	US-10-340-189-87	Sequence 87, Appli	334	40	71.4	128	4	US-10-265-713-10	Sequence 10, Appli
262	40	71.4	107	4	US-10-325-696-27	Sequence 27, App	335	40	71.4	128	4	US-10-265-713-19	Sequence 19, Appli
263	40	71.4	107	4	US-10-325-696-65	Sequence 65, Appli	336	40	71.4	128	4	US-10-166-626-10	Sequence 10, Appli
264	40	71.4	107	4	US-10-663-244-79	Sequence 79, Appli	337	40	71.4	128	4	US-10-166-626-19	Sequence 19, Appli
265	40	71.4	107	4	US-10-723-434-1	Sequence 1, Appli	338	40	71.4	213	4	US-10-379-392-135	Sequence 135, App
266	40	71.4	107	4	US-10-723-434-2	Sequence 2, Appli	339	40	71.4	213	4	US-10-379-392-137	Sequence 137, App
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270	40	71.4	107	4	US-10-723-434-6	Sequence 6, Appli	343	40	71.4	213	4	US-10-379-392-157	Sequence 157, App
271	40	71.4	107	4	US-10-723-434-7	Sequence 7, Appli	344	40	71.4	214	4	US-10-364-953-1	Sequence 1, Appli
272	40	71.4	107	4	US-10-723-434-8	Sequence 8, Appli	345	40	71.4	233	4	US-10-663-244-150	Sequence 150, App
273	40	71.4	107	4	US-10-723-434-9	Sequence 9, Appli	346	40	71.4	237	3	US-09-056-1608-100	Sequence 100, App
274	40	71.4	107	4	US-10-723-434-10	Sequence 10, Appli	347	40	71.4	237	4	US-10-020-786-10	Sequence 10, Appli
275	40	71.4	107	4	US-10-723-434-11	Sequence 11, Appli	348	40	71.4	237	4	US-10-234-671-100	Sequence 100, App
276	40	71.4	107	4	US-10-723-434-12	Sequence 12, Appli	349	40	71.4	237	5	US-10-697-995-8	Sequence 8, Appli
277	40	71.4	107	4	US-10-723-434-13	Sequence 13, Appli	350	40	71.4	237	5	US-10-697-995-11	Sequence 11, Appli
278	40	71.4	107	4	US-10-723-434-14	Sequence 14, Appli	351	40	71.4	237	5	US-10-974-591-100	Sequence 100, App
279	40	71.4	107	4	US-10-482-630-89	Sequence 89, Appli	352	40	71.4	237	6	US-11-071-291-10	Sequence 10, Appli
280	40	71.4	107	5	US-10-717-243-125	Sequence 125, App	353	40	71.4	240	4	US-10-127-890-147	Sequence 147, App
281	40	71.4	107	5	US-10-974-591-13	Sequence 13, Appli	354	40	71.4	240	4	US-10-127-890-148	Sequence 148, App
282	40	71.4	107	5	US-10-974-591-15	Sequence 15, Appli	355	40	71.4	240	5	US-10-717-243-147	Sequence 147, App
283	40	71.4	107	5	US-10-837-904-115	Sequence 115, App	356	40	71.4	240	5	US-10-717-243-148	Sequence 148, App
284	40	71.4	107	6	US-10-506-997-37	Sequence 37, Appli	357	40	71.4	253	3	US-09-811-737-18	Sequence 18, Appli
285	40	71.4	107	6	US-11-133-775-27	Sequence 27, App	358	40	71.4	255	3	US-09-811-737-15	Sequence 15, Appli
286	40	71.4	107	6	US-11-133-775-65	Sequence 65, Appli	359	40	71.4	260	3	US-09-811-737-16	Sequence 16, Appli
287	40	71.4	108	3	US-09-056-1608-8	Sequence 8, Appli	360	40	71.4	260	3	US-09-811-737-17	Sequence 17, Appli
288	40	71.4	108	3	US-09-056-1608-10	Sequence 10, Appli	361	40	71.4	262	3	US-09-811-737-19	Sequence 19, Appli
289	40	71.4	108	3	US-09-056-1608-126	Sequence 126, App	362	40	71.4	491	4	US-10-011-125-2	Sequence 2, Appli
290	40	71.4	108	4	US-10-153-159-2	Sequence 2, Appli	363	40	71.4	491	5	US-10-764-428-7	Sequence 7, Appli
291	40	71.4	108	4	US-10-153-159-4	Sequence 4, Appli	364	40	71.4	667	5	US-10-764-428-13	Sequence 13, Appli
292	40	71.4	108	4	US-10-153-159-16	Sequence 16, Appli	365	40	71.4	667	5	US-10-764-428-25	Sequence 25, Appli
293	40	71.4	108	4	US-10-153-176-2	Sequence 2, Appli	366	40	71.4	670	5	US-10-764-428-5	Sequence 5, Appli
294	40	71.4	108	4	US-10-153-176-4	Sequence 4, Appli	367	40	71.4	670	5	US-10-764-428-9	Sequence 9, Appli
295	40	71.4	108	4	US-10-153-176-16	Sequence 16, Appli	368	40	71.4	670	5	US-10-764-428-11	Sequence 11, Appli
296	40	71.4	108	4	US-10-234-671-10	Sequence 10, Appli	369	40	71.4	670	5	US-10-764-428-27	Sequence 27, Appli
297	40	71.4	108	4	US-10-234-671-124	Sequence 124, App	370	39	69.6	11	3	US-09-977-797A-18	Sequence 18, Appli
298	40	71.4	108	4	US-10-443-134A-2	Sequence 2, Appli	371	39	69.6	11	3	US-09-977-797A-22	Sequence 22, Appli
299	40	71.4	108	4	US-10-443-134A-4	Sequence 4, Appli	372	39	69.6	11	3	US-09-977-797A-2	Sequence 2, Appli
300	40	71.4	108	4	US-10-443-134A-16	Sequence 16, Appli	373	39	69.6	11	4	US-10-203-754A-42	Sequence 42, Appli
301	40	71.4	108	4	US-10-443-134A-127	Sequence 127, App	374	39	69.6	11	4	US-10-203-754A-45	Sequence 45, Appli
302	40	71.4	108	5	US-10-877-532-7	Sequence 7, Appli	375	39	69.6	11	4	US-10-279-633-59	Sequence 59, Appli
303	40	71.4	108	5	US-10-974-591-10	Sequence 10, Appli	376	39	69.6	11	4	US-10-279-633-61	Sequence 61, Appli
304	40	71.4	108	5	US-10-974-591-124	Sequence 124, App	377	39	69.6	11	4	US-10-396-578-17	Sequence 17, Appli
305	40	71.4	109	3	US-09-229-200A-7	Sequence 7, Appli	378	39	69.6	11	5	US-10-949-135-12	Sequence 12, Appli
306	40	71.4	109	4	US-10-197-080-4	Sequence 4, Appli	379	39	69.6	11	6	US-11-074-803-17	Sequence 17, Appli
307	40	71.4	109	5	US-10-484-031-4	Sequence 4, Appli	380	39	69.6	88	3	US-09-905-243-36	Sequence 36, Appli
308	40	71.4	110	3	US-09-056-1608-103	Sequence 103, App	381	39	69.6	88	6	US-11-099-331-36	Sequence 36, Appli
309	40	71.4	110	3	US-09-056-1608-105	Sequence 105, App	382	39	69.6	102	4	US-10-078-958-14	Sequence 14, Appli
310	40	71.4	110	3	US-09-056-1608-107	Sequence 107, App	383	39	69.6	102	4	US-10-803-622-173	Sequence 173, App
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312	40	71.4	110	4	US-10-234-671-8	Sequence 8, Appli	385	39	69.6	103	4	US-10-473-977-66	Sequence 70, Appli
313	40	71.4	110	4	US-10-234-671-101	Sequence 101, App	386	39	69.6	103	5	US-10-791-153A-70	Sequence 66, Appli
314	40	71.4	110	4	US-10-234-671-103	Sequence 103, App	387	39	69.6	107	3	US-09-848-798-173	Sequence 173, App
315	40	71.4	110	4	US-10-234-671-105	Sequence 105, App	388	39	69.6	107	3	US-09-848-798-179	Sequence 179, App
316	40	71.4	110	4	US-10-234-671-115	Sequence 115, App	389	39	69.6	107	4	US-10-268-501-5	Sequence 5, Appli
317	40	71.4	110	4	US-10-624-153-94	Sequence 94, Appli	390	39	69.6	107	4	US-10-046-986-107	Sequence 107, App
318	40	71.4	110	5	US-10-683-043-1	Sequence 1, Appli	391	39	69.6	107	4	US-10-608-626-5	Sequence 5, Appli
319	40	71.4	110	5	US-10-683-043-5	Sequence 5, Appli	392	39	69.6	107	4	US-10-600-152-14	Sequence 14, Appli

393	39	69.6	107	4	US-10-619-754-5	Sequence 5, Appli	466	38	67.9	107	4	US-10-041-860-32	Sequence 32, Appl
394	39	69.6	107	5	US-10-835-641-18	Sequence 18, Appl	467	38	67.9	107	4	US-10-041-860-34	Sequence 34, Appl
395	39	69.6	107	5	US-10-719-310-5	Sequence 5, Appli	468	38	67.9	107	4	US-10-041-860-223	Sequence 223, App
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399	39	69.6	107	5	US-10-916-840-159	Sequence 159, App	472	38	67.9	107	4	US-10-041-860-334	Sequence 334, App
400	39	69.6	107	5	US-10-994-091A-28	Sequence 28, Appl	473	38	67.9	107	4	US-10-016-986-82	Sequence 82, Appl
401	39	69.6	107	6	US-11-044-749-5	Sequence 5, Appli	474	38	67.9	107	4	US-10-016-986-84	Sequence 84, Appl
402	39	69.6	107	6	US-11-154-465-5	Sequence 5, Appli	475	38	67.9	107	4	US-10-309-762-86	Sequence 86, Appl
403	39	69.6	108	3	US-09-056-160B-12	Sequence 12, Appl	476	38	67.9	107	4	US-10-665-383-44	Sequence 44, Appl
404	39	69.6	108	3	US-09-795-798-3	Sequence 3, Appli	477	38	67.9	107	4	US-10-665-383-48	Sequence 48, Appl
405	39	69.6	108	4	US-10-016-986-102	Sequence 102, App	478	38	67.9	107	5	US-10-727-155-264	Sequence 264, App
406	39	69.6	108	4	US-10-234-671-12	Sequence 12, Appl	479	38	67.9	107	5	US-10-727-155-306	Sequence 306, App
407	39	69.6	108	4	US-10-727-737-3	Sequence 3, Appli	480	38	67.9	107	6	US-11-021-715-97	Sequence 97, Appl
408	39	69.6	108	5	US-10-726-332-22	Sequence 22, Appl	481	38	67.9	108	3	US-09-905-243-73	Sequence 73, Appl
409	39	69.6	108	5	US-10-861-049-38	Sequence 38, Appl	482	38	67.9	108	4	US-10-141-908-7	Sequence 7, Appli
410	39	69.6	108	5	US-10-974-591-12	Sequence 12, Appl	483	38	67.9	108	4	US-10-141-908-14	Sequence 14, Appl
411	39	69.6	108	6	US-11-021-874-38	Sequence 38, Appl	484	38	67.9	108	4	US-10-041-860-328	Sequence 328, App
412	39	69.6	109	3	US-09-811-123-6	Sequence 6, Appli	485	38	67.9	108	4	US-10-016-986-109	Sequence 109, App
413	39	69.6	109	4	US-10-330-613-10	Sequence 10, Appl	486	38	67.9	108	5	US-10-725-962-36	Sequence 36, Appl
414	39	69.6	109	4	US-10-330-530-10	Sequence 10, Appl	487	38	67.9	108	5	US-10-725-962-38	Sequence 38, Appl
415	39	69.6	109	4	US-10-371-942-72	Sequence 72, Appl	488	38	67.9	108	5	US-10-725-962-39	Sequence 39, Appl
416	39	69.6	109	4	US-10-371-942-76	Sequence 76, Appl	489	38	67.9	108	5	US-10-725-962-40	Sequence 40, Appl
417	39	69.6	109	4	US-10-660-357-10	Sequence 10, Appl	490	38	67.9	108	5	US-10-625-307A-39	Sequence 39, Appl
418	39	69.6	109	5	US-10-835-641-3	Sequence 3, Appli	491	38	67.9	108	5	US-10-625-307A-67	Sequence 67, Appl
419	39	69.6	110	4	US-10-044-896-4	Sequence 4, Appli	492	38	67.9	108	6	US-11-099-331-73	Sequence 73, Appl
420	39	69.6	111	4	US-10-203-754A-54	Sequence 54, Appl	493	38	67.9	110	4	US-10-251-215-41	Sequence 41, Appl
421	39	69.6	112	4	US-10-203-754A-55	Sequence 55, Appl	494	38	67.9	110	4	US-10-251-215-43	Sequence 43, Appl
422	39	69.6	113	4	US-10-364-743-55	Sequence 55, Appl	495	38	67.9	112	4	US-10-148-737-2	Sequence 2, Appli
423	39	69.6	113	5	US-10-452-593-55	Sequence 55, Appl	496	38	67.9	112	6	US-11-054-041-2	Sequence 2, Appli
424	39	69.6	115	4	US-10-364-743-50	Sequence 50, Appl	497	38	67.9	113	4	US-10-364-743-57	Sequence 57, Appl
425	39	69.6	115	5	US-10-452-593-50	Sequence 50, Appl	498	38	67.9	113	5	US-10-452-593-57	Sequence 57, Appl
426	39	69.6	126	4	US-10-469-125-8	Sequence 8, Appli	499	38	67.9	116	5	US-10-783-311-158	Sequence 158, App
427	39	69.6	166	4	US-10-364-743-22	Sequence 22, Appl	500	38	67.9	125	5	US-10-473-287-48	Sequence 48, Appl
428	39	69.6	166	5	US-10-452-593-22	Sequence 22, Appl	501	38	67.9	127	4	US-10-395-894-17	Sequence 17, Appl
429	39	69.6	215	3	US-09-791-153A-47	Sequence 47, Appl	502	38	67.9	127	4	US-10-695-667-17	Sequence 17, Appl
430	39	69.6	248	3	US-09-880-748-1360	Sequence 1360, Ap	503	38	67.9	127	5	US-10-976-352-17	Sequence 17, Appl
431	39	69.6	248	4	US-10-293-418-1360	Sequence 2296, Ap	504	38	67.9	136	5	US-10-473-287-49	Sequence 49, Appl
432	39	69.6	260	4	US-10-284-049-2296	Sequence 2296, Ap	505	38	67.9	138	4	US-10-425-115-210486	Sequence 210486,
433	39	69.6	634	4	US-10-416-011-2	Sequence 2, Appli	506	38	67.9	211	3	US-09-974-449-36	Sequence 36, Appl
434	38	67.9	11	3	US-09-974-449-46	Sequence 46, Appl	507	38	67.9	238	6	US-11-031-485-28	Sequence 28, Appl
435	38	67.9	11	4	US-10-279-633-52	Sequence 52, Appl	508	38	67.9	239	5	US-10-935-290-80	Sequence 80, Appl
436	38	67.9	11	5	US-10-783-311-160	Sequence 160, App	509	38	67.9	241	3	US-09-880-748-1577	Sequence 1577, Ap
437	38	67.9	11	5	US-10-725-962-107	Sequence 107, App	510	38	67.9	241	3	US-10-293-418-1577	Sequence 1577, Ap
438	38	67.9	88	3	US-09-905-243-29	Sequence 29, Appl	511	38	67.9	242	3	US-09-880-748-1915	Sequence 1915, Ap
439	38	67.9	88	6	US-11-099-331-29	Sequence 29, Appl	512	38	67.9	242	4	US-10-293-418-1915	Sequence 1915, Ap
440	38	67.9	95	4	US-10-194-975-58	Sequence 58, Appl	513	38	67.9	243	6	US-11-017-030-6	Sequence 6, Appli
441	38	67.9	95	4	US-10-194-975-61	Sequence 61, Appl	514	38	67.9	244	6	US-11-090-847-69	Sequence 69, Appl
442	38	67.9	95	4	US-10-041-860-9	Sequence 9, Appli	515	38	67.9	247	4	US-10-293-418-3240	Sequence 3240, Ap
443	38	67.9	95	4	US-10-041-860-333	Sequence 333, App	516	38	67.9	248	3	US-09-880-748-1446	Sequence 1446, Ap
444	38	67.9	95	4	US-10-041-860-335	Sequence 335, App	517	38	67.9	248	4	US-10-293-418-1446	Sequence 1446, Ap
445	38	67.9	95	4	US-10-041-860-345	Sequence 345, App	518	38	67.9	251	3	US-09-880-748-1921	Sequence 1921, Ap
446	38	67.9	95	4	US-10-308-817-5	Sequence 5, Appli	519	38	67.9	251	4	US-10-293-418-1921	Sequence 1921, Ap
447	38	67.9	95	4	US-10-308-817-8	Sequence 8, Appli	520	38	67.9	251	6	US-11-017-030-2	Sequence 2, Appli
448	38	67.9	95	4	US-10-453-698-5	Sequence 5, Appli	521	38	67.9	251	6	US-11-017-030-19	Sequence 19, Appl
449	38	67.9	95	4	US-10-453-698-8	Sequence 8, Appli	522	37	66.1	11	3	US-09-924-099-3	Sequence 3, Appli
450	38	67.9	95	4	US-10-379-392-68	Sequence 68, Appl	523	37	66.1	11	4	US-10-203-754A-51	Sequence 51, Appl
451	38	67.9	95	4	US-10-379-392-72	Sequence 72, Appl	524	37	66.1	11	4	US-10-401-344-14	Sequence 14, Appl
452	38	67.9	95	5	US-10-986-089A-42	Sequence 42, Appl	525	37	66.1	11	5	US-10-813-977-21	Sequence 21, Appl
453	38	67.9	96	4	US-10-041-860-327	Sequence 327, App	526	37	66.1	81	3	US-09-864-408A-5628	Sequence 5628, Ap
454	38	67.9	96	4	US-10-041-860-329	Sequence 329, App	527	37	66.1	95	4	US-10-194-975-93	Sequence 93, Appl
455	38	67.9	96	5	US-10-041-860-333	Sequence 33, Appl	528	37	66.1	95	4	US-10-308-817-40	Sequence 40, Appl
456	38	67.9	102	4	US-10-723-860-33	Sequence 10, Appl	529	37	66.1	95	4	US-10-453-698-40	Sequence 40, Appl
457	38	67.9	102	4	US-10-141-908-10	Sequence 10, Appl	530	37	66.1	95	4	US-10-379-392-107	Sequence 107, App
458	38	67.9	102	4	US-10-141-908-29	Sequence 29, Appl	531	37	66.1	100	3	US-09-899-896-8	Sequence 8, Appli
459	38	67.9	102	4	US-10-010-729-35	Sequence 35, Appl	532	37	66.1	102	3	US-09-864-761-48570	Sequence 48570, A
460	38	67.9	105	3	US-09-974-449-4	Sequence 4, Appli	533	37	66.1	106	6	US-11-004-054-5	Sequence 5, Appli
461	38	67.9	105	3	US-10-141-908-31	Sequence 31, Appl	534	37	66.1	107	4	US-10-127-890-123	Sequence 123, App
462	38	67.9	106	4	US-10-016-986-89	Sequence 89, Appl	535	37	66.1	107	4	US-10-340-189-26	Sequence 26, Appl
463	38	67.9	106	4	US-10-016-986-83	Sequence 83, Appl	536	37	66.1	107	4	US-10-325-696-26	Sequence 26, Appl
464	38	67.9	106	4	US-10-016-986-85	Sequence 85, Appl	537	37	66.1	107	4	US-10-309-762-66	Sequence 66, Appl
465	38	67.9	107	3	US-09-848-798-169	Sequence 169, App	538	37	66.1	107	4	US-10-309-762-69	Sequence 69, Appl

539	37	66.1	107	4	US-10-424-599-225078	Sequence 225078,	612	36	64.3	11	3	US-09-968-561A-316	Sequence 316, Appl
540	37	66.1	107	4	US-10-723-434-20	Sequence 20, Appl	613	36	64.3	11	4	US-10-367-506-22	Sequence 22, Appl
541	37	66.1	107	4	US-10-723-434-22	Sequence 22, Appl	614	36	64.3	11	4	US-10-133-715-7	Sequence 7, Appl
542	37	66.1	107	4	US-10-774-076-3	Sequence 3, Appl	615	36	64.3	11	4	US-10-302-356A-7	Sequence 7, Appl
543	37	66.1	107	4	US-10-774-076-14	Sequence 14, Appl	616	36	64.3	11	4	US-10-163-356A-7	Sequence 7, Appl
544	37	66.1	107	5	US-10-717-243-123	Sequence 123, Appl	617	36	64.3	11	4	US-10-422-287-7	Sequence 7, Appl
545	37	66.1	107	6	US-11-133-775-26	Sequence 26, Appl	618	36	64.3	11	4	US-10-307-276B-38	Sequence 38, Appl
546	37	66.1	108	3	US-09-924-099-1	Sequence 1, Appl	619	36	64.3	11	4	US-10-622-932-7	Sequence 7, Appl
547	37	66.1	108	4	US-10-010-729-45	Sequence 45, Appl	620	36	64.3	11	4	US-10-623-065-7	Sequence 7, Appl
548	37	66.1	108	4	US-10-803-622-267	Sequence 267, Appl	621	36	64.3	11	4	US-10-623-076-7	Sequence 7, Appl
549	37	66.1	108	4	US-10-803-653-267	Sequence 267, Appl	622	36	64.3	11	4	US-10-623-210-7	Sequence 7, Appl
550	37	66.1	109	3	US-09-943-906-74	Sequence 74, Appl	623	36	64.3	11	4	US-10-623-035-7	Sequence 7, Appl
551	37	66.1	109	4	US-10-435-602-74	Sequence 74, Appl	624	36	64.3	11	4	US-10-623-075-7	Sequence 7, Appl
552	37	66.1	109	6	US-11-027-139-74	Sequence 74, Appl	625	36	64.3	11	4	US-10-622-928-7	Sequence 7, Appl
553	37	66.1	110	5	US-10-996-316-209	Sequence 209, Appl	626	36	64.3	11	5	US-10-622-205-7	Sequence 7, Appl
554	37	66.1	111	4	US-10-203-754A-57	Sequence 57, Appl	627	36	64.3	11	6	US-11-061-956-38	Sequence 38, Appl
555	37	66.1	113	4	US-10-364-743-44	Sequence 44, Appl	628	36	64.3	11	6	US-11-115-682-316	Sequence 316, Appl
556	37	66.1	113	4	US-10-364-743-45	Sequence 45, Appl	629	36	64.3	12	4	US-10-411-869A-39	Sequence 39, Appl
557	37	66.1	113	4	US-10-364-743-46	Sequence 46, Appl	630	36	64.3	12	4	US-10-222-140A-7	Sequence 7, Appl
558	37	66.1	113	5	US-10-452-593-44	Sequence 44, Appl	631	36	64.3	31	3	US-09-956-206A-3	Sequence 3, Appl
559	37	66.1	113	5	US-10-452-593-45	Sequence 45, Appl	632	36	64.3	31	5	US-10-965-616-3	Sequence 3, Appl
560	37	66.1	113	5	US-10-452-593-46	Sequence 46, Appl	633	36	64.3	88	3	US-09-905-243-62	Sequence 62, Appl
561	37	66.1	113	5	US-10-916-758-78	Sequence 78, Appl	634	36	64.3	88	6	US-11-099-331-62	Sequence 62, Appl
562	37	66.1	127	4	US-10-774-076-11	Sequence 11, Appl	635	36	64.3	107	3	US-09-158-120A-20	Sequence 20, Appl
563	37	66.1	127	4	US-10-774-076-19	Sequence 19, Appl	636	36	64.3	107	3	US-09-158-120A-21	Sequence 21, Appl
564	37	66.1	130	2	US-08-779-784-35	Sequence 35, Appl	637	36	64.3	107	3	US-09-801-185A-1	Sequence 1, Appl
565	37	66.1	130	4	US-10-010-729-71	Sequence 71, Appl	638	36	64.3	107	3	US-09-801-185A-9	Sequence 9, Appl
566	37	66.1	130	5	US-10-683-451-33	Sequence 33, Appl	639	36	64.3	107	4	US-10-269-010-2	Sequence 2, Appl
567	37	66.1	139	6	US-11-131-648-16	Sequence 16, Appl	640	36	64.3	107	4	US-10-268-883-6	Sequence 6, Appl
568	37	66.1	139	6	US-11-131-648-41	Sequence 41, Appl	641	36	64.3	107	4	US-10-330-613-30	Sequence 30, Appl
569	37	66.1	144	4	US-10-642-120-4	Sequence 4, Appl	642	36	64.3	107	4	US-10-330-530-30	Sequence 30, Appl
570	37	66.1	144	4	US-10-642-060-4	Sequence 4, Appl	643	36	64.3	107	4	US-10-016-986-108	Sequence 108, Appl
571	37	66.1	144	4	US-10-642-122-4	Sequence 4, Appl	644	36	64.3	107	4	US-10-133-715-9	Sequence 9, Appl
572	37	66.1	144	4	US-10-642-059-4	Sequence 4, Appl	645	36	64.3	107	4	US-10-133-715-9	Sequence 9, Appl
573	37	66.1	144	4	US-10-642-124-4	Sequence 4, Appl	646	36	64.3	107	4	US-10-302-356A-1	Sequence 1, Appl
574	37	66.1	144	4	US-10-621-269-4	Sequence 4, Appl	647	36	64.3	107	4	US-10-302-356A-9	Sequence 9, Appl
575	37	66.1	144	4	US-10-620-850-4	Sequence 4, Appl	648	36	64.3	107	4	US-10-340-189-1	Sequence 1, Appl
576	37	66.1	144	4	US-10-642-118-4	Sequence 4, Appl	649	36	64.3	107	4	US-10-163-657A-1	Sequence 1, Appl
577	37	66.1	144	4	US-10-642-119-4	Sequence 4, Appl	650	36	64.3	107	4	US-10-163-657A-9	Sequence 9, Appl
578	37	66.1	144	4	US-10-642-117-4	Sequence 4, Appl	651	36	64.3	107	4	US-10-325-696-1	Sequence 1, Appl
579	37	66.1	144	5	US-10-642-099-4	Sequence 4, Appl	652	36	64.3	107	4	US-10-422-287-1	Sequence 1, Appl
580	37	66.1	144	5	US-10-642-064-4	Sequence 4, Appl	653	36	64.3	107	4	US-10-422-287-9	Sequence 9, Appl
581	37	66.1	144	5	US-10-642-116-4	Sequence 4, Appl	654	36	64.3	107	4	US-10-660-337-30	Sequence 30, Appl
582	37	66.1	144	5	US-10-642-100-4	Sequence 4, Appl	655	36	64.3	107	4	US-10-622-932-1	Sequence 1, Appl
583	37	66.1	144	5	US-10-642-058-4	Sequence 4, Appl	656	36	64.3	107	4	US-10-622-932-9	Sequence 9, Appl
584	37	66.1	144	5	US-10-642-121-4	Sequence 4, Appl	657	36	64.3	107	4	US-10-623-065-1	Sequence 1, Appl
585	37	66.1	144	5	US-10-642-065-4	Sequence 4, Appl	658	36	64.3	107	4	US-10-623-065-9	Sequence 9, Appl
586	37	66.1	144	5	US-10-642-071-4	Sequence 4, Appl	659	36	64.3	107	4	US-10-623-076-1	Sequence 1, Appl
587	37	66.1	162	4	US-10-156-761-7786	Sequence 7786, Ap	660	36	64.3	107	4	US-10-623-076-9	Sequence 9, Appl
588	37	66.1	214	5	US-10-916-758-20	Sequence 20, Appl	661	36	64.3	107	4	US-10-723-434-19	Sequence 19, Appl
589	37	66.1	226	5	US-10-813-977-17	Sequence 17, Appl	662	36	64.3	107	4	US-10-723-434-23	Sequence 23, Appl
590	37	66.1	236	4	US-10-401-344-4	Sequence 4, Appl	663	36	64.3	107	4	US-10-723-434-24	Sequence 24, Appl
591	37	66.1	236	5	US-10-879-994-6	Sequence 6, Appl	664	36	64.3	107	4	US-10-622-210-1	Sequence 1, Appl
592	37	66.1	236	5	US-10-610-452-6	Sequence 6, Appl	665	36	64.3	107	4	US-10-622-210-9	Sequence 9, Appl
593	37	66.1	237	3	US-09-924-099-9	Sequence 9, Appl	666	36	64.3	107	4	US-10-623-035-1	Sequence 1, Appl
594	37	66.1	243	3	US-09-924-099-10	Sequence 10, Appl	667	36	64.3	107	4	US-10-623-035-9	Sequence 9, Appl
595	37	66.1	252	4	US-10-239-656-55	Sequence 55, Appl	668	36	64.3	107	4	US-10-623-075-1	Sequence 1, Appl
596	37	66.1	257	4	US-10-239-656-67	Sequence 67, Appl	669	36	64.3	107	4	US-10-623-075-9	Sequence 9, Appl
597	37	66.1	428	5	US-10-450-763-39125	Sequence 39125, A	670	36	64.3	107	4	US-10-622-928-1	Sequence 1, Appl
598	37	66.1	470	4	US-10-369-493-6721	Sequence 6721, Ap	671	36	64.3	107	4	US-10-622-928-9	Sequence 9, Appl
599	37	66.1	499	4	US-10-239-656-73	Sequence 73, Appl	672	36	64.3	107	5	US-10-622-205-1	Sequence 1, Appl
600	37	66.1	623	4	US-10-452-024-72	Sequence 72, Appl	673	36	64.3	107	5	US-10-622-205-9	Sequence 9, Appl
601	37	66.1	623	4	US-10-452-024-73	Sequence 73, Appl	674	36	64.3	107	6	US-11-133-775-1	Sequence 1, Appl
602	37	66.1	623	4	US-10-452-024-170	Sequence 170, App	675	36	64.3	108	3	US-09-229-200A-11	Sequence 11, Appl
603	37	66.1	623	4	US-10-452-024-171	Sequence 171, App	676	36	64.3	108	3	US-09-229-200A-15	Sequence 15, Appl
604	37	66.1	623	4	US-10-452-024-172	Sequence 172, App	677	36	64.3	108	4	US-10-222-140A-1	Sequence 1, Appl
605	37	66.1	626	4	US-10-452-024-74	Sequence 74, Appl	678	36	64.3	108	4	US-10-307-276B-4	Sequence 4, Appl
606	37	66.1	1832	4	US-10-282-132A-62735	Sequence 62735, A	679	36	64.3	108	4	US-10-307-276B-6	Sequence 6, Appl
607	36	64.3	11	3	US-09-192-854-178	Sequence 178, App	680	36	64.3	108	5	US-10-706-689-11	Sequence 11, Appl
608	36	64.3	11	3	US-09-861-294-22	Sequence 22, Appl	681	36	64.3	108	5	US-10-988-360-11	Sequence 11, Appl
609	36	64.3	11	3	US-09-968-561A-316	Sequence 316, Appl	682	36	64.3	108	6	US-11-061-956-4	Sequence 4, Appl
610	36	64.3	11	3	US-09-801-185A-7	Sequence 7, Appl	683	36	64.3	108	6	US-11-061-956-6	Sequence 6, Appl
611	36	64.3	11	3	US-09-968-744A-316	Sequence 316, Appl	684	36	64.3	109	4	US-10-078-757B-49	Sequence 49, Appl

685	36	64.3	113	4	US-10-364-743-52	Sequence 52, Appl	758	35	62.5	107	5	US-10-503-504-7	Sequence 7, Appl
686	36	64.3	113	5	US-10-452-593-52	Sequence 52, Appl	759	35	62.5	107	5	US-10-484-280-2	Sequence 2, Appl
687	36	64.3	127	4	US-10-288-883-5	Sequence 5, Appl	760	35	62.5	107	5	US-10-484-280-12	Sequence 12, Appl
688	36	64.3	127	4	US-10-395-894-21	Sequence 21, Appl	761	35	62.5	107	5	US-10-484-280-27	Sequence 27, Appl
689	36	64.3	127	4	US-10-695-667-21	Sequence 21, Appl	762	35	62.5	107	5	US-10-949-135-26	Sequence 46, Appl
690	36	64.3	127	5	US-10-976-352-21	Sequence 21, Appl	763	35	62.5	107	5	US-10-506-997-43	Sequence 43, Appl
691	36	64.3	127	5	US-09-797-481-2	Sequence 2, Appl	764	35	62.5	108	3	US-09-848-798-41	Sequence 41, Appl
692	36	64.3	142	3	US-09-844-736-4	Sequence 4, Appl	765	35	62.5	108	3	US-10-268-883-12	Sequence 12, Appl
693	36	64.3	142	4	US-10-162-396-4	Sequence 4, Appl	766	35	62.5	108	5	US-10-726-332-26	Sequence 26, Appl
694	36	64.3	142	5	US-10-819-493-4	Sequence 4, Appl	767	35	62.5	109	3	US-09-798-058-4	Sequence 4, Appl
695	36	64.3	150	4	US-10-153-382-33	Sequence 33, Appl	768	35	62.5	109	4	US-10-220-418-4	Sequence 4, Appl
696	36	64.3	150	5	US-10-612-497-24	Sequence 24, Appl	769	35	62.5	111	4	US-10-203-754A-19	Sequence 19, Appl
697	36	64.3	150	5	US-10-612-497-98	Sequence 98, Appl	770	35	62.5	111	4	US-10-251-215-42	Sequence 42, Appl
698	36	64.3	150	5	US-10-776-649-24	Sequence 24, Appl	771	35	62.5	127	4	US-10-309-762-99	Sequence 99, Appl
699	36	64.3	150	5	US-10-776-649-98	Sequence 98, Appl	772	35	62.5	128	4	US-10-687-035-31	Sequence 31, Appl
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701	36	64.3	150	6	US-11-085-368-79	Sequence 79, Appl	774	35	62.5	129	3	US-09-007-093-2	Sequence 2, Appl
702	36	64.3	203	4	US-10-424-599-148081	Sequence 148081,	775	35	62.5	129	4	US-10-428-754-2	Sequence 2, Appl
703	36	64.3	239	4	US-10-423-847-18	Sequence 18, Appl	776	35	62.5	129	6	US-11-003-839-38	Sequence 38, Appl
704	36	64.3	239	5	US-10-831-063-18	Sequence 18, Appl	777	35	62.5	130	4	US-10-268-883-11	Sequence 11, Appl
705	36	64.3	244	3	US-09-880-748-82	Sequence 82, Appl	778	35	62.5	144	4	US-10-607-095-4	Sequence 4, Appl
706	36	64.3	244	3	US-09-880-748-164	Sequence 164, App	779	35	62.5	148	4	US-10-222-026A-25	Sequence 25, Appl
707	36	64.3	244	3	US-09-880-748-261	Sequence 261, App	780	35	62.5	159	4	US-10-767-701-38406	Sequence 38406, A
708	36	64.3	244	3	US-09-880-748-280	Sequence 280, App	781	35	62.5	187	4	US-10-094-749-1922	Sequence 1922, Ap
709	36	64.3	244	3	US-10-293-418-82	Sequence 82, Appl	782	35	62.5	187	4	US-09-738-626-4300	Sequence 4300, Ap
710	36	64.3	244	4	US-10-293-418-164	Sequence 164, App	783	35	62.5	214	5	US-10-503-504-8	Sequence 8, Appl
711	36	64.3	244	4	US-10-293-418-261	Sequence 261, App	784	35	62.5	214	5	US-10-484-280-14	Sequence 14, Appl
712	36	64.3	244	4	US-10-293-418-280	Sequence 280, App	785	35	62.5	214	5	US-10-880-028-41	Sequence 41, Appl
713	36	64.3	247	4	US-10-423-847-13	Sequence 13, Appl	786	35	62.5	214	5	US-10-880-320-41	Sequence 41, Appl
714	36	64.3	247	5	US-10-831-063-13	Sequence 13, Appl	787	35	62.5	232	3	US-09-778-320-294	Sequence 294, App
715	36	64.3	249	4	US-10-423-847-16	Sequence 16, Appl	788	35	62.5	232	3	US-09-910-689-294	Sequence 294, App
716	36	64.3	249	5	US-10-831-063-16	Sequence 16, Appl	789	35	62.5	232	4	US-10-010-742-294	Sequence 294, App
717	36	64.3	250	4	US-10-423-847-12	Sequence 12, Appl	790	35	62.5	232	4	US-10-714-389-294	Sequence 294, App
718	36	64.3	250	4	US-10-423-847-15	Sequence 15, Appl	791	35	62.5	232	4	US-10-717-296-294	Sequence 294, App
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726	36	64.3	253	5	US-10-831-063-11	Sequence 11, Appl	799	35	62.5	253	4	US-10-293-418-936	Sequence 936, App
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729	36	64.3	416	4	US-10-421-467A-68	Sequence 68, Appl	802	35	62.5	265	3	US-09-910-689-41	Sequence 41, Appl
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734	35.5	63.4	129	3	US-10-309-764-85	Sequence 85, Appl	807	35	62.5	287	4	US-10-222-026A-37	Sequence 37, Appl
735	35	62.5	11	3	US-08-798-058-8	Sequence 8, Appl	808	35	62.5	287	4	US-10-406-830-5	Sequence 5, Appl
736	35	62.5	11	4	US-10-220-418-8	Sequence 8, Appl	809	35	62.5	289	3	US-09-778-320-40	Sequence 40, Appl
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738	35	62.5	118	5	US-10-482-630-118	Sequence 118, App	811	35	62.5	289	3	US-09-510-662A-40	Sequence 40, Appl
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752	35	62.5	106	4	US-10-466-242-8	Sequence 8, Appl	825	35	62.5	440	4	US-10-058-270A-120	Sequence 120, App
753	35	62.5	106	4	US-10-466-242-34	Sequence 34, Appl	826	35	62.5	440	4	US-10-714-389-39	Sequence 39, Appl
754	35	62.5	107	4	US-10-091-300-43	Sequence 43, Appl	827	35	62.5	440	4	US-10-717-296-39	Sequence 39, Appl
755	35	62.5	107	4	US-10-309-762-87	Sequence 87, Appl	828	35	62.5	440	5	US-10-643-795A-104	Sequence 104, App
756	35	62.5	107	4	US-10-723-434-28	Sequence 28, Appl	829	35	62.5	440	5	US-10-948-518-104	Sequence 104, App
757	35	62.5	107	5	US-10-482-630-95	Sequence 95, Appl	830	35	62.5	440	5	US-10-482-630A-164	Sequence 164, App

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833	35	62.5	602	4	US-10-369-493-3842	Sequence 3842, App	906	34	60.7	11	3	US-09-968-744A-172	Sequence 172, App
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842	35	62.5	1216	6	US-11-084-955-2	Sequence 2, App	915	34	60.7	11	3	US-09-968-744A-280	Sequence 280, App
843	35	62.5	1428	4	US-10-437-963-103290	Sequence 103290, A	916	34	60.7	11	3	US-09-968-744A-292	Sequence 292, App
844	35	62.5	1457	4	US-10-327-288-2	Sequence 2, App	917	34	60.7	11	3	US-09-968-744A-304	Sequence 304, App
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846	35	62.5	1469	4	US-10-607-095-16	Sequence 16, App	919	34	60.7	11	3	US-09-968-561A-16	Sequence 16, App
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879	34	60.7	11	3	US-09-968-561A-226	Sequence 226, App	952	34	60.7	11	4	US-10-203-754A-7	Sequence 7, App
880	34	60.7	11	3	US-09-968-561A-232	Sequence 232, App	953	34	60.7	11	4	US-10-203-754A-48	Sequence 48, App
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882	34	60.7	11	3	US-09-968-561A-250	Sequence 250, App	955	34	60.7	11	4	US-10-279-633-51	Sequence 51, App
883	34	60.7	11	3	US-09-968-561A-256	Sequence 256, App	956	34	60.7	11	4	US-10-279-633-54	Sequence 54, App
884	34	60.7	11	3	US-09-968-561A-280	Sequence 280, App	957	34	60.7	11	4	US-10-745-455-10	Sequence 10, App
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889	34	60.7	11	3	US-09-968-744A-16	Sequence 16, App	962	34	60.7	11	5	US-10-631-722-1	Sequence 1, App
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903	34	60.7	11	3	US-09-968-744A-154	Sequence 154, App	976	34	60.7	11	6	US-11-115-682-64	Sequence 64, App

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977      34      60.7      11      6      US-11-115-682-100      Sequence 100, App
978      34      60.7      11      6      US-11-115-682-106      Sequence 106, App
979      34      60.7      11      6      US-11-115-682-112      Sequence 112, App
980      34      60.7      11      6      US-11-115-682-118      Sequence 118, App
981      34      60.7      11      6      US-11-115-682-124      Sequence 124, App
982      34      60.7      11      6      US-11-115-682-136      Sequence 136, App
983      34      60.7      11      6      US-11-115-682-154      Sequence 154, App
984      34      60.7      11      6      US-11-115-682-160      Sequence 160, App
985      34      60.7      11      6      US-11-115-682-166      Sequence 166, App
986      34      60.7      11      6      US-11-115-682-172      Sequence 172, App
987      34      60.7      11      6      US-11-115-682-178      Sequence 178, App
988      34      60.7      11      6      US-11-115-682-202      Sequence 202, App
989      34      60.7      11      6      US-11-115-682-208      Sequence 208, App
990      34      60.7      11      6      US-11-115-682-226      Sequence 226, App
991      34      60.7      11      6      US-11-115-682-232      Sequence 232, App
992      34      60.7      11      6      US-11-115-682-244      Sequence 244, App
993      34      60.7      11      6      US-11-115-682-250      Sequence 250, App
994      34      60.7      11      6      US-11-115-682-256      Sequence 256, App
995      34      60.7      11      6      US-11-115-682-280      Sequence 280, App
996      34      60.7      11      6      US-11-115-682-292      Sequence 292, App
997      34      60.7      11      6      US-11-115-682-304      Sequence 304, App
998      34      60.7      11      6      US-11-010-797-10      Sequence 10, Appl
999      34      60.7      12      3      US-09-791-551-18      Sequence 18, Appl
1000     34      60.7      13      5      US-10-496-869-15      Sequence 15, Appl
```

ALIGNMENTS

```
RESULT 1
US-09-155-106-4
; Sequence 4, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09155,106
; FILING DATE: 20-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: peptide
US-09-155-106-4
```

```
Query Match      100.0%; Score 56; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1      RASQDIGNYL 11
      |||||
Db      1      RASQDIGNYL 11
```

```
RESULT 2
US-10-808-538-4
; Sequence 4, Application US/10808538
```

```
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-808-538-4

Query Match      100.0%; Score 56; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      RASQDIGNYL 11
      |||||
Db      1      RASQDIGNYL 11

RESULT 3
US-09-155-106-22
; Sequence 22, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22
  Query Match      100.0%; Score 56; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.026;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
    |||||
Db 24 RASQDIGNYL 34

RESULT 4
US-09-155-106-23
; Sequence 23, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23
  Query Match      100.0%; Score 56; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.026;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
    |||||
Db 24 RASQDIGNYL 34

RESULT 5
US-09-155-106-24
; Sequence 24, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-24
  Query Match      100.0%; Score 56; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.026;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
    |||||
Db 24 RASQDIGNYL 34

RESULT 6
US-09-155-106-28
; Sequence 28, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-28
  Query Match      100.0%; Score 56; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.026;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
    |||||
Db 24 RASQDIGNYL 34

RESULT 7
US-09-155-106-30
; Sequence 30, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/155,106
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-155-106-30

Query Match 100.0%; Score 56; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
| | | | | | | | | |
Db 24 RASQDIGNYL 34

RESULT 8

US-10-808-538-22
; Sequence 22, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106

FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-808-538-22

Query Match 100.0%; Score 56; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
| | | | | | | | | |
Db 24 RASQDIGNYL 34

RESULT 9

US-10-808-538-23
; Sequence 23, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106

FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-808-538-23

Query Match 100.0%; Score 56; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 11
| | | | | | | | | |
Db 24 RASQDIGNYL 34

RESULT 10

US-10-808-538-24
; Sequence 24, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible


```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-808-538-24

```

Query Match 100.0%; Score 56; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 RASQDIGNYL 11
   |||||
Db 24 RASQDIGNYL 34

```

```

RESULT 11
US-10-808-538-28
; Sequence 28, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-808-538-28

```

Query Match 100.0%; Score 56; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 RASQDIGNYL 11
   |||||
Db 24 RASQDIGNYL 34

RESULT 12
US-10-808-538-30
; Sequence 30, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-808-538-30

```

Query Match 100.0%; Score 56; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 RASQDIGNYL 11
   |||||
Db 24 RASQDIGNYL 34

```

```

RESULT 13
US-10-466-242-20
; Sequence 20, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens

```



```
;
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(106)
; OTHER INFORMATION: Clone 2a:4 VK
US-10-466-242-20

Query Match      83.9%; Score 47; DB 4; Length 106;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 23 QASQDIGNYL 32

RESULT 14
US-10-140-555-8
; Sequence 8, Application US/10140555
; Publication No. US2002012727A1
; GENERAL INFORMATION:
; APPLICANT: Julie A. Abrahamson
; APPLICANT: Stephen D. Holmes
; APPLICANT: Jeffrey R. Jackson
; TITLE OF INVENTION: RHAMM Antagonist Antibodies
; FILE REFERENCE: P50857
; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(11)
; OTHER INFORMATION: light chain CDR 1
US-10-140-555-8

Query Match      80.4%; Score 45; DB 4; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 1 RASQDIGNYL 10

RESULT 15
US-10-279-633-47
; Sequence 47, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; TITLE OF INVENTION: VARIATION
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-47
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```
Query Match      80.4%; Score 45; DB 4; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 1 RASQDIGNYL 10

RESULT 16
US-10-473-977-18
; Sequence 18, Application US/10473977
; Publication No. US20040253233A1
; GENERAL INFORMATION:
; APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al
; TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND THE USE THEREOF
; FILE REFERENCE: 4565-0107P
; CURRENT APPLICATION NUMBER: US/10/473,977
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/CU02/00003
; PRIOR FILING DATE: 2002-04-06
; PRIOR APPLICATION NUMBER: CU 84/2001
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(11)
US-10-473-977-18
```

```
Query Match      80.4%; Score 45; DB 5; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 1 RASQDIGNYL 10

RESULT 17
US-10-783-311-152
; Sequence 152, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-152
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Query Match      80.4%; Score 45; DB 5; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
```

	Db	1 RASQDISNYL 10		
	RESULT 18			
	US-10-725-962-102			
	; Sequence 102, Application US/10725962			
	; Publication No. US20050013809A1			
	; GENERAL INFORMATION:			
	; APPLICANT: Samuel M. Owens			
	; APPLICANT: Frank I. Carroll			
	; APPLICANT: Philip Abraham			
	; APPLICANT: Melinda G. Gunnell			
	; APPLICANT: Mary Haak-Frendscho			
	; APPLICANT: Xiao Feng			
	; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE			
	; FILE REFERENCE: ABGENIX.071A			
	; CURRENT APPLICATION NUMBER: US/10/725,962			
	; CURRENT FILING DATE: 2003-12-02			
	; PRIOR APPLICATION NUMBER: 60/430717			
	; PRIOR FILING DATE: 2002-12-02			
	; NUMBER OF SEQ ID NOS: 141			
	; SOFTWARE: FastSeq for Windows Version 4.0			
	; SEQ ID NO 102			
	; LENGTH: 11			
	; TYPE: PRT			
	; ORGANISM: Mus musculus			
	US-10-725-962-102			
	Query Match	80.4%;	Score 45;	DB 5; Length 11;
	Best Local Similarity	90.0%;	Pred. No. 0.24;	
	Matches	9; Conservative	0; Mismatches	1; Indels
				0; Gaps
				0;
	QY	1 RASQDISNYL 10		
	Db	1 RASQDISNYL 10		
	RESULT 19			
	US-09-956-206A-5			
	; Sequence 5, Application US/09956206A			
	; Patent No. US20020164339A1			
	; GENERAL INFORMATION:			
	; APPLICANT: DO COUTO, FERNANDO J.R.			
	; CERIANI, ROBERTO L.			
	; PETERSON, JERRY A.			
	; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE			
	; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND			
	; METHODS OF HUMANIZING ANTIBODY PEPTIDES			
	NUMBER OF SEQUENCES: 81			
	CORRESPONDENCE ADDRESS:			
	ADDRESSEE: MORRISON & FOERSTER			
	STREET: 755 Page Mill Road			
	CITY: Palo Alto			
	STATE: CA			
	COUNTRY: USA			
	ZIP: 94304-1018			
	COMPUTER READABLE FORM:			
	MEDIUM TYPE: Floppy disk			
	OPERATING SYSTEM: PC-DOS/MS-DOS			
	SOFTWARE: PatentIn Release #1.0, Version #1.30			
	CURRENT APPLICATION DATA:			
	APPLICATION NUMBER: US/09/956,206A			
	FILING DATE: 19-Apr-2002			
	CLASSIFICATION: <Unknown>			
	PRIOR APPLICATION DATA:			
	APPLICATION NUMBER: US 08/525,539			
	FILING DATE: 14-SEP-1995			
	APPLICATION NUMBER: PCT/US95/11683			
	FILING DATE: 14-SEP-1995			
	APPLICATION NUMBER: 08/487,598			
	FILING DATE: 14-SEP-1995			
	APPLICATION NUMBER: 08/487,598			
	FILING DATE: 14-SEP-1995			
	ATTORNEY/AGENT INFORMATION:			
	NAME: WITT, ERIC			
	REGISTRATION NUMBER: 44,408			
	REFERENCE/DOCKET NUMBER: 276332000101			
	TELECOMMUNICATION INFORMATION:			
	TELEPHONE: (650) 813-5600			
	TELEFAX: (650) 494-0792			
	INFORMATION FOR SEQ ID NO: 5:			
	SEQUENCE CHARACTERISTICS:			
	LENGTH: 31 amino acids			
	TYPE: amino acid			
	STRANDEDNESS: single			
	TOPOLOGY: linear			
	SEQUENCE DESCRIPTION: SEQ ID NO: 5:			
	US-09-956-206A-5			
	Query Match	80.4%;	Score 45;	DB 3; Length 31;
	Best Local Similarity	90.0%;	Pred. No. 0.71;	
	Matches	9; Conservative	0; Mismatches	1; Indels
				0; Gaps
				0;
	QY	1 RASQDISNYL 10		
	Db	1 RASQDISNYL 20		
	RESULT 20			
	US-10-965-616-5			
	; Sequence 5, Application US/10965616			
	; Publication No. US20050169915A1			
	; GENERAL INFORMATION:			
	; APPLICANT: DO COUTO, FERNANDO J.R.			
	; CERIANI, ROBERTO L.			
	; PETERSON, JERRY A.			
	; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE			
	; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND			
	; METHODS OF HUMANIZING ANTIBODY PEPTIDES			
	NUMBER OF SEQUENCES: 81			
	CORRESPONDENCE ADDRESS:			
	ADDRESSEE: MORRISON & FOERSTER			
	STREET: 755 Page Mill Road			
	CITY: Palo Alto			
	STATE: CA			
	COUNTRY: USA			
	ZIP: 94304-1018			
	COMPUTER READABLE FORM:			
	MEDIUM TYPE: Floppy disk			

;
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-965-616-5

Query Match 80.4%; Score 45; DB 5; Length 31;
Best Local Similarity 90.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 11 RASQDISNYL 20

RESULT 21
US-09-892-613C-10
; Sequence 10, Application US/09892613C
; Publication No. US20030040606A1
; GENERAL INFORMATION:
; APPLICANT: Leung, Shawn Shui-on
; TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-PATCHING
; FILE REFERENCE: 655
; CURRENT APPLICATION NUMBER: US/09/892.613C
; CURRENT FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Chimaera sp.
US-09-892-613C-10

Query Match 80.4%; Score 45; DB 3; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 24 RASQDISNYL 33

RESULT 22
US-10-011-931-4
; Sequence 4, Application US/10011931
; Publication No. US20030028606A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING OF AN ANTIBODY TO AN IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011.931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-011-931-4

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;

Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 24 RASQDISNYL 33

RESULT 23
US-10-411-037-51
; Sequence 51, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411.037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-51

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 RASQDIGNYL 10
| | | | | | | |
Db 24 RASQDINNLY 33

RESULT 24
US-10-411-037-52
; Sequence 52, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411.037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523

;
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-52

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDINNYL 33

RESULT 25
US-10-411-026-51
; Sequence 51, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-51

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10

Db 24 RASQDINNYL 33
|||||
|||

RESULT 26
US-10-411-026-52
; Sequence 52, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-026-52

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDINNYL 33

RESULT 27
US-10-251-085B-145
; Sequence 145, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human

US-10-251-0858-145

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||

Db 24 RASQDISNYL 33

RESULT 28

US-10-410-962-51
; Sequence 51, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-410-962-51

US-10-410-962-51

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||

Db 24 RASQDINNLY 33

RESULT 29

US-10-410-962-52
; Sequence 52, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-410-962-51

FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-410-962-52

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||

Db 24 RASQDINNLY 33

RESULT 30

US-10-411-049-51
; Sequence 51, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-411-049-51

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Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 31
US-10-411-049-52
; Sequence 52, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-049-52

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 32
US-10-410-930-51
; Sequence 51, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
```

```
Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 33
US-10-410-930-52
; Sequence 52, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-930-51

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
DB      24 RASQDINNLY 33

RESULT 34
US-10-410-930-53
; Sequence 53, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5057
; CURRENT APPLICATION NUMBER: US/10/410,930
```

```
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQDIGNYL 10
    ||||| |||
Db 24 RASQDINNYL 33

RESULT 34
US-10-410-997-51
; Sequence 51, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-51

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
    ||||| |||
Db 24 RASQDINNYL 33

RESULT 35
US-10-410-997-52
; Sequence 52, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
```

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; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-997-52

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
    ||||| |||
Db 24 RASQDINNYL 33

RESULT 36
US-10-411-012-51
; Sequence 51, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GLYCOEGLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-012-51

Query Match 80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 RASQDIGNYL 10
Db      24 RASQDINNVL 33

US-10-411-012-52
; Sequence 52, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GLYCOREGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-012-52

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 RASQDINNVL 33

US-10-411-012-52
; Sequence 51, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-287-994-51

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 RASQDINNVL 33

US-10-287-994-51
; Sequence 52, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-287-994-52

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 RASQDINNVL 33

US-10-287-994-52
; Sequence 52, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-287-994-52

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 RASQDINNVL 33

US-10-287-994-52
; Sequence 51, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
```



```
RESULT 40
US-10-410-913-51
; Sequence 51, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-913-51

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
        ||||| |||
Db      24 RASQDINNYL 33

RESULT 41
US-10-410-913-52
; Sequence 52, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-913-51

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
        ||||| |||
Db      24 RASQDINNYL 33

RESULT 42
US-10-737-252-145
; Sequence 145, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdich, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-145

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
        ||||| |||
Db      24 RASQDISNYL 33

RESULT 43
US-10-741-657A-16
; Sequence 16, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 107
```

```
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-913-52
```

```
Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
        ||||| |||
Db      24 RASQDINNYL 33
```

```
RESULT 42
US-10-737-252-145
; Sequence 145, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdich, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-145
```

```
Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
        ||||| |||
Db      24 RASQDISNYL 33
```

```
RESULT 43
US-10-741-657A-16
; Sequence 16, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 107
```

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; TYPE: PRT
; ORGANISM: Mus sp.
US-10-741-657A-16

Query Match      80.4%; Score 45; DB 4; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
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Db 24 RASQDISNYL 33

RESULT 44
US-10-473-977-69
; Sequence 69, Application US/10473977
; Publication No. US2004025323A1
; GENERAL INFORMATION:
; APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al
; TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND THE USE THEREOF
; FILE REFERENCE: 4565-0107P
; CURRENT APPLICATION NUMBER: US/10/473,977
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/CU02/00003
; PRIOR FILING DATE: 2002-04-06
; PRIOR APPLICATION NUMBER: CU 84/2001
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(107)
US-10-473-977-69

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
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Db 24 RASQDISNYL 33

RESULT 45
US-10-410-980-51
; Sequence 51, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
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; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-980-51

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
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Db 24 RASQDINNYL 33

RESULT 46
US-10-410-980-52
; Sequence 52, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-980-52

Query Match      80.4%; Score 45; DB 5; Length 107;
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
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Db 24 RASQDINNYL 33

RESULT 47
US-10-482-759-10
; Sequence 10, Application US/10482759
; Publication No. US20050033028A1
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; GENERAL INFORMATION:
; APPLICANT: Leung, Shawn Shui-on
; TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-PATCHING
; FILE REFERENCE: 655
; CURRENT APPLICATION NUMBER: US/10/482,759
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 09/892,613
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Chimaera sp.
US-10-482-759-10

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 48
US-10-985-299-4
; Sequence 4, Application US/10985299
; Publication No. US20050084493A1
; GENERAL INFORMATION:
; APPLICANT: WITTE, ALISON
; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: SCREENING METHOD FOR ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING
; TITLE OF INVENTION: AGENTS THAT ALLOW BINDING TO IL-1 RECEPTOR BUT NOT ACTIVATION
; TITLE OF INVENTION: THEREOF (as amended)
; FILE REFERENCE: A-731A
; CURRENT APPLICATION NUMBER: US/10/985,299
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 10/011,931
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-985-299-4

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 49
US-10-410-897-51
; Sequence 51, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFreeze, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Rowe, Caryn
US-10-410-897-51

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDISNYL 33

RESULT 49
US-10-410-897-51
; Sequence 51, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFreeze, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Rowe, Caryn
US-10-410-897-51

; GENERAL INFORMATION:
; APPLICANT: Leung, Shawn Shui-on
; TITLE OF INVENTION: REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY FRAMEWORK-PATCHING
; FILE REFERENCE: 655
; CURRENT APPLICATION NUMBER: US/10/482,759
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 09/892,613
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-897-51

Query Match      80.4%; Score 45; DB 5; Length 107;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDINNVL 33

RESULT 50
US-10-410-897-52
; Sequence 52, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFreeze, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Rowe, Caryn
US-10-410-897-52

; TITLE OF INVENTION: FACTOR IX; REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-897-52

; TITLE OF INVENTION: FACTOR IX; REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
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; ORGANISM: Mus musculus
US-10-410-897-52
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Query Match 80.4%; Score 45; DB 5; Length 107;
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Qy 1 RASQDIGNYL 10
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 Db 24 RASQDINNYL 33

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Title: US-10-808-538-4
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Sequence: 1 RASQDIGNYLRL 11

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Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA.New.*

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- 4: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	45	80.4	107	US-11-183-205-52
6	45	80.4	108	US-10-981-300-23
7	45	80.4	127	US-11-089-872-5
8	45	80.4	214	US-10-981-300-14
9	45	80.4	214	US-11-183-218-55
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16	43	76.8	108	US-11-009-939-37
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18	43	76.8	247	US-11-084-717-21
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22	43	76.8	247	11	US-11-179-244-23	Sequence 23, Appl
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43	41	73.2	95	11	US-11-084-554-148	Sequence 148, App
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46	41	73.2	95	11	US-11-061-848-68	Sequence 68, Appl
47	41	73.2	95	11	US-11-004-590-68	Sequence 69, Appl
48	41	73.2	95	11	US-11-004-590-69	Sequence 69, Appl
49	41	73.2	95	11	US-11-136-250-145	Sequence 145, App
50	41	73.2	95	11	US-11-136-250-148	Sequence 148, App
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58	41	73.2	108	11	US-11-127-677-38	Sequence 38, Appl
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88	40	71.4	110	9	US-10-648-816-1	Sequence 1, Appl
89	40	71.4	110	9	US-10-648-816-5	Sequence 5, Appl
90	40	71.4	119	9	US-10-993-543-102	Sequence 102, App
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94	40	71.4	128	11	US-11-228-319-10	Sequence 10, Appl

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96	40	71.4	277	11	US-11-126-817-52	Sequence 52, Appl	169	38	67.9	108	11	US-11-098-758-188	Sequence 188, App
97	39	69.6	11	9	US-10-510-229-17	Sequence 17, Appl	170	38	67.9	108	11	US-11-098-758-190	Sequence 190, App
98	39	69.6	27	11	US-11-143-077-6	Sequence 6, Appl	171	38	67.9	109	11	US-11-049-536-324	Sequence 324, App
99	39	69.6	27	11	US-11-187-364-6	Sequence 6, Appl	172	38	67.9	109	11	US-11-199-739-324	Sequence 324, App
100	39	69.6	107	10	US-11-254-182-5	Sequence 5, Appl	173	38	67.9	119	9	US-10-993-543-122	Sequence 122, App
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104	39	69.6	107	11	US-11-182-308-5	Sequence 5, Appl	177	38	67.9	241	11	US-11-266-444-1577	Sequence 1577, App
105	39	69.6	107	11	US-11-049-536-116	Sequence 116, App	178	38	67.9	242	11	US-11-054-515-1915	Sequence 1915, App
106	39	69.6	107	11	US-11-049-536-159	Sequence 159, App	179	38	67.9	242	11	US-11-266-444-1915	Sequence 1915, App
107	39	69.6	107	11	US-11-102-120-5	Sequence 5, Appl	180	38	67.9	247	11	US-11-054-515-3240	Sequence 3240, App
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110	39	69.6	107	11	US-11-199-739-159	Sequence 159, App	183	38	67.9	251	11	US-11-054-515-1921	Sequence 1921, App
111	39	69.6	107	11	US-11-222-587-5	Sequence 5, Appl	184	38	67.9	251	11	US-11-266-444-1921	Sequence 1921, App
112	39	69.6	107	11	US-11-234-586-5	Sequence 5, Appl	185	37	66.1	95	10	US-11-239-308-60	Sequence 60, Appl
113	39	69.6	108	9	US-10-665-658-3	Sequence 3, Appl	186	37	66.1	95	11	US-11-054-669-93	Sequence 93, Appl
114	39	69.6	108	9	US-10-834-397-14	Sequence 14, Appl	187	37	66.1	95	11	US-11-084-554-106	Sequence 106, App
115	39	69.6	108	10	US-11-254-182-27	Sequence 27, Appl	188	37	66.1	95	11	US-11-061-848-49	Sequence 49, Appl
116	39	69.6	108	10	US-11-219-121-23	Sequence 23, Appl	189	37	66.1	95	11	US-11-004-590-98	Sequence 98, Appl
117	39	69.6	108	11	US-11-120-338-3	Sequence 3, Appl	190	37	66.1	95	11	US-11-136-250-106	Sequence 106, App
118	39	69.6	108	11	US-11-106-820-3	Sequence 3, Appl	191	37	66.1	106	11	US-11-004-590-388	Sequence 388, App
119	39	69.6	108	11	US-11-143-077-3	Sequence 3, Appl	192	37	66.1	107	11	US-11-126-798-47	Sequence 47, Appl
120	39	69.6	108	11	US-11-190-364-3	Sequence 3, Appl	193	37	66.1	108	9	US-10-925-366A-186	Sequence 186, App
121	39	69.6	108	11	US-11-147-780-3	Sequence 3, Appl	194	37	66.1	108	9	US-10-925-366A-205	Sequence 205, App
122	39	69.6	108	11	US-11-143-386-3	Sequence 3, Appl	195	37	66.1	108	10	US-11-239-308-28	Sequence 28, Appl
123	39	69.6	108	11	US-11-187-364-3	Sequence 3, Appl	196	37	66.1	108	11	US-11-098-758-186	Sequence 186, App
124	39	69.6	109	9	US-10-981-356A-5	Sequence 5, Appl	197	37	66.1	108	11	US-11-098-758-205	Sequence 205, App
125	39	69.6	109	11	US-11-096-046-5	Sequence 5, Appl	198	37	66.1	110	11	US-11-171-567-209	Sequence 209, App
126	39	69.6	120	9	US-10-993-543-126	Sequence 126, App	199	36	64.3	11	11	US-11-104-117-7	Sequence 7, Appl
127	39	69.6	214	10	US-11-219-121-27	Sequence 27, Appl	200	36	64.3	11	11	US-11-233-252-7	Sequence 7, Appl
128	39	69.6	214	11	US-11-049-536-700	Sequence 700, App	201	36	64.3	11	11	US-11-245-254-7	Sequence 7, Appl
129	39	69.6	214	11	US-11-199-739-700	Sequence 700, App	202	36	64.3	105	11	US-11-084-554-12	Sequence 12, Appl
130	39	69.6	214	11	US-11-199-739-724	Sequence 724, App	203	36	64.3	105	11	US-11-136-250-12	Sequence 12, Appl
131	39	69.6	248	11	US-11-054-515-1360	Sequence 1360, App	204	36	64.3	106	11	US-11-004-590-394	Sequence 394, App
132	39	69.6	248	11	US-11-266-444-1360	Sequence 1360, App	205	36	64.3	106	11	US-11-004-590-396	Sequence 396, App
133	38	67.9	11	8	US-10-981-300-30	Sequence 30, Appl	206	36	64.3	106	11	US-11-004-590-397	Sequence 397, App
134	38	67.9	95	9	US-10-993-543-281	Sequence 30, Appl	207	36	64.3	106	11	US-11-004-590-398	Sequence 398, App
135	38	67.9	95	10	US-11-221-902-75	Sequence 75, Appl	208	36	64.3	106	11	US-11-004-590-399	Sequence 399, App
136	38	67.9	95	10	US-11-221-902-76	Sequence 76, Appl	209	36	64.3	106	11	US-11-004-590-400	Sequence 400, App
137	38	67.9	95	10	US-11-239-308-31	Sequence 31, Appl	210	36	64.3	106	11	US-11-004-590-403	Sequence 403, App
138	38	67.9	95	10	US-11-239-308-34	Sequence 34, Appl	211	36	64.3	106	11	US-11-004-590-405	Sequence 405, App
139	38	67.9	95	11	US-11-054-669-58	Sequence 58, Appl	212	36	64.3	106	11	US-11-004-590-407	Sequence 407, App
140	38	67.9	95	11	US-11-054-669-61	Sequence 61, Appl	213	36	64.3	106	11	US-11-004-590-408	Sequence 408, App
141	38	67.9	95	11	US-11-084-554-111	Sequence 111, App	214	36	64.3	106	11	US-11-004-590-410	Sequence 410, App
142	38	67.9	95	11	US-11-084-554-121	Sequence 121, App	215	36	64.3	107	11	US-11-084-554-1	Sequence 1, Appl
143	38	67.9	95	11	US-11-061-848-35	Sequence 35, Appl	216	36	64.3	107	11	US-11-104-117-1	Sequence 1, Appl
144	38	67.9	95	11	US-11-061-848-70	Sequence 70, Appl	217	36	64.3	107	11	US-11-104-117-9	Sequence 9, Appl
145	38	67.9	95	11	US-11-004-590-63	Sequence 63, Appl	218	36	64.3	107	11	US-11-136-250-1	Sequence 1, Appl
146	38	67.9	95	11	US-11-004-590-67	Sequence 67, Appl	219	36	64.3	107	11	US-11-233-252-1	Sequence 1, Appl
147	38	67.9	95	11	US-11-136-250-111	Sequence 111, App	220	36	64.3	107	11	US-11-233-252-9	Sequence 9, Appl
148	38	67.9	95	11	US-11-136-250-121	Sequence 121, App	221	36	64.3	107	11	US-11-245-254-1	Sequence 1, Appl
149	38	67.9	102	9	US-10-771-257-108	Sequence 108, App	222	36	64.3	107	11	US-11-245-254-9	Sequence 9, Appl
150	38	67.9	103	9	US-10-771-257-102	Sequence 102, App	223	36	64.3	150	11	US-11-128-900-24	Sequence 24, Appl
151	38	67.9	103	9	US-10-771-257-114	Sequence 114, App	224	36	64.3	150	11	US-11-128-900-98	Sequence 98, Appl
152	38	67.9	107	11	US-11-064-174-169	Sequence 169, App	225	36	64.3	244	11	US-11-054-515-82	Sequence 82, Appl
153	38	67.9	108	8	US-10-981-300-21	Sequence 21, Appl	226	36	64.3	244	11	US-11-054-515-164	Sequence 164, App
154	38	67.9	108	8	US-10-981-300-22	Sequence 22, App	227	36	64.3	244	11	US-11-054-515-261	Sequence 261, App
155	38	67.9	108	9	US-10-925-366A-159	Sequence 159, App	228	36	64.3	244	11	US-11-054-515-280	Sequence 280, App
156	38	67.9	108	9	US-10-925-366A-174	Sequence 174, App	229	36	64.3	244	11	US-11-266-444-82	Sequence 82, Appl
157	38	67.9	108	9	US-10-925-366A-188	Sequence 188, App	230	36	64.3	244	11	US-11-266-444-164	Sequence 164, App
158	38	67.9	108	9	US-10-925-366A-190	Sequence 190, App	231	36	64.3	244	11	US-11-266-444-261	Sequence 261, App
159	38	67.9	108	11	US-11-049-536-248	Sequence 248, App	232	36	64.3	264	11	US-11-176-525-1	Sequence 1, Appl
160	38	67.9	108	11	US-11-049-536-316	Sequence 316, App	233	36	64.3	264	11	US-11-108-135-38	Sequence 38, Appl
161	38	67.9	108	11	US-11-049-536-480	Sequence 480, App	234	35	62.5	11	11	US-11-126-978-38	Sequence 38, Appl
162	38	67.9	108	11	US-11-049-536-604	Sequence 604, App	235	35	62.5	11	11	US-11-217-995-4	Sequence 4, Appl
163	38	67.9	108	11	US-11-199-739-248	Sequence 248, App	236	35	62.5	11	11	US-11-049-536-22	Sequence 22, Appl
164	38	67.9	108	11	US-11-199-739-316	Sequence 316, App	237	35	62.5	102	11	US-11-199-739-22	Sequence 22, Appl
165	38	67.9	108	11	US-11-199-739-480	Sequence 480, App	238	35	62.5	102	11	US-11-004-590-395	Sequence 395, App
166	38	67.9	108	11	US-11-199-739-604	Sequence 604, App	239	35	62.5	106	11	US-11-004-590-402	Sequence 402, App
167	38	67.9	108	11	US-11-098-758-159	Sequence 159, App	240	35	62.5	106	11		

241	35	62.5	106	11	US-11-004-590-406	Sequence 406, App	314	60.7	108	9	US-10-925-366A-199	Sequence 199, App
242	35	62.5	106	11	US-11-004-590-409	Sequence 409, App	315	60.7	108	9	US-10-925-366A-232	Sequence 232, App
243	35	62.5	107	9	US-10-507-662-40	Sequence 40, Appl	316	60.7	108	9	US-10-771-257-28	Sequence 28, Appl
244	35	62.5	107	9	US-10-507-662-41	Sequence 41, Appl	317	60.7	108	9	US-10-771-257-36	Sequence 36, Appl
245	35	62.5	107	11	US-11-108-135-46	Sequence 46, Appl	318	60.7	108	9	US-10-771-257-63	Sequence 63, Appl
246	35	62.5	107	11	US-11-126-978-46	Sequence 46, Appl	319	60.7	108	9	US-10-771-257-69	Sequence 69, Appl
247	35	62.5	107	11	US-11-049-536-632	Sequence 632, App	320	60.7	108	9	US-10-515-241-9	Sequence 9, Appl
248	35	62.5	107	11	US-11-199-739-632	Sequence 632, App	321	60.7	108	11	US-11-127-677-28	Sequence 28, Appl
249	35	62.5	108	9	US-10-925-366A-93	Sequence 93, Appl	322	60.7	108	11	US-11-127-677-36	Sequence 36, Appl
250	35	62.5	108	9	US-10-925-366A-155	Sequence 155, App	323	60.7	108	11	US-11-127-677-61	Sequence 61, Appl
251	35	62.5	108	9	US-10-925-366A-194	Sequence 194, App	324	60.7	108	11	US-11-127-677-67	Sequence 67, Appl
252	35	62.5	108	11	US-11-064-174-41	Sequence 41, Appl	325	60.7	108	11	US-11-127-932-19	Sequence 19, Appl
253	35	62.5	108	11	US-11-049-536-228	Sequence 228, App	326	60.7	108	11	US-11-064-174-32	Sequence 32, Appl
254	35	62.5	108	11	US-11-199-739-228	Sequence 228, App	327	60.7	108	11	US-11-064-174-43	Sequence 43, Appl
255	35	62.5	108	11	US-11-098-758-93	Sequence 93, Appl	328	60.7	108	11	US-11-064-174-163	Sequence 163, App
256	35	62.5	108	11	US-11-098-758-155	Sequence 155, App	329	60.7	108	11	US-11-064-174-167	Sequence 167, App
257	35	62.5	108	11	US-11-098-758-194	Sequence 194, App	330	60.7	108	11	US-11-127-903-19	Sequence 19, Appl
258	35	62.5	129	11	US-11-230-462-38	Sequence 38, Appl	331	60.7	108	11	US-11-049-536-172	Sequence 172, App
259	35	62.5	214	11	US-11-217-995-8	Sequence 8, Appl	332	60.7	108	11	US-11-049-536-452	Sequence 452, App
260	35	62.5	253	11	US-11-054-515-936	Sequence 936, App	333	60.7	108	11	US-11-049-536-560	Sequence 560, App
261	35	62.5	253	11	US-11-266-444-936	Sequence 936, App	334	60.7	108	11	US-11-199-739-172	Sequence 172, App
262	35	62.5	257	11	US-11-056-825-10	Sequence 10, Appl	335	60.7	108	11	US-11-199-739-452	Sequence 452, App
263	35	62.5	421	9	US-10-467-657-4102	Sequence 4102, App	336	60.7	108	11	US-11-199-739-560	Sequence 560, App
264	35	62.5	660	11	US-11-188-238-14270	Sequence 14270, A	337	60.7	108	11	US-11-102-512-3	Sequence 3, Appl
265	34.5	61.6	109	11	US-11-096-074-52	Sequence 52, Appl	338	60.7	108	11	US-11-102-512-6	Sequence 6, Appl
266	34.5	61.6	109	11	US-11-095-822-52	Sequence 52, Appl	339	60.7	108	11	US-11-098-758-3	Sequence 3, Appl
267	34	60.7	11	9	US-10-510-229-29	Sequence 29, Appl	340	60.7	108	11	US-11-098-758-6	Sequence 6, Appl
268	34	60.7	11	9	US-10-510-229-77	Sequence 77, Appl	341	60.7	108	11	US-11-098-758-148	Sequence 148, App
269	34	60.7	11	9	US-10-510-229-89	Sequence 89, Appl	342	60.7	108	11	US-11-098-758-163	Sequence 163, App
270	34	60.7	95	9	US-10-993-543-274	Sequence 274, App	343	60.7	108	11	US-11-098-758-176	Sequence 176, App
271	34	60.7	95	9	US-10-496-3498-54	Sequence 54, Appl	344	60.7	108	11	US-11-098-758-199	Sequence 199, App
272	34	60.7	95	10	US-11-221-902-71	Sequence 71, Appl	345	60.7	108	11	US-11-098-758-232	Sequence 232, App
273	34	60.7	95	10	US-11-221-902-72	Sequence 72, Appl	346	60.7	108	11	US-11-166-496-10	Sequence 10, Appl
274	34	60.7	95	10	US-11-239-308-29	Sequence 29, Appl	347	60.7	109	11	US-11-127-932-14	Sequence 14, Appl
275	34	60.7	95	11	US-11-054-669-54	Sequence 54, Appl	348	60.7	109	11	US-11-127-932-18	Sequence 18, Appl
276	34	60.7	95	11	US-11-054-669-55	Sequence 55, Appl	349	60.7	109	11	US-11-127-903-14	Sequence 14, Appl
277	34	60.7	95	11	US-11-084-554-143	Sequence 143, App	350	60.7	109	11	US-11-127-903-18	Sequence 18, Appl
278	34	60.7	95	11	US-11-084-554-146	Sequence 146, App	351	60.7	111	11	US-11-049-536-86	Sequence 86, Appl
279	34	60.7	95	11	US-11-061-848-36	Sequence 36, Appl	352	60.7	111	11	US-11-199-739-86	Sequence 86, Appl
280	34	60.7	95	11	US-11-061-848-37	Sequence 37, Appl	353	60.7	111	9	US-10-993-543-178	Sequence 178, App
281	34	60.7	95	11	US-11-061-848-63	Sequence 63, Appl	354	60.7	121	9	US-10-993-543-30	Sequence 30, Appl
282	34	60.7	95	11	US-11-128-900-94	Sequence 94, Appl	355	60.7	134	11	US-11-128-900-23	Sequence 23, Appl
283	34	60.7	95	11	US-11-004-590-72	Sequence 72, Appl	356	60.7	134	11	US-11-128-900-97	Sequence 97, Appl
284	34	60.7	95	11	US-11-004-590-73	Sequence 73, Appl	357	60.7	139	11	US-11-128-900-22	Sequence 22, Appl
285	34	60.7	95	11	US-11-136-250-143	Sequence 143, App	358	60.7	139	11	US-11-128-900-96	Sequence 96, Appl
286	34	60.7	95	11	US-11-136-250-146	Sequence 146, App	359	60.7	145	11	US-11-126-798-2	Sequence 2, Appl
287	34	60.7	96	11	US-11-144-248-42	Sequence 42, App	360	60.7	145	11	US-11-126-798-58	Sequence 58, Appl
288	34	60.7	96	11	US-11-144-222-42	Sequence 42, App	361	60.7	214	11	US-11-128-900-71	Sequence 71, Appl
289	34	60.7	96	11	US-11-182-343-42	Sequence 42, App	362	60.7	236	11	US-11-086-289-8	Sequence 8, Appl
290	34	60.7	102	11	US-11-049-536-42	Sequence 42, App	363	60.7	240	11	US-10-925-366A-219	Sequence 219, App
291	34	60.7	102	11	US-11-199-739-42	Sequence 42, App	364	60.7	240	11	US-11-098-758-219	Sequence 219, App
292	34	60.7	103	11	US-11-064-174-42	Sequence 42, App	365	60.7	243	9	US-10-537-061-2	Sequence 2, Appl
293	34	60.7	105	8	US-10-981-300-24	Sequence 24, Appl	366	60.7	243	9	US-10-537-061-3	Sequence 3, Appl
294	34	60.7	105	11	US-11-155-775-52	Sequence 52, Appl	367	60.7	245	11	US-11-054-515-1972	Sequence 1972, App
295	34	60.7	107	9	US-10-925-366A-234	Sequence 234, App	368	60.7	245	11	US-11-266-444-1972	Sequence 1972, App
296	34	60.7	107	9	US-10-537-061-8	Sequence 8, Appl	369	60.7	246	11	US-11-054-515-2075	Sequence 2075, App
297	34	60.7	107	11	US-11-064-174-33	Sequence 33, Appl	370	60.7	246	11	US-11-266-444-2075	Sequence 2075, App
298	34	60.7	107	11	US-11-064-174-37	Sequence 37, Appl	371	60.7	250	11	US-11-054-515-1174	Sequence 1174, App
299	34	60.7	107	11	US-11-064-174-38	Sequence 38, Appl	372	60.7	250	11	US-11-266-444-1174	Sequence 1174, App
300	34	60.7	107	11	US-11-064-174-39	Sequence 39, Appl	373	60.7	257	9	US-10-496-3498-53	Sequence 53, Appl
301	34	60.7	107	11	US-11-064-174-40	Sequence 40, Appl	374	60.7	396	11	US-11-188-298-8932	Sequence 8932, App
302	34	60.7	107	11	US-11-064-174-156	Sequence 156, App	375	60.7	482	11	US-11-045-004-2627	Sequence 2627, App
303	34	60.7	107	11	US-11-064-174-158	Sequence 158, App	376	60.7	515	11	US-11-188-298-6279	Sequence 6279, App
304	34	60.7	107	11	US-11-064-174-168	Sequence 168, App	377	60.7	521	11	US-11-188-298-19766	Sequence 19766, A
305	34	60.7	107	11	US-11-064-174-175	Sequence 175, App	378	60.7	708	11	US-11-174-150-25	Sequence 25, Appl
306	34	60.7	107	11	US-11-064-174-176	Sequence 176, App	379	60.7	736	11	US-11-174-150-26	Sequence 26, Appl
307	34	60.7	107	11	US-11-049-536-158	Sequence 158, App	380	60.7	736	11	US-11-078-189-9	Sequence 9, Appl
308	34	60.7	107	11	US-11-098-758-234	Sequence 234, App	381	60.7	739	11	US-11-078-189-12	Sequence 12, Appl
309	34	60.7	108	9	US-10-925-366A-3	Sequence 3, Appl	382	58.9	11	9	US-10-981-356A-7	Sequence 7, Appl
310	34	60.7	108	9	US-10-925-366A-5	Sequence 5, Appl	383	58.9	11	9	US-10-510-229-35	Sequence 35, Appl
311	34	60.7	108	9	US-10-925-366A-148	Sequence 148, App	384	58.9	11	9	US-10-510-229-83	Sequence 83, Appl
312	34	60.7	108	9	US-10-925-366A-163	Sequence 163, App	385	58.9	11	11	US-11-093-274-10	Sequence 10, Appl
313	34	60.7	108	9	US-10-925-366A-176	Sequence 176, App	386	58.9	11	11	US-11-093-274-11	Sequence 11, Appl

387	33	58.9	11	11	US-11-093-274-12	Sequence 12, Appl	460	33	58.9	108	11	US-11-127-903-12	Sequence 12, Appl
388	33	58.9	11	11	US-11-096-046-7	Sequence 7, Appl	461	33	58.9	108	11	US-11-127-903-13	Sequence 13, Appl
389	33	58.9	11	11	US-11-051-453-19	Sequence 19, Appl	462	33	58.9	108	11	US-11-049-536-216	Sequence 216, App
390	33	58.9	94	11	US-11-093-274-33	Sequence 33, Appl	463	33	58.9	108	11	US-11-049-536-260	Sequence 260, App
391	33	58.9	95	9	US-10-993-543-273	Sequence 273, App	464	33	58.9	108	11	US-11-049-536-264	Sequence 264, App
392	33	58.9	95	9	US-10-993-543-283	Sequence 283, App	465	33	58.9	108	11	US-11-049-536-280	Sequence 280, App
393	33	58.9	95	9	US-10-993-543-284	Sequence 284, App	466	33	58.9	108	11	US-11-049-536-304	Sequence 304, App
394	33	58.9	95	10	US-11-221-902-68	Sequence 68, Appl	467	33	58.9	108	11	US-11-049-536-392	Sequence 392, App
395	33	58.9	95	10	US-11-221-902-78	Sequence 78, Appl	468	33	58.9	108	11	US-11-049-536-440	Sequence 440, App
396	33	58.9	95	10	US-11-239-308-33	Sequence 33, Appl	469	33	58.9	108	11	US-11-049-536-512	Sequence 512, App
397	33	58.9	95	10	US-11-239-308-38	Sequence 38, Appl	470	33	58.9	108	11	US-11-049-536-564	Sequence 564, App
398	33	58.9	95	10	US-11-239-308-40	Sequence 40, Appl	471	33	58.9	108	11	US-11-049-536-628	Sequence 628, App
399	33	58.9	95	10	US-11-239-308-54	Sequence 54, Appl	472	33	58.9	108	11	US-11-199-739-216	Sequence 216, App
400	33	58.9	95	11	US-11-054-669-60	Sequence 60, Appl	473	33	58.9	108	11	US-11-199-739-260	Sequence 260, App
401	33	58.9	95	11	US-11-054-669-67	Sequence 67, Appl	474	33	58.9	108	11	US-11-199-739-264	Sequence 264, App
402	33	58.9	95	11	US-11-054-669-69	Sequence 69, Appl	475	33	58.9	108	11	US-11-199-739-280	Sequence 280, App
403	33	58.9	95	11	US-11-054-669-86	Sequence 86, Appl	476	33	58.9	108	11	US-11-199-739-304	Sequence 304, App
404	33	58.9	95	11	US-11-084-554-125	Sequence 125, App	477	33	58.9	108	11	US-11-199-739-392	Sequence 392, App
405	33	58.9	95	11	US-11-084-554-138	Sequence 138, App	478	33	58.9	108	11	US-11-199-739-440	Sequence 440, App
406	33	58.9	95	11	US-11-084-554-139	Sequence 139, App	479	33	58.9	108	11	US-11-199-739-512	Sequence 512, App
407	33	58.9	95	11	US-11-084-554-140	Sequence 140, App	480	33	58.9	108	11	US-11-199-739-564	Sequence 564, App
408	33	58.9	95	11	US-11-061-848-34	Sequence 34, Appl	481	33	58.9	108	11	US-11-199-739-628	Sequence 628, App
409	33	58.9	95	11	US-11-061-848-44	Sequence 44, Appl	482	33	58.9	108	11	US-11-217-919-93	Sequence 93, Appl
410	33	58.9	95	11	US-11-061-848-46	Sequence 46, Appl	483	33	58.9	108	11	US-11-098-758-154	Sequence 154, App
411	33	58.9	95	11	US-11-061-848-52	Sequence 52, Appl	484	33	58.9	108	11	US-11-098-758-175	Sequence 175, App
412	33	58.9	95	11	US-11-061-848-57	Sequence 57, Appl	485	33	58.9	108	11	US-11-098-758-177	Sequence 177, App
413	33	58.9	95	11	US-11-061-848-65	Sequence 65, Appl	486	33	58.9	108	11	US-11-098-758-181	Sequence 181, App
414	33	58.9	95	11	US-11-061-848-66	Sequence 66, Appl	487	33	58.9	108	11	US-11-098-758-197	Sequence 197, App
415	33	58.9	95	11	US-11-061-848-72	Sequence 72, Appl	488	33	58.9	108	11	US-11-098-758-233	Sequence 233, App
416	33	58.9	95	11	US-11-061-848-73	Sequence 73, Appl	489	33	58.9	108	11	US-11-098-758-288	Sequence 288, App
417	33	58.9	95	11	US-11-004-590-56	Sequence 56, Appl	490	33	58.9	108	11	US-11-166-496-11	Sequence 11, Appl
418	33	58.9	95	11	US-11-004-590-58	Sequence 58, Appl	491	33	58.9	108	9	US-10-771-257-29	Sequence 29, Appl
419	33	58.9	95	11	US-11-004-590-66	Sequence 66, Appl	492	33	58.9	109	9	US-10-834-397-28	Sequence 28, Appl
420	33	58.9	95	11	US-11-004-590-88	Sequence 88, Appl	493	33	58.9	109	9	US-10-834-397-43	Sequence 43, Appl
421	33	58.9	95	11	US-11-136-250-125	Sequence 125, App	494	33	58.9	109	11	US-11-040-159-7	Sequence 7, Appl
422	33	58.9	95	11	US-11-136-250-138	Sequence 138, App	495	33	58.9	109	11	US-11-040-159-9	Sequence 9, Appl
423	33	58.9	95	11	US-11-136-250-139	Sequence 139, App	496	33	58.9	109	11	US-11-040-159-11	Sequence 11, Appl
424	33	58.9	95	11	US-11-136-250-140	Sequence 140, App	497	33	58.9	109	11	US-11-040-159-13	Sequence 13, Appl
425	33	58.9	99	11	US-11-195-095-14	Sequence 14, Appl	498	33	58.9	109	11	US-11-127-677-29	Sequence 29, Appl
426	33	58.9	102	9	US-10-771-257-104	Sequence 104, Appl	499	33	58.9	109	11	US-11-127-932-16	Sequence 16, Appl
427	33	58.9	102	11	US-11-049-536-30	Sequence 30, Appl	500	33	58.9	109	11	US-11-127-932-17	Sequence 17, App
428	33	58.9	102	11	US-11-049-536-38	Sequence 38, Appl	501	33	58.9	109	11	US-11-127-932-20	Sequence 20, Appl
429	33	58.9	102	11	US-11-199-739-30	Sequence 30, Appl	502	33	58.9	109	11	US-11-127-903-16	Sequence 16, Appl
430	33	58.9	102	11	US-11-199-739-38	Sequence 38, Appl	503	33	58.9	109	11	US-11-127-903-17	Sequence 17, Appl
431	33	58.9	103	9	US-10-771-257-98	Sequence 98, Appl	504	33	58.9	109	11	US-11-127-903-20	Sequence 20, Appl
432	33	58.9	103	9	US-10-771-257-100	Sequence 100, App	505	33	58.9	109	11	US-11-049-536-176	Sequence 176, App
433	33	58.9	103	9	US-10-771-257-109	Sequence 109, App	506	33	58.9	109	11	US-11-049-536-372	Sequence 372, App
434	33	58.9	106	11	US-11-149-943-54	Sequence 54, Appl	507	33	58.9	109	11	US-11-049-536-636	Sequence 636, App
435	33	58.9	107	11	US-11-239-308-10	Sequence 10, Appl	508	33	58.9	109	11	US-11-049-536-660	Sequence 660, App
436	33	58.9	107	11	US-11-040-159-17	Sequence 17, Appl	509	33	58.9	109	11	US-11-199-739-176	Sequence 176, App
437	33	58.9	107	11	US-11-093-274-24	Sequence 24, Appl	510	33	58.9	109	11	US-11-199-739-372	Sequence 372, App
438	33	58.9	107	11	US-11-064-174-44	Sequence 44, Appl	511	33	58.9	109	11	US-11-199-739-636	Sequence 636, App
439	33	58.9	107	11	US-11-064-174-162	Sequence 162, App	512	33	58.9	109	11	US-11-199-739-660	Sequence 660, App
440	33	58.9	107	11	US-11-049-536-157	Sequence 157, App	513	33	58.9	110	11	US-11-049-536-376	Sequence 376, App
441	33	58.9	107	11	US-11-049-536-428	Sequence 428, App	514	33	58.9	110	11	US-11-049-536-544	Sequence 544, App
442	33	58.9	107	11	US-11-199-739-428	Sequence 428, App	515	33	58.9	110	11	US-11-049-536-672	Sequence 672, App
443	33	58.9	108	9	US-10-925-366A-154	Sequence 154, App	516	33	58.9	110	11	US-11-049-536-680	Sequence 680, App
444	33	58.9	108	9	US-10-925-366A-175	Sequence 175, App	517	33	58.9	110	11	US-11-199-739-376	Sequence 376, App
445	33	58.9	108	9	US-10-925-366A-177	Sequence 177, App	518	33	58.9	110	11	US-11-199-739-544	Sequence 544, App
446	33	58.9	108	9	US-10-925-366A-181	Sequence 181, App	519	33	58.9	110	11	US-11-199-739-672	Sequence 672, App
447	33	58.9	108	9	US-10-925-366A-197	Sequence 197, App	520	33	58.9	110	11	US-11-199-739-680	Sequence 680, App
448	33	58.9	108	9	US-10-925-366A-233	Sequence 233, App	521	33	58.9	111	11	US-11-049-536-66	Sequence 66, Appl
449	33	58.9	108	9	US-10-925-366A-288	Sequence 288, App	522	33	58.9	111	11	US-11-049-536-100	Sequence 100, App
450	33	58.9	108	9	US-10-771-257-35	Sequence 35, Appl	523	33	58.9	111	11	US-11-199-739-66	Sequence 66, Appl
451	33	58.9	108	9	US-10-886-383-2	Sequence 2, Appl	524	33	58.9	111	11	US-11-199-739-100	Sequence 100, App
452	33	58.9	108	9	US-10-886-383-4	Sequence 4, Appl	525	33	58.9	114	9	US-10-925-366A-12	Sequence 12, Appl
453	33	58.9	108	11	US-11-093-274-22	Sequence 22, Appl	526	33	58.9	114	11	US-11-098-758-12	Sequence 12, Appl
454	33	58.9	108	11	US-11-093-274-23	Sequence 23, Appl	527	33	58.9	115	11	US-11-098-8408-307	Sequence 307, App
455	33	58.9	108	11	US-11-127-677-35	Sequence 35, Appl	528	33	58.9	115	11	US-11-009-873A-307	Sequence 307, App
456	33	58.9	108	11	US-11-127-932-12	Sequence 12, Appl	529	33	58.9	115	9	US-11-009-769A-307	Sequence 307, App
457	33	58.9	108	11	US-11-127-932-13	Sequence 13, Appl	530	33	58.9	119	9	US-10-993-543-26	Sequence 26, Appl
458	33	58.9	108	11	US-11-064-174-181	Sequence 181, App	531	33	58.9	119	9	US-10-993-543-82	Sequence 82, Appl
459	33	58.9	108	11	US-11-051-453-5	Sequence 5, Appl	532	33	58.9	119	11	US-11-217-919-3	Sequence 3, Appl

533	33	58.9	120	9	US-10-993-543-78	Sequence 78, Appl	606	32	57.1	108	11	US-11-098-758-171	Sequence 171, App
534	33	58.9	128	9	US-10-721-763-31	Sequence 31, Appl	607	32	57.1	108	11	US-11-098-758-179	Sequence 179, App
535	33	58.9	128	11	US-11-051-453-50	Sequence 50, Appl	608	32	57.1	108	11	US-11-098-758-184	Sequence 184, App
536	33	58.9	139	11	US-11-128-900-16	Sequence 16, Appl	609	32	57.1	109	11	US-11-049-536-588	Sequence 588, App
537	33	58.9	139	11	US-11-128-900-90	Sequence 90, Appl	610	32	57.1	109	11	US-11-049-536-620	Sequence 620, App
538	33	58.9	142	11	US-11-128-900-91	Sequence 91, Appl	611	32	57.1	109	11	US-11-049-536-644	Sequence 644, App
539	33	58.9	146	11	US-11-128-900-21	Sequence 21, Appl	612	32	57.1	109	11	US-11-049-536-684	Sequence 684, App
540	33	58.9	146	11	US-11-128-900-93	Sequence 93, Appl	613	32	57.1	109	11	US-11-199-739-588	Sequence 588, App
541	33	58.9	152	11	US-11-128-900-98	Sequence 18, Appl	614	32	57.1	109	11	US-11-199-739-620	Sequence 620, App
542	33	58.9	152	11	US-11-128-900-95	Sequence 95, Appl	615	32	57.1	109	11	US-11-199-739-644	Sequence 644, App
543	33	58.9	234	11	US-11-128-900-17	Sequence 17, Appl	616	32	57.1	109	11	US-11-199-739-684	Sequence 684, App
544	33	58.9	234	11	US-11-128-900-69	Sequence 69, Appl	617	32	57.1	110	11	US-11-049-536-516	Sequence 516, App
545	33	58.9	236	11	US-11-086-289-4	Sequence 4, Appli	618	32	57.1	110	11	US-11-199-739-516	Sequence 516, App
546	33	58.9	236	11	US-11-086-289-20	Sequence 20, Appl	619	32	57.1	115	11	US-11-009-870A-309	Sequence 309, App
547	33	58.9	236	11	US-11-264-096-237	Sequence 237, App	620	32	57.1	115	11	US-11-009-870A-309	Sequence 309, App
548	33	58.9	241	11	US-11-054-515-1932	Sequence 1932, Ap	621	32	57.1	115	9	US-11-009-769A-309	Sequence 6, Appli
549	33	58.9	241	11	US-11-054-515-2054	Sequence 2054, Ap	622	32	57.1	120	9	US-10-993-543-6	Sequence 62, Appl
550	33	58.9	241	11	US-11-266-444-1932	Sequence 1932, Ap	623	32	57.1	120	9	US-10-993-543-162	Sequence 162, App
551	33	58.9	241	11	US-11-266-444-2054	Sequence 2054, Ap	624	32	57.1	120	9	US-10-993-543-154	Sequence 154, App
552	33	58.9	248	11	US-11-054-515-1104	Sequence 1104, Ap	625	32	57.1	121	9	US-10-993-543-106	Sequence 106, App
553	33	58.9	248	11	US-11-266-444-1104	Sequence 1104, Ap	626	32	57.1	122	9	US-10-993-543-137	Sequence 137, App
554	33	58.9	249	11	US-11-054-515-919	Sequence 919, App	627	32	57.1	129	9	US-10-873-528-137	Sequence 137, App
555	33	58.9	249	11	US-11-054-515-1635	Sequence 1635, Ap	628	32	57.1	150	9	US-10-496-284-57	Sequence 57, Appl
556	33	58.9	249	11	US-11-266-444-919	Sequence 919, App	629	32	57.1	154	11	US-11-045-004-2044	Sequence 2044, Ap
557	33	58.9	249	11	US-11-266-444-1635	Sequence 1635, Ap	630	32	57.1	187	9	US-10-667-235-72	Sequence 72, Appl
558	33	58.9	251	11	US-11-054-515-1049	Sequence 1049, Ap	631	32	57.1	211	9	US-10-667-235-71	Sequence 71, Appl
559	33	58.9	251	11	US-11-266-444-1049	Sequence 1049, Ap	632	32	57.1	239	9	US-10-496-284-11	Sequence 11, Appl
560	33	58.9	310	11	US-11-136-079-2	Sequence 2, Appli	633	32	57.1	248	9	US-10-793-626-464	Sequence 464, App
561	33	58.9	440	11	US-11-166-496-2	Sequence 2, Appli	634	32	57.1	252	7	US-09-978-360A-485	Sequence 485, App
562	33	58.9	452	10	US-11-264-558-6	Sequence 6, Appli	635	32	57.1	283	11	US-11-241-677-4	Sequence 4, Appli
563	33	58.9	478	11	US-11-087-099-6302	Sequence 6302, Ap	636	32	57.1	367	11	US-11-096-568A-21077	Sequence 21077, A
564	33	58.9	544	9	US-10-793-626-38	Sequence 38, Appl	637	32	57.1	369	11	US-11-096-568A-21076	Sequence 21076, A
565	33	58.9	549	11	US-11-096-568A-31281	Sequence 31281, A	638	32	57.1	390	7	US-09-978-360A-487	Sequence 487, App
566	33	58.9	566	9	US-10-467-657-3302	Sequence 3302, Ap	639	32	57.1	403	11	US-11-096-568A-21075	Sequence 21075, A
567	33	58.9	630	11	US-11-096-568A-31280	Sequence 31280, A	640	32	57.1	522	11	US-11-079-463-5994	Sequence 5994, Ap
568	33	58.9	705	11	US-11-096-568A-31279	Sequence 31279, A	641	32	57.1	523	11	US-11-188-298-16556	Sequence 16556, A
569	33	58.9	1114	11	US-11-217-972-2	Sequence 2, Appli	642	32	57.1	523	11	US-11-188-298-18815	Sequence 18815, A
570	33	58.9	1235	11	US-11-124-367A-366	Sequence 366, App	643	32	57.1	527	11	US-11-188-298-12153	Sequence 12153, A
571	33	58.9	3028	9	US-10-455-772-276	Sequence 276, App	644	32	57.1	528	11	US-11-188-298-16802	Sequence 16802, A
572	33	58.9	3028	9	US-10-455-772-284	Sequence 284, App	645	32	57.1	565	11	US-11-188-298-17564	Sequence 17564, A
573	33	58.9	3028	9	US-10-455-772-286	Sequence 286, App	646	32	57.1	587	11	US-11-072-512-3783	Sequence 3783, Ap
574	33	58.9	3028	9	US-10-455-772-288	Sequence 288, App	647	32	57.1	612	11	US-11-079-463-8781	Sequence 8781, Ap
575	32.5	58.0	245	11	US-11-054-515-1896	Sequence 1896, Ap	648	32	57.1	647	11	US-11-188-298-1041	Sequence 1041, Ap
576	32.5	58.0	245	11	US-11-266-444-1896	Sequence 1896, Ap	649	32	57.1	658	11	US-11-045-004-2685	Sequence 2685, Ap
577	32	57.1	11	11	US-11-171-567-4	Sequence 4, Appli	650	32	57.1	660	11	US-11-188-298-9237	Sequence 9237, Ap
578	32	57.1	11	11	US-11-171-567-7	Sequence 7, Appli	651	32	57.1	660	11	US-11-188-298-10905	Sequence 10905, A
579	32	57.1	13	11	US-11-152-974A-442	Sequence 442, App	652	32	57.1	667	11	US-11-188-298-5319	Sequence 5319, Ap
580	32	57.1	13	11	US-11-153-143A-442	Sequence 442, App	653	32	57.1	697	11	US-11-052-554A-110	Sequence 110, App
581	32	57.1	94	11	US-11-037-812-9	Sequence 9, Appli	654	32	57.1	754	11	US-11-188-298-9686	Sequence 9686, App
582	32	57.1	95	10	US-11-239-308-55	Sequence 55, Appl	655	32	57.1	754	11	US-11-188-298-19237	Sequence 19237, A
583	32	57.1	95	11	US-11-054-669-87	Sequence 87, Appl	656	32	57.1	1042	11	US-11-037-243-74	Sequence 74, Appl
584	32	57.1	95	11	US-11-084-554-131	Sequence 131, App	657	31	55.4	11	8	US-10-981-300-32	Sequence 32, Appl
585	32	57.1	95	11	US-11-004-590-89	Sequence 89, Appl	658	31	55.4	11	11	US-11-152-846-19	Sequence 19, Appl
586	32	57.1	95	11	US-11-136-250-131	Sequence 131, App	659	31	55.4	11	11	US-11-223-834-4	Sequence 4, Appli
587	32	57.1	102	11	US-11-172-740-1076	Sequence 1076, Ap	660	31	55.4	11	11	US-11-203-253A-73	Sequence 73, Appl
588	32	57.1	102	11	US-11-049-536-26	Sequence 26, Appl	661	31	55.4	11	11	US-11-171-567-16	Sequence 16, Appl
589	32	57.1	102	11	US-11-199-739-26	Sequence 26, Appl	662	31	55.4	85	11	US-11-284-260-8	Sequence 8, Appli
590	32	57.1	107	10	US-11-239-308-20	Sequence 20, Appl	663	31	55.4	85	11	US-11-284-261-8	Sequence 8, Appli
591	32	57.1	107	11	US-11-112-240-8	Sequence 8, Appli	664	31	55.4	90	11	US-11-173-071-23	Sequence 23, Appl
592	32	57.1	107	11	US-11-112-304A-8	Sequence 8, Appli	665	31	55.4	95	10	US-11-239-308-59	Sequence 59, Appl
593	32	57.1	108	9	US-10-925-366A-141	Sequence 141, App	666	31	55.4	95	11	US-11-054-669-91	Sequence 91, Appl
594	32	57.1	108	9	US-10-925-366A-149	Sequence 149, App	667	31	55.4	95	11	US-11-054-669-92	Sequence 92, Appl
595	32	57.1	108	9	US-10-925-366A-171	Sequence 171, App	668	31	55.4	95	11	US-11-084-554-104	Sequence 104, App
596	32	57.1	108	9	US-10-925-366A-179	Sequence 179, App	669	31	55.4	95	11	US-11-084-554-113	Sequence 113, App
597	32	57.1	108	9	US-10-925-366A-184	Sequence 184, App	670	31	55.4	95	11	US-11-061-848-53	Sequence 53, App
598	32	57.1	108	11	US-11-049-536-556	Sequence 556, App	671	31	55.4	95	11	US-11-061-848-54	Sequence 54, Appl
599	32	57.1	108	11	US-11-049-536-596	Sequence 596, App	672	31	55.4	95	11	US-11-004-590-96	Sequence 96, Appl
600	32	57.1	108	11	US-11-199-739-556	Sequence 556, App	673	31	55.4	95	11	US-11-004-590-97	Sequence 97, Appl
601	32	57.1	108	11	US-11-199-739-596	Sequence 596, App	674	31	55.4	95	11	US-11-136-250-104	Sequence 104, App
602	32	57.1	108	11	US-11-102-512-89	Sequence 89, Appl	675	31	55.4	95	11	US-11-136-250-113	Sequence 113, App
603	32	57.1	108	11	US-11-221-281-45	Sequence 45, Appl	676	31	55.4	96	11	US-11-128-900-99	Sequence 99, Appl
604	32	57.1	108	11	US-11-098-758-141	Sequence 141, App	677	31	55.4	105	11	US-11-223-834-12	Sequence 12, Appl
605	32	57.1	108	11	US-11-098-758-149	Sequence 149, App	678	31	55.4	105	11	US-11-049-536-224	Sequence 224, App

679	31	55.4	105	11	US-11-199-739-224	Sequence 224, App	752	30	53.6	93	9	US-10-667-295-52	Sequence 52, Appl
680	31	55.4	106	11	US-11-223-834-9	Sequence 9, Appli	753	30	53.6	93	11	US-11-172-740-2398	Sequence 2398, Ap
681	31	55.4	106	11	US-11-223-834-10	Sequence 10, Appl	754	30	53.6	101	11	US-11-049-536-34	Sequence 34, Appl
682	31	55.4	106	11	US-11-223-834-11	Sequence 11, Appl	755	30	53.6	101	11	US-11-199-739-34	Sequence 34, Appl
683	31	55.4	107	10	US-11-239-308-24	Sequence 24, Appl	756	30	53.6	103	9	US-10-510-720-6	Sequence 6, Appli
684	31	55.4	107	10	US-11-239-308-26	Sequence 26, Appl	757	30	53.6	105	11	US-11-096-074-55	Sequence 55, Appl
685	31	55.4	107	11	US-11-096-074-54	Sequence 54, Appl	758	30	53.6	105	11	US-11-097-812-53	Sequence 53, Appl
686	31	55.4	107	11	US-11-064-174-36	Sequence 36, Appl	759	30	53.6	105	11	US-11-095-823-55	Sequence 55, Appl
687	31	55.4	107	11	US-11-064-174-172	Sequence 172, App	760	30	53.6	106	11	US-11-096-074-51	Sequence 51, Appl
688	31	55.4	107	11	US-11-064-174-174	Sequence 174, App	761	30	53.6	106	11	US-11-155-775-8	Sequence 8, Appli
689	31	55.4	107	11	US-11-095-822-54	Sequence 54, Appl	762	30	53.6	106	11	US-11-107-028-8	Sequence 8, Appli
690	31	55.4	107	11	US-11-165-023-7	Sequence 7, Appli	763	30	53.6	106	11	US-11-107-028-9	Sequence 9, Appli
691	31	55.4	107	11	US-11-203-251A-4	Sequence 4, Appli	764	30	53.6	106	11	US-11-095-823-51	Sequence 51, Appl
692	31	55.4	107	11	US-11-203-253A-4	Sequence 4, Appli	765	30	53.6	106	11	US-11-049-536-432	Sequence 432, App
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694	31	55.4	108	9	US-10-771-257-4	Sequence 4, Appli	767	30	53.6	106	11	US-11-199-739-432	Sequence 432, App
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717	31	55.4	155	11	US-11-128-900-112	Sequence 112, App	790	30	53.6	107	11	US-11-165-023-5	Sequence 5, Appli
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990 29 51.8 200 9 US-10-455-772-1114 Sequence 1116, Ap
991 29 51.8 200 9 US-10-455-772-1116 Sequence 13879, A
992 29 51.8 220 11 US-11-096-568A-13879 Sequence 6439, Ap
993 29 51.8 229 11 US-11-079-463-6439 Sequence 7800, Ap
994 29 51.8 230 9 US-10-467-657-7800 Sequence 132, App
995 29 51.8 234 8 US-10-546-594-132 Sequence 58, Appl
996 29 51.8 236 9 US-10-496-284-58 Sequence 62, Appl
997 29 51.8 236 9 US-10-496-284-62 Sequence 12, Appl
998 29 51.8 240 9 US-10-902-546-12 Sequence 1118, Ap
999 29 51.8 251 9 US-10-455-772-1118 Sequence 1893, Ap
1000 29 51.8 254 11 US-11-054-515-1893
```

ALIGNMENTS

```
RESULT 1
US-10-981-300-31
; Sequence 31, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-10-981-300-31
```

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Query Match 80.4%; Score 45; DB 8; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Oy 1 RASQDIGNYL 10
||| ||| |||
Db 1 RASQDISNYL 10
```

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RESULT 2
US-11-183-218-51
; Sequence 51, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
```

```
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONGUATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-11-183-218-51
```

```
Query Match 80.4%; Score 45; DB 10; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 RASQDIGNYL 10
||| ||| |||
Db 24 RASQDINNLY 33
```

```
RESULT 3
US-11-183-218-52
; Sequence 52, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONGUATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
```

; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: US 60/334,301
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; PRIOR FILING DATE: 2001-11-28
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 52
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-183-218-52

Query Match 80.4%; Score 45; DB 10; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 DB 24 RASQDINNLYL 33

RESULT 4
 US-11-183-205-51
 ; Sequence 51, Application US/11183205
 ; Publication No. US20060030521A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: DePree, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Bove, Caryn
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
 ; FILE REFERENCE: 040853-01-5052-US01
 ; CURRENT APPLICATION NUMBER: US/11/183,205
 ; CURRENT FILING DATE: 2005-07-15
 ; PRIOR APPLICATION NUMBER: US 11/183,205
 ; PRIOR FILING DATE: 2005-07-15
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,301
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: PCT/US2002/032263
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: US 10/287,994
 ; PRIOR FILING DATE: 2002-11-05
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 51
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-183-205-51

Query Match 80.4%; Score 45; DB 11; Length 107;

Best Local Similarity 90.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASQDIGNYL 10
 |||||
 DB 24 RASQDINNLYL 33
 RESULT 5
 US-11-183-205-52
 ; Sequence 52, Application US/11183205
 ; Publication No. US20060030521A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: DePree, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Bove, Caryn
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
 ; FILE REFERENCE: 040853-01-5052-US01
 ; CURRENT APPLICATION NUMBER: US/11/183,205
 ; CURRENT FILING DATE: 2005-07-15
 ; PRIOR APPLICATION NUMBER: US 11/183,205
 ; PRIOR FILING DATE: 2005-07-15
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,301
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: PCT/US2002/032263
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: US 10/287,994
 ; PRIOR FILING DATE: 2002-11-05
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 52
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-183-205-52

Query Match 80.4%; Score 45; DB 11; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
 |||||
 DB 24 RASQDINNLYL 33

RESULT 6
 US-10-981-300-23
 ; Sequence 23, Application US/10981300
 ; Publication No. US20060093599A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIORGIO SENALDI
 ; APPLICANT: GADI GAZIT-BORNSTEIN
 ; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
 ; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
 ; FILE REFERENCE: ABGX-005
 ; CURRENT APPLICATION NUMBER: US/10/981,300
 ; CURRENT FILING DATE: 2004-11-03

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; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapien
US-10-981-300-23

Query Match      80.4%; Score 45; DB 8; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 RASQDIGNYL 10
Db  24 RASQDISNYL 33

RESULT 7
US-11-089-872-5
; Sequence 5, Application US/11089872
; Publication No. US20050260212A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yongke
; APPLICANT: Ramakrishnan, Vanitha
; APPLICANT: Law, Debbie
; TITLE OF INVENTION: ANTI-LFL2 ANTIBODIES FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT
; FILE REFERENCE: 05882.0223.NFUS02
; CURRENT APPLICATION NUMBER: US/11/089,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/557,440
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 60/638,708
; PRIOR FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-089-872-5

Query Match      80.4%; Score 45; DB 11; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 RASQDIGNYL 10
Db  43 RASQDISNYL 52

RESULT 8
US-10-981-300-14
; Sequence 14, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 214
; TYPE: PRT
; ORGANISM: homo sapien
US-10-981-300-14

Query Match      80.4%; Score 45; DB 8; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.51;
```

```
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 RASQDIGNYL 10
Db  24 RASQDISNYL 33

RESULT 9
US-11-183-218-55
; Sequence 55, Application US/11183218
; Publication No. US2006008906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-55

Query Match      80.4%; Score 45; DB 10; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 RASQDIGNYL 10
Db  24 RASQDISNYL 33

RESULT 10
US-11-025-712-11
; Sequence 11, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/025,712
FILING DATE: 28-Dec-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/404,286
FILING DATE: 31-Mar-2003
APPLICATION NUMBER: 09/811384
FILING DATE: 20-DEC-2000
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, David W.
REGISTRATION NUMBER: NONE
REFERENCE/DOCKET NUMBER: P1729C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-025-712-11

Query Match 80.4%; Score 45; DB 11; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 24 RASQDINNLY 33

RESULT 11
US-11-173-564-1
Sequence 1, Application US/11173564
Publication No. US20050271654A1
GENERAL INFORMATION:
APPLICANT: Rinderknecht, Ernst H.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY PURIFICATION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/173,564

FILING DATE: 01-JUL-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/811,757
FILING DATE: 06-MAR-1997
CLASSIFICATION:
APPLICATION NUMBER: 08/425,763
FILING DATE: 20-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 941
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-11-173-564-1

Query Match 80.4%; Score 45; DB 11; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
Db 24 RASQDINNLY 33

RESULT 12
US-11-183-205-55
Sequence 55, Application US/11183205
Publication No. US2006003052A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DePrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Howe, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-US01
CURRENT APPLICATION NUMBER: US/11/183,205
CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 11/183,205
PRIOR FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/334,301
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: PCT/US2002/032263
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 10/287,994
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 214
TYPE: PRT


```
; ORGANISM: Homo sapiens
US-11-183-205-55

Query Match      80.4%; Score 45; DB 11; Length 214;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDIGNYL 33

RESULT 13
US-10-999-866-55
; Sequence 55, Application US/10999866
; Publication No. US20050266004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11)
; OTHER INFORMATION: LC CDR1
US-10-999-866-55

Query Match      76.8%; Score 43; DB 9; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 1 RASQDITNYL 10

RESULT 14
US-11-009-939-38
; Sequence 38, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-38

Query Match      76.8%; Score 43; DB 11; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 RASQDIGNYL 10
Db 1 RASQDITNYL 10

RESULT 15
US-10-999-866-43
; Sequence 43, Application US/10999866
; Publication No. US20050266004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(107)
; OTHER INFORMATION: LC variable region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(23)
; OTHER INFORMATION: Framework 1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (24)..(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (35)..(50)
; OTHER INFORMATION: Framework 2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (51)..(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (57)..(89)
; OTHER INFORMATION: Framework 3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (90)..(97)
; OTHER INFORMATION: CDR3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (98)..(107)
; OTHER INFORMATION: JK2
US-10-999-866-43

Query Match      76.8%; Score 43; DB 9; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDITNYL 33

RESULT 16
US-11-009-939-37
; Sequence 37, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
```

FILE REFERENCE: 23135-402
CURRENT APPLICATION NUMBER: US/11/009,939
CURRENT FILING DATE: 2005-12-10
PRIOR APPLICATION NUMBER: 60/528,811
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/528,812
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/528,962
PRIOR FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 108
TYPE: PRT
ORGANISM: Mus musculus
US-11-009-939-37

Query Match 76.8%; Score 43; DB 11; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDITNYL 33
|||||

RESULT 17

US-10-236-051-8
Sequence 8, Application US/10236051
Publication No. US20060073145A1
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: LETURCO, Didier J.
APPLICANT: MORIARTY, Ann M.
APPLICANT: ULEVITCH, Richard J.
APPLICANT: TOBIAS, Peter S.
APPLICANT: MATHISON, John C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA

FILE REFERENCE: SCRIP1140-4
CURRENT APPLICATION NUMBER: US/10/236,051
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 09/170,769
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/373,297
PRIOR FILING DATE: 1995-01-23
PRIOR APPLICATION NUMBER: PCT/US94/05898
PRIOR FILING DATE: 1994-05-27
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR FILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8

LENGTH: 211
TYPE: PRT
ORGANISM: Murine
US-10-236-051-8

Query Match 76.8%; Score 43; DB 9; Length 211;
Best Local Similarity 90.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 21 RASQDIKNYL 30
|||||

RESULT 18

US-11-084-717-21
Sequence 21, Application US/11084717
Publication No. US20050260736A1
GENERAL INFORMATION:
APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI-JUN

APPLICANT: HARVEY, BARRETT R.
APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSB:723US
CURRENT APPLICATION NUMBER: US/11/084,717
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,324
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 10/620,278
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-084-717-21

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDIRNYL 33
|||||

RESULT 19

US-11-084-717-23
Sequence 23, Application US/11084717
Publication No. US20050260736A1
GENERAL INFORMATION:
APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI-JUN
APPLICANT: HARVEY, BARRETT R.
APPLICANT: IVERSON, BRENT L.
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: UTSB:723US
CURRENT APPLICATION NUMBER: US/11/084,717
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,324
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 10/620,278
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-11-084-717-23

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
Db 24 RASQDIRNYL 33
|||||

RESULT 20

US-11-084-717-25

; Sequence 25, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
; FILE REFERENCE: UTSB:723US
; CURRENT APPLICATION NUMBER: US/11/084,717
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,324
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 10/620,278
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-717-25

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 21
US-11-179-244-21
; Sequence 21, Application US/11179244
; Publication No. US20050267294A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
; FILE REFERENCE: UTSB:721US
; CURRENT APPLICATION NUMBER: US/11/179,244
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/10/620,049
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-179-244-21

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 22
US-11-179-244-23
; Sequence 23, Application US/11179244
; Publication No. US20050267294A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
; FILE REFERENCE: UTSB:721US
; CURRENT APPLICATION NUMBER: US/11/179,244
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/10/620,049
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-179-244-23

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 23
US-11-179-244-25
; Sequence 25, Application US/11179244
; Publication No. US20050267294A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
; FILE REFERENCE: UTSB:721US
; CURRENT APPLICATION NUMBER: US/11/179,244
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/10/620,049
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-179-244-25

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 24

US-11-084-055B-21
; Sequence 21, Application US/11084055B
; Publication No. US20060029947A1

; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI JUN
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
; FILE REFERENCE: UTSS:722US
; CURRENT APPLICATION NUMBER: US/11/084,055B
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,260
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-055B-21

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 25
US-11-084-055B-23
; Sequence 23, Application US/11084055B
; Publication No. US20060029947A1

; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI JUN
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
; FILE REFERENCE: UTSS:722US
; CURRENT APPLICATION NUMBER: US/11/084,055B
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,260
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-055B-23

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 26
US-11-084-055B-25
; Sequence 25, Application US/11084055B
; Publication No. US20060029947A1

; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI JUN
; APPLICANT: IVERSON, BRENT L.
; TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
; FILE REFERENCE: UTSS:722US
; CURRENT APPLICATION NUMBER: US/11/084,055B
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,260
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-084-055B-25

Query Match 76.8%; Score 43; DB 11; Length 247;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
|||||
Db 24 RASQDIRNYL 33

RESULT 27
US-11-061-848-2
; Sequence 2, Application US/11061848
; Publication No. US20050288491A1

; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-061-848-2

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 KASQDIRNYL 33

RESULT 28
US-11-061-848-10
; Sequence 10, Application US/11061848
; Publication No. US20050288491A1

; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848

; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-10

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 29

US-11-061-848-11
; Sequence 11, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-11

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 30

US-11-061-848-12
; Sequence 12, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-12

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 31

US-11-061-848-13
; Sequence 13, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-13

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 32

US-11-061-848-14
; Sequence 14, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-14

Query Match 75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQDIGNYL 10
:|||||
Db 24 KASQDINNYL 33

RESULT 33

US-11-061-848-15

```
; Sequence 15, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-15

Query Match      75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
      :|||||
Db      24 RASQDINNYL 33

RESULT 34
US-11-102-512-40
; Sequence 40, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-40

Query Match      75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
      :|||||
Db      24 RASQDIGNNL 33

RESULT 35
US-11-102-512-54
; Sequence 54, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
```

```
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-54

Query Match      75.0%; Score 42; DB 11; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.89;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 11
      :|||||
Db      24 RASQDIGSALR 34

RESULT 36
US-10-981-300-33
; Sequence 33, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-981-300-33

Query Match      73.2%; Score 41; DB 8; Length 11;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
      :|||||
Db      1 QASQDISNYL 10

RESULT 37
US-11-221-902-73
; Sequence 73, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGA
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-902-73

Query Match      73.2%; Score 41; DB 10; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQDIGNYL 10
      :|||||
Db      24 QASQDISNYL 33

RESULT 38
US-11-221-902-74
; Sequence 74, Application US/11221902
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; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATES
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-902-74

Query Match      73.2%; Score 41; DB 10; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 QASQDISNYL 33

RESULT 39
US-11-239-308-30
; Sequence 30, Application US/11239308
; Publication No. US20060088883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: IntegriGen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-30

Query Match      73.2%; Score 41; DB 10; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 QASQDISNYL 33

RESULT 40
US-11-054-669-56
; Sequence 56, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 56
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-56

Query Match      73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 QASQDISNYL 33

RESULT 41
US-11-054-669-57
; Sequence 57, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-57

Query Match      73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQDIGNYL 10
Db      24 QASQDISNYL 33

RESULT 42
US-11-084-554-145
; Sequence 145, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-145

Query Match      73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
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Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 43

US-11-084-554-148
; Sequence 148, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-148

Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 44

US-11-061-848-33
; Sequence 33, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-33

Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 45

US-11-061-848-62
; Sequence 62, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-62

Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 46

US-11-061-848-68
; Sequence 68, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-68

Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33

RESULT 47

US-11-004-590-68
; Sequence 68, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRINC
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590


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; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-004-590-68
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```
Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33
```

RESULT 48

```
US-11-004-590-69
; Sequence 69, Application US/11004590
; Publication No. US2006000883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 69
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-004-590-69
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Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33
```

RESULT 49

```
US-11-136-250-145
; Sequence 145, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
```

```
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: AGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-136-250-145
```

```
Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33
```

RESULT 50

```
US-11-136-250-148
; Sequence 148, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-136-250-148
```

```
Query Match 73.2%; Score 41; DB 11; Length 95;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 RASQDIGNYL 10
:|||||
Db 24 QASQDISNYL 33
```

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Search completed: May 11, 2006, 16:50:31
Job time : 17.7049 secs
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GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2006, 16:15:30 ; Search time 64.7213 Seconds
(without alignments)
47.521 Million cell updates/sec

Title: US-10-808-538-5
Perfect score: 33
Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	7	2 AAW23434	Aaw23434 CDR-2 of
2	33	100.0	108	2 AAW23439	Aaw23439 Modified
3	33	100.0	108	2 AAW23440	Aaw23440 Modified
4	33	100.0	108	2 AAW23442	Aaw23442 hWI2 ligh
5	33	100.0	108	2 AAW23436	Aaw23436 rWI2 ligh
6	29	87.9	13	5 ADG67276	Adg67276 Human SGI
7	29	87.9	13	5 ADG67278	Adg67278 Human SGI
8	29	87.9	13	5 ADG67279	Adg67279 Human SGI
9	29	87.9	13	5 ADG67277	Adg67277 Human SGI
10	29	87.9	93	4 AAU40729	Aau40729 Propionib
11	29	87.9	93	6 ABM37248	Abm37248 Propionib
12	29	87.9	107	8 ADO26410	Ado26410 Murine an
13	29	87.9	145	8 ADJ78464	Adj78464 Mouse per
14	29	87.9	158	4 AAB94485	Aab94485 Human pro
15	29	87.9	235	8 ADG28555	Adg28555 Paramyxov
16	29	87.9	236	2 AAR77614	Aar77614 Humanised
17	29	87.9	236	5 ABP51696	Abp51696 SGI.1 lig
18	29	87.9	236	8 ADQ16649	Adq16649 Immunoglo
19	29	87.9	236	9 ADV44387	Adv44387 SGI.1 lig
20	29	87.9	236	9 AEB12860	Aeb12860 Antibody
21	29	87.9	240	2 AAR77612	Aar77612 Humanised
22	29	87.9	241	2 AAR77613	Aar77613 Humanised
23	29	87.9	241	2 AAR77608	Aar77608 ChimERIC
24	29	87.9	248	2 AAR77606	Aar77606 Murine 5G

25	29	87.9	248	2 AAR77616	Aar77616 Humanised
26	29	87.9	248	2 AAR77607	Aar77607 Humanised
27	29	87.9	336	7 ADM05455	Adm05455 Human pro
28	29	87.9	422	2 AAW11301	Aaw11301 Perilipin
29	29	87.9	422	3 AAB12394	Aab12394 Rat peril
30	29	87.9	517	2 AAW11300	Aaw11300 Perilipin
31	29	87.9	517	3 AAB12393	Aab12393 Rat peril
32	29	87.9	702	9 ASC08432	Aec08432 Amino aci
33	29	87.9	702	9 ASC08433	Aec08433 Amino aci
34	29	87.9	731	9 AEC08431	Aec08431 ScFv-2-1G
35	29	87.9	734	9 AEC08430	Aec08430 ScFv-1-1F
36	29	87.9	878	2 AAR13793	Aar13793 Bcdysone
37	29	87.9	878	2 AAR32889	Aar32889 DHR23aloh
38	29	87.9	878	5 AEG93745	Aeg93745 Fruit fly
39	29	87.9	881	4 ABB58488	Aeb58488 Drosophil
40	29	87.9	881	4 ABB58488	Aeb58488 Drosophil
41	29	87.9	945	4 ARG02406	Arg02406 Novel hum
42	28	84.8	226	8 ADX67119	Adx67119 Plant ful
43	28	84.8	233	6 ABU35172	Abu35172 Protein e
44	28	84.8	289	8 ADI42942	Adi42942 Plant tra
45	28	84.8	289	8 ADQ16242	Adq16242 Rice AT-h
46	28	84.8	289	8 ADQ16220	Adq16220 Rice AT-h
47	28	84.8	289	9 ADZ00558	Adz00558 G3407 pol
48	28	84.8	289	9 ADZ00580	Adz00580 G3407 pol
49	28	84.8	289	9 AEA26513	Aea26513 Stress to
50	28	84.8	323	6 ADA34821	Ada34821 Acinetoba
51	28	84.8	354	6 AAU01214	Aau01214 Enterococ
52	28	84.8	354	6 ABU30089	Abu30089 Protein e
53	28	84.8	361	7 ADC95655	Adc95655 E. faeciu
54	28	84.8	399	4 ABB60245	Abb60245 Drosophil
55	28	84.8	497	8 ADY09306	Ady09306 Plant ful
56	28	84.8	518	6 ABU22710	Abu22710 Protein e
57	28	84.8	636	6 AAE37008	Aae37008 Micromono
58	28	84.8	665	6 ABP60064	Abp60064 B3GALT po
59	28	84.8	754	6 ADA55565	Ada55565 Human pro
60	28	84.8	898	2 AAW31853	Aaw31853 Mycobacte
61	28	84.8	957	6 ABU36437	Abu36437 Protein e
62	28	84.8	1122	7 ABM86070	Abm86070 Rice abio
63	28	84.8	1122	6 ABP79791	Abp79791 N. gonorr
64	28	84.8	1149	6 ABU16720	Abu16720 Protein e
65	28	84.8	1151	6 ADA33457	Ada33457 Acinetoba
66	28	84.8	1161	6 ABU37856	Abu37856 Protein e
67	28	84.8	1161	6 ABU37439	Abu37439 Protein e
68	28	84.8	1199	6 ABU35345	Abu35345 Protein e
69	28	84.8	1220	8 ADL05325	Adl05325 M. catarr
70	28	84.8	2408	2 AAR24306	Aar24306 Translati
71	28	84.8	4904	4 ABB62249	Abb62249 Drosophil
72	28	84.8	1938	6 ABP76681	Abp76681 Streptomy
73	27	81.8	64	2 AAW15271	Aaw15271 Salmonell
74	27	81.8	111	5 ABP03359	Abp03359 Human ORF
75	27	81.8	142	4 AAU57052	Aau57052 Propionib
76	27	81.8	142	6 ABM53571	Abm53571 Propionib
77	27	81.8	164	8 ADX94053	Adx94053 Plant ful
78	27	81.8	164	8 ADX96805	Adx96805 Plant ful
79	27	81.8	199	8 ADY12877	Ady12877 Plant ful
80	27	81.8	250	6 ADB08682	Adb08682 Alloiococ
81	27	81.8	278	8 ADU00626	Adu00626 Amino aci
82	27	81.8	286	8 ADS44472	Ads44472 Bacterial
83	27	81.8	289	6 ABM67918	Abm67918 Photorhab
84	27	81.8	296	6 AAU44328	Aau44328 Propionib
85	27	81.8	296	6 ABM40847	Abm40847 Propionib
86	27	81.8	336	6 ADB08684	Adb08684 Alloiococ
87	27	81.8	336	8 ADJ27099	Adj27099 Alloiococ
88	27	81.8	354	4 ABP80365	Abp80365 N. gonorr
89	27	81.8	363	4 AAB79956	Aab79956 Corynebac
90	27	81.8	376	4 AAG91110	Aag91110 C Glutami
91	27	81.8	395	6 ABU22268	Abu22268 Protein e
92	27	81.8	395	8 ADS43956	Ads43956 Bacterial
93	27	81.8	432	7 ABO65782	Ab065782 Klebsiell
94	27	81.8	439	8 ADW69751	Adw69751 Refractor
95	27	81.8	440	3 AAY69549	Aay69549 Aspergill
96	27	81.8	440	3 AAY69551	Aay69551 Aspergill
97	27	81.8	440	3 AAY69553	Aay69553 Aspergill

98 27 81.8 440 3 AAY69550 Aspergill 171 26 78.8 6 ABR47755 Human sec
99 27 81.8 440 3 AAY69552 Aspergill 172 26 78.8 6 ABR00080 Human gen
100 27 81.8 440 3 AAB20508 Aspergill 173 26 78.8 4 ADB91548 Human sec
101 27 81.8 440 3 AAB20507 Aspergill 174 26 78.8 4 ADC74148 Human sec
102 27 81.8 440 3 AAB20510 Aspergill 175 26 78.8 4 AAU21177 Human nov
103 27 81.8 440 3 AAB20506 Aspergill 176 26 78.8 7 AAG20547 Arabidops
104 27 81.8 440 3 AAB20509 Aspergill 177 26 78.8 7 AAG53061 Arabidops
105 27 81.8 440 8 AAB20505 Aspergill 178 26 78.8 77 3 AAG11678 Arabidops
106 27 81.8 440 8 ADL73074 Aspergill 179 26 78.8 80 3 AAB56349 Human sec
107 27 81.8 440 8 ADL73071 Aspergill 180 26 78.8 100 3 AAG28172 Arabidops
108 27 81.8 440 8 ADL73073 Aspergill 181 26 78.8 106 3 AAG28171 Arabidops
109 27 81.8 440 8 ADL73072 Aspergill 182 26 78.8 107 9 AEA40463 Anti-VEGF
110 27 81.8 440 8 ADZ42192 Aspergill 183 26 78.8 107 9 AEA40456 Anti-VEGF
111 27 81.8 440 8 ADZ42193 Aspergill 184 26 78.8 107 9 AEA40453 Anti-VEGF
112 27 81.8 440 8 ADZ42195 Aspergill 185 26 78.8 107 9 AEA40466 Anti-VEGF
113 27 81.8 440 8 ADZ42194 Aspergill 186 26 78.8 107 9 AEA40472 Anti-VEGF
114 27 81.8 440 8 ADZ42196 Aspergill 187 26 78.8 107 9 AEA40454 Anti-VEGF
115 27 81.8 465 2 AAH84356 Aspergill 188 26 78.8 107 9 AEA40455 Anti-VEGF
116 27 81.8 465 2 AAY39905 A. fumiga 189 26 78.8 107 9 AEA40459 Anti-VEGF
117 27 81.8 465 7 ADK90742 Broad-epe 190 26 78.8 107 9 AEA40464 Anti-VEGF
118 27 81.8 465 8 ADL91250 Mutant ph 191 26 78.8 107 9 AEA40469 Anti-VEGF
119 27 81.8 465 8 ADL91244 Wild-type 192 26 78.8 110 3 AAG28170 Arabidops
120 27 81.8 467 2 AAY43171 A. fumiga 193 26 78.8 111 7 ADH85907 Enterococ
121 27 81.8 467 3 AAY69570 Mutant As 194 26 78.8 124 6 ABP70684 Kohnia sp
122 27 81.8 467 3 AAY69574 Mutant As 195 26 78.8 132 2 AAY37569 Chlamydia
123 27 81.8 467 3 AAB20528 Aspergill 196 26 78.8 143 3 AAG05488 Arabidops
124 27 81.8 467 4 AAU02112 A. fumiga 197 26 78.8 143 3 AAG20546 Arabidops
125 27 81.8 467 4 AAU02117 A. fumiga 198 26 78.8 143 3 AAG53058 Arabidops
126 27 81.8 467 8 ADL73098 Aspergill 199 26 78.8 149 3 AAG20545 Arabidops
127 27 81.8 474 6 ABB80171 A. fumiga 200 26 78.8 149 3 AAG53057 Arabidops
128 27 81.8 481 4 ABB52992 Escherich 201 26 78.8 149 3 AAG05487 Arabidops
129 27 81.8 487 4 ABB59931 Drosophil 202 26 78.8 155 3 AAG05486 Arabidops
130 27 81.8 493 7 ADP04332 Bacterial 203 26 78.8 169 3 AAG53056 Arabidops
131 27 81.8 493 8 ADN31594 Mouse for 204 26 78.8 185 3 AAG21459 Arabidops
132 27 81.8 494 5 AAU79818 Mouse mes 205 26 78.8 207 5 ABB47790 Listeria
133 27 81.8 494 8 ADN31596 Mouse for 206 26 78.8 239 8 ADT56926 Plant pol
134 27 81.8 494 8 ADN31597 Mouse for 207 26 78.8 240 6 ADA33137 Acinetoba
135 27 81.8 511 2 AAY37593 Protein i 208 26 78.8 311 4 ABB08018 Novel hum
136 27 81.8 554 7 ADP06601 Bacterial 209 26 78.8 316 9 AEB40359 L. pneumo
137 27 81.8 558 4 ABB63561 Drosophil 210 26 78.8 318 9 AEB36999 L. pneumo
138 27 81.8 573 6 ABU45104 Protein e 211 26 78.8 320 2 AAR62044 Leptospir
139 27 81.8 581 6 ABU38600 Protein e 212 26 78.8 320 2 AAU14278 Leptospir
140 27 81.8 588 6 ABU22735 Protein e 213 26 78.8 320 5 AAE25831 Leptospir
141 27 81.8 603 8 ADO07904 Fly poly 214 26 78.8 320 7 ADF61051 Outf mem
142 27 81.8 607 8 ADM98179 Environme 215 26 78.8 334 3 AAG21458 Arabidops
143 27 81.8 620 7 ABO72364 Pseudomon 216 26 78.8 337 2 AAR34498 Internal
144 27 81.8 698 8 ADS42225 Bacterial 217 26 78.8 362 3 AAG21457 Arabidops
145 27 81.8 784 5 ABB93947 Herbicida 218 26 78.8 412 5 ABB90911 Herbicida
146 27 81.8 784 8 ADN73567 Thale cre 219 26 78.8 416 8 ADS44629 Bacterial
147 27 81.8 852 8 ADS24105 Bacterial 220 26 78.8 421 7 ADC00281 Enterohae
148 27 81.8 983 4 ABB70130 Drosophil 221 26 78.8 427 5 ABB49079 Listeria
149 27 81.8 1013 8 ADJ49302 Oil-asso 222 26 78.8 427 6 ABU32600 Protein e
150 27 81.8 1013 8 ADJ50402 Oil-asso 223 26 78.8 432 5 ABB91019 Chlamydia
151 27 81.8 1013 8 ADJ65043 Thalecres 224 26 78.8 432 7 ADD43868 Chlamydia
152 27 81.8 1021 8 ADJ49300 Oil-asso 225 26 78.8 432 9 ADW29040 C trachom
153 27 81.8 1088 8 ADJ49079 Oil-asso 226 26 78.8 432 9 AEA19160 Chlamydia
154 27 81.8 1089 8 ADJ49650 Oil-asso 227 26 78.8 440 8 ADS28995 Bacterial
155 27 81.8 1089 8 ADL00239 Arabidops 228 26 78.8 467 8 ADS29122 Bacterial
156 27 81.8 1162 6 ABU40048 Protein e 229 26 78.8 510 2 AAR60863 Hydrogen
157 27 81.8 1162 6 ABU41801 Protein e 230 26 78.8 510 8 ADO62573 Transcrip
158 27 81.8 1162 8 ADS24694 Bacterial 231 26 78.8 513 7 ABM87822 Rice abio
159 27 81.8 1164 9 AEB40781 L. pneumo 232 26 78.8 525 8 ADX79634 Acremoniu
160 27 81.8 1168 9 AEB37467 L. pneumo 233 26 78.8 529 4 AAB81926 Arabidops
161 27 81.8 1246 6 ABR53786 Protein s 234 26 78.8 547 3 AAG54288 Arabidops
162 27 81.8 1246 7 ADK63824 Disease t 235 26 78.8 556 7 ADF50204 Partial T
163 27 81.8 1246 8 ADS43969 Bacterial 236 26 78.8 557 1 AAP81151 Herbicide
164 27 81.8 1418 8 ADN18012 Bacterial 237 26 78.8 557 7 ADF50223 Partial A
165 27 81.8 2049 9 ADZ51729 PKS FecF, 238 26 78.8 557 7 ADF50229 Partial A
166 27 81.8 2086 4 AAU34143 Staphyloc 239 26 78.8 557 7 ADF50217 Partial A
167 27 81.8 3705 6 ABU50020 Protein e 240 26 78.8 557 7 ADF50221 Partial A
168 27 81.8 5795 4 AAU37017 Staphyloc 241 26 78.8 557 7 ADF50227 Partial A
169 26 78.8 7 9 AEA40633 Anti-VEGF 242 26 78.8 557 7 ADF50219 Partial A
170 26 78.8 44 3 AAB56205 Human sec 243 26 78.8 557 7 ADF50231 Partial A

244	26	78.8	557	7	ADP50235	Adf50235 Partial A	317	26	78.8	665	2	AAR28614	Aar28614 Amino aci
245	26	78.8	557	7	ADP50202	Adf50202 Partial T	318	26	78.8	666	2	AAR28610	Aar28610 Amino aci
246	26	78.8	557	7	ADP50233	Adf50233 Partial A	319	26	78.8	666	2	AAR28616	Aar28616 Amino aci
247	26	78.8	558	7	ADP50225	Adf50225 Partial A	320	26	78.8	666	2	AAR28609	Aar28609 Amino aci
248	26	78.8	568	7	ADH80255	Adh80255 Chicory a	321	26	78.8	666	2	AAW13729	Aaw13729 Herbicide
249	26	78.8	568	7	ADH80253	Adh80253 Chicory a	322	26	78.8	666	2	AAW79141	Aaw79141 Plant ace
250	26	78.8	570	9	ADH80253	Adh80253 Chicory a	323	26	78.8	666	5	ABM08419	Abm08419 N. plumba
251	26	78.8	574	9	ADV11377	Adv11377 AHAS prot	324	26	78.8	667	1	AAW08419	Aaw08419 N. plumba
252	26	78.8	574	9	ADV11359	Adv11359 AHAS prot	325	26	78.8	667	1	AAW08419	Aaw08419 N. plumba
253	26	78.8	585	9	ADV11375	Adv11375 AHAS prot	326	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
254	26	78.8	585	9	ADV11363	Adv11363 AHAS prot	327	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
255	26	78.8	589	9	ADV11371	Adv11371 AHAS prot	328	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
256	26	78.8	589	9	ADV11365	Adv11365 AHAS prot	329	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
257	26	78.8	596	9	ADV11373	Adv11373 AHAS prot	330	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
258	26	78.8	596	9	ADV11355	Adv11355 AHAS prot	331	26	78.8	667	2	AAW1150	Aaw1150 Herbicide
259	26	78.8	597	4	AAU08231	Aau08231 Polypepti	332	26	78.8	668	2	AAW1150	Aaw1150 Herbicide
260	26	78.8	599	2	AAW16597	Aaw16597 Corn acet	333	26	78.8	668	2	AAW1150	Aaw1150 Herbicide
261	26	78.8	599	2	AAW16598	Aaw16598 Corn acet	334	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
262	26	78.8	599	2	AAW16599	Aaw16599 Corn acet	335	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
263	26	78.8	599	2	AAW03692	Aaw03692 Corn acet	336	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
264	26	78.8	614	8	ADR23158	Adr23158 Smooth pi	337	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
265	26	78.8	618	8	ADR23169	Adr23169 Smooth pi	338	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
266	26	78.8	618	8	ADR23161	Adr23161 Smooth pi	339	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
267	26	78.8	620	7	ABO61172	AbO61172 Klebsiell	340	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
268	26	78.8	624	8	ADM99163	Adm99163 Environme	341	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
269	26	78.8	633	5	AAU10029	Aau10029 Rice herb	342	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
270	26	78.8	633	5	AAU10029	Aau10029 Rice herb	343	26	78.8	669	2	AAW1150	Aaw1150 Herbicide
271	26	78.8	633	9	ADY79257	Ady79257 Partial R	344	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
272	26	78.8	633	9	ADY79259	Ady79259 Partial R	345	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
273	26	78.8	638	2	AAW05588	Aar05588 Acetohydr	346	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
274	26	78.8	638	2	AAW05589	Aar05589 Acetohydr	347	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
275	26	78.8	638	2	AAW32007	Aar32007 Herbicide	348	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
276	26	78.8	638	2	AAW32008	Aar32008 Herbicide	349	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
277	26	78.8	638	2	AAW32006	Aar32006 Herbicide	350	26	78.8	670	2	AAW1150	Aaw1150 Herbicide
278	26	78.8	638	2	AAW54055	Aaw54055 AHAS cion	351	26	78.8	670	3	AAW1150	Aaw1150 Herbicide
279	26	78.8	638	2	AAW54054	Aaw54054 AHAS cion	352	26	78.8	670	3	AAW1150	Aaw1150 Herbicide
280	26	78.8	638	2	AAW54053	Aaw54053 AHAS cion	353	26	78.8	670	5	AAW1150	Aaw1150 Herbicide
281	26	78.8	638	5	ABG71110	Abg71110 Maize ace	354	26	78.8	670	6	AAW1150	Aaw1150 Herbicide
282	26	78.8	638	5	ABG71110	Abg71110 Maize ace	355	26	78.8	670	6	AAW1150	Aaw1150 Herbicide
283	26	78.8	638	5	ABG71109	Abg71109 Maize ace	356	26	78.8	670	7	AAW1150	Aaw1150 Herbicide
284	26	78.8	638	9	ADY79261	Ady79261 Partial R	357	26	78.8	670	7	AAW1150	Aaw1150 Herbicide
285	26	78.8	639	9	ADY79265	Ady79265 Consensus	358	26	78.8	670	7	AAW1150	Aaw1150 Herbicide
286	26	78.8	644	5	AAU10027	Aau10027 Rice herb	359	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
287	26	78.8	644	5	AAU10025	Aau10025 Rice herb	360	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
288	26	78.8	644	5	AAU10024	Aau10024 Rice herb	361	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
289	26	78.8	644	5	AAU10028	Aau10028 Rice herb	362	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
290	26	78.8	644	5	ABM81482	Abm81482 Rice acet	363	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
291	26	78.8	644	6	ABF70882	Abf70882 Rice acet	364	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
292	26	78.8	644	7	ADD42027	Add42027 Rice acet	365	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
293	26	78.8	644	7	ADD42025	Add42025 Rice acet	366	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
294	26	78.8	644	7	ADD42021	Add42021 Rice acet	367	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
295	26	78.8	644	7	ADD42021	Add42021 Rice acet	368	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
296	26	78.8	644	7	ADP50215	Adp50215 Rice ALS/	369	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
297	26	78.8	644	9	ADY79263	Ady79263 Wild-type	370	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
298	26	78.8	644	9	ADY79267	Ady79267 Rice acet	371	26	78.8	670	8	AAW1150	Aaw1150 Herbicide
299	26	78.8	648	2	AAW24472	Aaw24472 Acetolact	372	25	75.8	10	8	ADK07445	Adk07445 Hepatitis
300	26	78.8	648	8	AAW24473	Aaw24473 Herbicide	373	25	75.8	10	8	ADK07445	Adk07445 Hepatitis
301	26	78.8	648	8	ADY06593	Ady06593 Plant ful	374	25	75.8	10	8	ADK01420	Adk01420 Hepatitis
302	26	78.8	649	6	ABP71594	Abp71594 H. annus	375	25	75.8	12	8	ADK02131	Adk02131 Hepatitis
303	26	78.8	649	6	ABP71595	Abp71595 H. annus	376	25	75.8	12	8	ADK02131	Adk02131 Hepatitis
304	26	78.8	652	8	ADN43339	Adn43339 Brassica	377	25	75.8	15	5	AAE17823	Aae17823 HSVII UL4
305	26	78.8	652	8	ADN43337	Adn43337 Brassica	378	25	75.8	15	5	ADG74959	Adg74959 Human her
306	26	78.8	655	8	ADN43336	Adn43336 Brassica	379	25	75.8	16	5	ABP62289	Abp62289 Human imm
307	26	78.8	655	8	ADN43338	Adn43338 Brassica	380	25	75.8	16	5	ABP62288	Abp62288 Human imm
308	26	78.8	660	2	AAR28615	Aar28615 Amino aci	381	25	75.8	16	5	ABP62291	Abp62291 Human imm
309	26	78.8	662	2	AAR28611	Aar28611 Amino aci	382	25	75.8	20	7	ADP71091	Adp71091 Saccharom
310	26	78.8	664	2	AAR11973	Aar11973 Tobacco S	383	25	75.8	35	5	AAU81892	Aau81892 Bacillus
311	26	78.8	664	2	AAR28613	Aar28613 Amino aci	384	25	75.8	36	7	ADK14935	Adk14935 Urinary s
312	26	78.8	664	2	AAR26911	Aar26911 ALS Hra m	385	25	75.8	50	4	AAU61628	Aau61628 Propionib
313	26	78.8	664	2	AAR63080	Aar63080 ALS SURB-	386	25	75.8	50	6	ABM58147	Abm58147 Propionib
314	26	78.8	664	2	AAW00211	Aaw00211 Tobacco H	387	25	75.8	52	4	AAU60727	Aau60727 Propionib
315	26	78.8	664	2	AAW22463	Aaw22463 Tobacco S	388	25	75.8	52	6	ABM57246	Abm57246 Propionib
316	26	78.8	664	2	AAW22455	Aaw22455 Tobacco w	389	25	75.8	58	4	AAU43171	Aau43171 Propionib

390	25	75.8	58	6	ABM33690	Abm33690 Propionib	463	25	75.8	178	9	ABE336018	Abb336018 L. pneumo
391	25	75.8	63	8	ADS64737	Adg64737 Human cyc	464	25	75.8	180	5	ABP54907	Abp54907 Von Wille
392	25	75.8	64	4	RAU42501	Rau42501 Propionib	465	25	75.8	190	5	ABE92302	Abp92302 Nematode
393	25	75.8	64	6	ABM33020	Abm33020 Propionib	466	25	75.8	191	6	ABU31820	Abu31820 Protein e
394	25	75.8	68	6	AAU59072	Aau59072 Propionib	467	25	75.8	193	5	AAE17838	Aae17838 Herpes si
395	25	75.8	68	6	ABM55591	Abm55591 Propionib	468	25	75.8	193	7	ADG74983	Adg74983 Human her
396	25	75.8	68	4	AAU51919	Aau51919 Propionib	469	25	75.8	193	7	ADG75161	Adg75161 Human her
397	25	75.8	72	4	AAU65898	Aau65898 Propionib	470	25	75.8	195	6	ABU47826	Abu47826 Protein e
398	25	75.8	72	6	ABM62417	Abm62417 Propionib	471	25	75.8	195	7	ADC96167	Adc96167 E. faeciu
399	25	75.8	72	6	ABM48438	Abm48438 Propionib	472	25	75.8	198	4	AAU38296	Aau38296 Salmonell
400	25	75.8	73	4	AAU47130	Aau47130 Propionib	473	25	75.8	199	7	ABO66691	Abp66691 Klebsiell
401	25	75.8	73	6	ABM43649	Abm43649 Propionib	474	25	75.8	200	2	AAW72158	Aaw72158 HSV-2 str
402	25	75.8	75	4	AAU50270	Aau50270 Propionib	475	25	75.8	202	4	AAU36248	Aau36248 Pseudomon
403	25	75.8	75	6	ABM46789	Abm46789 Propionib	476	25	75.8	210	5	ABB47352	Abb47352 Listeria
404	25	75.8	82	4	AAO13908	Aao13908 Human pol	477	25	75.8	214	7	ABO75209	Abp75209 Pseudomon
405	25	75.8	82	5	ABU10950	Abj10950 Yeast sel	478	25	75.8	217	2	AAW72085	Aaw72085 HSV-2 str
406	25	75.8	83	4	AAU44467	Aau44467 Propionib	479	25	75.8	217	7	ABO65369	Abp65369 Klebsiell
407	25	75.8	83	6	ABM40986	Abm40986 Propionib	480	25	75.8	220	4	AAU67708	Aau67708 Propionib
408	25	75.8	85	8	ADG64734	Adg64734 Human cyc	481	25	75.8	220	6	ABM64227	Abm64227 Propionib
409	25	75.8	87	2	AAU10279	Aau10279 Sinian im	482	25	75.8	229	4	AAU66716	Aau66716 Propionib
410	25	75.8	106	5	AAE17809	Aae17809 Herpes si	483	25	75.8	229	6	ABM63235	Abm63235 Propionib
411	25	75.8	106	5	ABP33331	Abp33331 Human tra	484	25	75.8	231	4	ABY79359	Abp79359 Corynebac
412	25	75.8	106	7	ADG74942	Adg74942 Human her	485	25	75.8	241	8	ADY22306	Ady22306 Plant ful
413	25	75.8	108	4	AAU61576	Aau61576 Propionib	486	25	75.8	245	3	AAU92824	Aau92824 C. pneumo
414	25	75.8	108	6	ABM58095	Abm58095 Propionib	487	25	75.8	245	5	ABP45889	Abp45889 Human Bly
415	25	75.8	112	4	AAU65603	Aau65603 Propionib	488	25	75.8	245	7	ADG96716	Adg96716 Single ch
416	25	75.8	112	6	ABM62122	Abm62122 Propionib	489	25	75.8	251	4	AAU24365	Aau24365 Murine ES
417	25	75.8	117	4	AAU67662	Abp67662 Corynebac	490	25	75.8	251	4	ABY93363	Abp93363 Human pro
418	25	75.8	122	7	ABO75539	Abp75539 Pseudomon	491	25	75.8	255	5	ABN49861	Abb49861 Listeria
419	25	75.8	124	8	ADX71575	Adx71575 Plant ful	492	25	75.8	257	8	ADN99550	Adn99550 Novel hum
420	25	75.8	125	2	AAU39822	Aau39822 Llana ant	493	25	75.8	258	4	AAU93113	Aau93113 C glutami
421	25	75.8	126	4	AAU91039	Aau91039 C glutami	494	25	75.8	258	7	ABO65521	Abp65521 Klebsiell
422	25	75.8	130	5	ABP62182	Abp62182 Human imm	495	25	75.8	259	8	ADS23019	Ads23019 Bacterial
423	25	75.8	130	5	ABP62181	Abp62181 Human imm	496	25	75.8	262	7	ABO60801	Abp60801 Klebsiell
424	25	75.8	130	5	ABP62180	Abp62180 Human imm	497	25	75.8	266	8	ADN24576	Adn24576 Bacterial
425	25	75.8	130	5	ABP62183	Abp62183 Human imm	498	25	75.8	266	8	ADN21816	Adn21816 Bacterial
426	25	75.8	131	4	AAU56581	Aau56581 Propionib	499	25	75.8	268	8	ADX73188	Adx73188 Plant ful
427	25	75.8	131	4	AAU39826	Aau39826 Propionib	500	25	75.8	275	7	ABM67980	Abm67980 Rice abio
428	25	75.8	131	6	ABM36345	Abm36345 Propionib	501	25	75.8	275	6	ABM65636	Abm65636 Propionib
429	25	75.8	131	6	ABM53100	Abm53100 Propionib	502	25	75.8	276	8	ADY10683	Ady10683 Plant ful
430	25	75.8	136	5	ABP09783	Abp09783 Human ORF	503	25	75.8	276	8	ADY10723	Ady10723 Plant ful
431	25	75.8	136	7	ADC95946	Adc95946 E. faeciu	504	25	75.8	276	8	ADX66631	Adx66631 Plant ful
432	25	75.8	137	4	ABB70698	Abb70698 Drosophil	505	25	75.8	277	7	ADG75162	Adg75162 Human her
433	25	75.8	138	5	ABP06821	Abp06821 Human ORF	506	25	75.8	279	7	ADC46595	Adc46595 Bacillus
434	25	75.8	138	9	ABM94044	Abm94044 M. xanthu	507	25	75.8	280	6	ADA35072	Ada35072 Acinetoba
435	25	75.8	139	5	ADJ33796	Adj33796 Protein o	508	25	75.8	282	9	ABE42625	Abp42625 L. pneumo
436	25	75.8	141	4	AAU64190	Aau64190 Propionib	509	25	75.8	292	4	AAG98866	Aag98866 E. coli g
437	25	75.8	141	6	ABM60709	Abm60709 Propionib	510	25	75.8	292	7	ADC00496	Adc00496 Enteroha
438	25	75.8	142	6	ADA54275	Ada54275 Human pro	511	25	75.8	295	2	AAW87931	Aaw87931 A rat HRP
439	25	75.8	143	4	ABM64890	Abm64890 Drosophil	512	25	75.8	295	2	AAW78474	Aaw78474 Human HRP
440	25	75.8	143	6	ABU43552	Abu43552 Protein e	513	25	75.8	295	7	ABO64248	Abp64248 Klebsiell
441	25	75.8	143	6	ABU47459	Abu47459 Protein e	514	25	75.8	299	4	ABY79837	Abp79837 Coryneb
442	25	75.8	144	5	ABP60845	Abp60845 Trypanoso	515	25	75.8	299	6	ABU36824	Abu36824 Protein e
443	25	75.8	146	9	ABM94296	Abm94296 M. xanthu	516	25	75.8	299	6	ADA12190	Ada12190 Acinetoba
444	25	75.8	151	4	ABB64395	Abb64395 Drosophil	517	25	75.8	299	7	AAE339413	Aae339413 Acinetoba
445	25	75.8	168	2	AAU88501	Aau88501 Cyclin de	518	25	75.8	300	6	ABU26152	Abu26152 Protein e
446	25	75.8	168	2	AAU98368	Aau98368 Human p18	519	25	75.8	300	7	ADH85750	Adh85750 Enterococ
447	25	75.8	168	5	AAU47883	Abu47883 p18 Ink4c	520	25	75.8	301	2	AAU92999	Aau92999 Rhodobact
448	25	75.8	168	5	AAU85613	Aau85613 Lung tumo	521	25	75.8	301	5	AAE17873	Aae17873 Sequence
449	25	75.8	168	6	ABU69585	Abu69585 Genbank p	522	25	75.8	302	8	ADS24640	Ads24640 Bacterial
450	25	75.8	168	6	ABU66488	Abu66488 Lung can	523	25	75.8	303	6	ABU33867	Abu33867 Protein e
451	25	75.8	168	7	ABR92060	Abp92060 Human cer	524	25	75.8	305	5	ABG69041	Abp69041 Amino aci
452	25	75.8	168	8	ADQ20295	Adq20295 Human sof	525	25	75.8	305	6	ABU34440	Abu34440 Protein e
453	25	75.8	168	8	ADQ20295	Adq20295 Human sof	526	25	75.8	307	6	ABU35778	Abu35778 Protein e
454	25	75.8	168	8	ADJ21345	Adj21345 Lung can	527	25	75.8	309	4	AAU53911	Aau53911 Propionib
455	25	75.8	168	8	ABM80090	Abm80090 Tumour-as	528	25	75.8	309	6	ABM50430	Abm50430 Propionib
456	25	75.8	168	8	ADS64721	Ads64721 Human cyc	529	25	75.8	310	4	AAU52133	Aau52133 Propionib
457	25	75.8	168	8	ADU18058	Adu18058 Human can	530	25	75.8	310	6	ABM48652	Abm48652 Propionib
458	25	75.8	168	9	ADX06618	Adx06618 Cyclin-de	531	25	75.8	313	8	ADS27030	Ads27030 Bacterial
459	25	75.8	168	9	ADY15270	Ady15270 PRO poly	532	25	75.8	313	8	ADS26640	Ads26640 Bacterial
460	25	75.8	168	9	ADY20275	Ady20275 PRO poly	533	25	75.8	316	8	ADS41835	Ads41835 Bacterial
461	25	75.8	169	9	ABE39447	Abp39447 L. pneumo	534	25	75.8	317	4	AAG90625	Aag90625 C Glutami
462	25	75.8	176	4	ABM65551	Abm65551 Drosophil	535	25	75.8	320	6	ADA48416	Ada48416 Rice prot

536	25	75.8	322	8	ADY12358	Ady12358 Plant ful	609	25	75.8	436	2	AAV35293	Aay35293 Chlamydia
537	25	75.8	327	4	AAU34814	Aau34814 E. coli c	610	25	75.8	436	3	AY92823	Aay92823 C. pneumo
538	25	75.8	328	4	AAU346055	Aag46055 Arabidops	611	25	75.8	439	3	AE86694	Ade86694 Chicken t
539	25	75.8	329	2	AAW77071	Rat Catho-	612	25	75.8	441	2	AA54223	Aay54223 L.lactic
540	25	75.8	329	7	AD560395	Ad560395 Rat Prote	613	25	75.8	441	8	ADY08265	Ady08265 Plant ful
541	25	75.8	329	7	ADP45859	Adp45859 Rat Prote	614	25	75.8	443	5	AAO20953	Aao20953 Human-N-k
542	25	75.8	329	9	ABM90589	Abm90589 M. xanthu	615	25	75.8	443	8	ADJ70539	Adj70539 Human hea
543	25	75.8	331	3	AAQ24131	Aag24131 Arabidops	616	25	75.8	443	8	ADU60371	Adu60371 Housekeep
544	25	75.8	333	3	AAQ46079	Aag46079 Arabidops	617	25	75.8	448	9	ABE92298	Abe92298 Nematode
545	25	75.8	333	3	AAQ46054	Aag46054 Arabidops	618	25	75.8	459	6	ABU25303	Abu25303 Protein e
546	25	75.8	336	7	ADD24923	Add24923 Ralstonia	619	25	75.8	467	8	AD21822	Ad21822 Bacterial
547	25	75.8	336	3	AAQ46078	Aag46078 Arabidops	620	25	75.8	471	7	ADH39859	Adh39859 Wheat suc
548	25	75.8	336	3	AAQ24130	Aag24130 Arabidops	621	25	75.8	471	9	ADM28869	Adm28869 Wheat suc
549	25	75.8	340	6	ABU18517	Abu18517 Protein e	622	25	75.8	472	4	ABB69894	Abb69894 Drosophi
550	25	75.8	340	8	ADX76706	Adx76706 Plant ful	623	25	75.8	476	8	ADN24107	Adn24107 Bacterial
551	25	75.8	341	8	ADX78918	Adx78918 Plant ful	624	25	75.8	478	8	ADJ49523	Adj49523 Oil-assoc
552	25	75.8	341	8	ADX78918	Adx78918 Plant ful	625	25	75.8	482	8	ADS45101	Ads45101 Bacterial
553	25	75.8	342	3	AGS53242	Ags53242 Arabidops	626	25	75.8	485	6	ABP56884	Abp56884 Staphyloc
554	25	75.8	342	8	ADM48259	Adm48259 Polypepti	627	25	75.8	485	8	ADJ48956	Adj48956 Oil-assoc
555	25	75.8	343	8	ADS26274	Ads26274 Bacterial	628	25	75.8	486	7	ADH87667	Adh87667 Enterococ
556	25	75.8	347	3	AGI17390	Agi17390 Arabidops	629	25	75.8	487	7	ABO75166	Ab075166 Pseudomon
557	25	75.8	347	8	ADT56339	Adt56339 Plant pol	630	25	75.8	494	8	ADS43053	Ads43053 Bacterial
558	25	75.8	348	3	AGS53241	Ags53241 Arabidops	631	25	75.8	495	7	ADH39857	Adh39857 Wheat suc
559	25	75.8	349	6	ABU18333	Abu18333 Protein e	632	25	75.8	495	9	ADM28867	Adm28867 Wheat suc
560	25	75.8	353	3	AGS55042	Ags55042 Arabidops	633	25	75.8	496	4	AAH31991	Aah31991 Amino aci
561	25	75.8	353	6	ADA35434	Ada35434 Acinetoba	634	25	75.8	497	8	ADS42178	Ads42178 Bacterial
562	25	75.8	353	7	AAQ27376	Aaq27376 Distal up	635	25	75.8	500	3	AAQ23576	Aaq23576 Arabidops
563	25	75.8	353	8	ADT87103	Adt87103 Yeast Str	636	25	75.8	505	8	ADJ48883	Adj48883 Oil-assoc
564	25	75.8	354	3	AGI17389	Agi17389 Arabidops	637	25	75.8	506	8	ADN22411	Adn22411 Bacterial
565	25	75.8	355	3	AG46053	Aag46053 Arabidops	638	25	75.8	507	3	AAQ23575	Aaq23575 Arabidops
566	25	75.8	358	3	AAQ24129	Aag24129 Arabidops	639	25	75.8	509	5	ABH53645	Abh53645 Lactococc
567	25	75.8	358	3	AAQ46077	Aag46077 Arabidops	640	25	75.8	509	6	ABU48741	Abu48741 Protein e
568	25	75.8	358	8	ADY10110	Ady10110 Plant ful	641	25	75.8	510	7	ABO63654	Ab063654 Klebsiell
569	25	75.8	358	8	ADY08943	Ady08943 Plant ful	642	25	75.8	512	2	AAH80505	Aah80505 S. livida
570	25	75.8	358	8	ADX96764	Adx96764 Plant ful	643	25	75.8	512	2	AAW87797	Aaw87797 Protease
571	25	75.8	359	8	ADY06248	Ady06248 Plant ful	644	25	75.8	512	3	AAH19229	Aah19229 A subtili
572	25	75.8	363	8	ADY05318	Ady05318 Plant ful	645	25	75.8	516	4	AAQ62840	Aaq62840 Amino aci
573	25	75.8	370	8	ADX96197	Adx96197 Plant ful	646	25	75.8	520	4	ABH68718	Abh68718 Drosophi
574	25	75.8	370	8	ADY12445	Ady12445 Plant ful	647	25	75.8	520	4	ABG15666	Abg15666 Novel hum
575	25	75.8	372	6	ADN21562	Adn21562 Bacterial	648	25	75.8	527	3	AAQ90725	Aaq90725 Laccase-L
576	25	75.8	375	8	ABM65845	Abm65845 Propionib	649	25	75.8	527	3	AAQ23574	Aaq23574 Arabidops
577	25	75.8	382	8	ADW44245	Adw44245 Protein r	650	25	75.8	527	8	ADN72493	Adn72493 Thale cre
578	25	75.8	383	4	ABG21795	Abg21795 Novel hum	651	25	75.8	532	8	ADS26040	Ads26040 Bacterial
579	25	75.8	384	2	AAQ24914	Aaq24914 Eiseinia f	652	25	75.8	536	8	ADX74878	Adx74878 Plant ful
580	25	75.8	385	4	ABG21796	Abg21796 Novel hum	653	25	75.8	540	2	AAW89777	Aaw89777 Staphyloc
581	25	75.8	391	8	ADG71674	Adg71674 Corn ZMNA	654	25	75.8	540	2	AAW89794	Aaw89794 Staphyloc
582	25	75.8	392	4	ABH64533	Abh64533 Drosophi	655	25	75.8	540	4	AAU01258	Aau01258 B. subtil
583	25	75.8	393	8	ADS24667	Ads24667 Bacterial	656	25	75.8	541	5	ABP25656	Abp25656 Streptoco
584	25	75.8	394	8	ADN22953	Adn22953 Bacterial	657	25	75.8	541	5	ABU02376	Abu02376 S. pneumo
585	25	75.8	400	6	ABU26444	Abu26444 Protein e	658	25	75.8	541	8	ADK46444	Adk46444 Streptoco
586	25	75.8	403	4	AAU54649	Aau54649 Propionib	659	25	75.8	541	8	ADV89808	Adv89808 Streptoco
587	25	75.8	403	6	ABM51168	Abm51168 Propionib	660	25	75.8	541	8	ADV83200	Adv83200 Streptoco
588	25	75.8	404	9	ADW43135	Adw43135 Fission y	661	25	75.8	541	8	ADV81061	Adv81061 Streptoco
589	25	75.8	405	8	ADS30212	Ads30212 Bacterial	662	25	75.8	542	5	ABP25657	Abp25657 Streptoco
590	25	75.8	409	4	ABH63762	Abh63762 Drosophi	663	25	75.8	545	9	ABM96689	Abm96689 M. xanthu
591	25	75.8	410	2	AAQ31664	Aaq31664 Mouse neu	664	25	75.8	546	6	ABU28075	Abu28075 Protein e
592	25	75.8	410	3	AAQ58173	Aaq58173 Murine ne	665	25	75.8	547	4	AAU36389	Aau36389 Pseudomon
593	25	75.8	411	6	ADA33392	Ada33392 Acinetoba	666	25	75.8	547	6	ABU40182	Abu40182 Protein e
594	25	75.8	414	6	ABU20217	Abu20217 Protein e	667	25	75.8	547	6	ABU40390	Abu40390 Protein e
595	25	75.8	414	9	ABM96703	Abm96703 M. xanthu	668	25	75.8	547	6	ABU38686	Abu38686 Protein e
596	25	75.8	416	5	ABH54559	Abh54559 Lactococc	669	25	75.8	548	2	AAH86881	Aah86881 E. coli t
597	25	75.8	416	8	ADN17897	Adn17897 Bacterial	670	25	75.8	548	2	AAH88842	Aah88842 E. coli i
598	25	75.8	417	9	ABM95859	Abm95859 M. xanthu	671	25	75.8	548	2	AAW22460	Aaw22460 B. coli a
599	25	75.8	420	9	ABM97586	Abm97586 M. xanthu	672	25	75.8	548	2	AAW13731	Aaw13731 Protein p
600	25	75.8	421	8	ADN27083	Adn27083 Bacterial	673	25	75.8	548	4	AAU38442	Aau38442 Salmonell
601	25	75.8	430	5	ABH47515	Abh47515 Listeria	674	25	75.8	548	6	ABU47033	Abu47033 Protein e
602	25	75.8	430	8	ADSL5405	Adsl5405 HSV-1 pol	675	25	75.8	548	6	ABU47887	Abu47887 Protein e
603	25	75.8	431	6	ABU17834	Abu17834 Protein e	676	25	75.8	548	6	ABU45314	Abu45314 Protein e
604	25	75.8	431	6	ABU18722	Abu18722 Protein e	677	25	75.8	548	6	ABU31711	Abu31711 Protein e
605	25	75.8	433	2	AAH86672	Aah86672 Allergen	678	25	75.8	549	6	ABM67989	Abm67989 Photorhab
606	25	75.8	433	8	ADN25068	Adn25068 Bacterial	679	25	75.8	550	4	AAU35163	Aau35163 Enterococ
607	25	75.8	433	8	ADN22310	Adn22310 Bacterial	680	25	75.8	550	6	ABU21729	Abu21729 Protein e
608	25	75.8	435	4	ABH61663	Abh61663 Drosophi	681	25	75.8	550	6	ABU29067	Abu29067 Protein e

682	25	75.8	554	6	ABU30054	Protein e	755	25	75.8	652	6	ABU25788	Protein e
683	25	75.8	554	6	ABU23680	Protein e	756	25	75.8	655	4	ABB60153	Drosophil
684	25	75.8	556	6	ADR94371	Novel S.	757	25	75.8	655	4	ABU34513	Protein e
685	25	75.8	556	9	AEA58241	Streptoco	758	25	75.8	660	4	AAG78363	GR1 homo
686	25	75.8	560	7	ADH87297	Enterococ	759	25	75.8	667	4	ABM64511	Drosophil
687	25	75.8	560	8	ADI37293	M. tuberc	760	25	75.8	673	8	ADM99173	Environme
688	25	75.8	562	1	NAP81153	Herbicide	761	25	75.8	679	2	AAR99394	Haemophil
689	25	75.8	562	2	AAW22459	E. coli a	762	25	75.8	679	3	AAB23855	Haemophil
690	25	75.8	562	4	AKG98315	Escherich	763	25	75.8	703	6	ABU19766	Protein e
691	25	75.8	562	7	ABO61494	Klebsiell	764	25	75.8	709	8	ADN23774	Bacterial
692	25	75.8	562	8	ADS43227	Bacterial	765	25	75.8	712	8	ADS44332	Bacterial
693	25	75.8	563	6	ABU23590	Protein e	766	25	75.8	715	4	ABG27848	Novel hum
694	25	75.8	563	5	ABB48522	Listeria	767	25	75.8	721	2	AAW72211	HSV-2 str
695	25	75.8	565	4	ABU33029	Protein e	768	25	75.8	722	5	AAE17810	Herpes si
696	25	75.8	565	7	ADM25925	Hyperther	769	25	75.8	722	7	ADG74943	Human her
697	25	75.8	569	7	ADF05481	Bacterial	770	25	75.8	722	7	ADG75163	Human her
698	25	75.8	570	6	ABU22491	Protein e	771	25	75.8	722	7	ADG75087	Human her
699	25	75.8	574	4	AAU01248	B. subtil	772	25	75.8	722	8	ADJ77801	Herpes si
700	25	75.8	575	4	ABB63508	Drosophil	773	25	75.8	727	3	AAW76841	Netrin pr
701	25	75.8	576	4	AAG89928	C glutami	774	25	75.8	727	5	AAW51612	Netrin pr
702	25	75.8	576	6	ABU22901	Protein e	775	25	75.8	727	7	ADB81218	Vertebrat
703	25	75.8	577	6	ABU21336	Protein e	776	25	75.8	737	4	AAB67047	Human imm
704	25	75.8	577	8	ADN73737	Thale cre	777	25	75.8	760	8	ADJ38205	Plastid d
705	25	75.8	578	8	ADT55733	Plant pol	778	25	75.8	760	9	ADK13793	E. coli i
706	25	75.8	578	6	ABU34743	Protein e	779	25	75.8	760	9	AEB91358	Microbial
707	25	75.8	579	4	AAB96355	Putative	780	25	75.8	775	5	AAG80763	Human his
708	25	75.8	582	6	ABU36859	Protein e	781	25	75.8	785	3	AAW82220	Humicola
709	25	75.8	582	9	AEB92297	Nematode	782	25	75.8	785	4	AAG55578	H. insole
710	25	75.8	592	8	ADN17947	Bacterial	783	25	75.8	786	6	ABU35071	Protein e
711	25	75.8	594	2	AAW47188	Aceto-hyd	784	25	75.8	790	3	AAB53164	Macaca mu
712	25	75.8	596	4	ABB71755	Drosophil	785	25	75.8	791	8	ADL04467	M. catarr
713	25	75.8	596	6	ABU19988	Protein e	786	25	75.8	796	6	ABR53413	Protein s
714	25	75.8	600	7	ADH39869	Wheat suc	787	25	75.8	796	7	ADK64704	Disease t
715	25	75.8	600	9	ABW95622	M. xanthu	788	25	75.8	798	6	ABU36064	Protein e
716	25	75.8	603	8	ADY12352	Plant ful	789	25	75.8	803	4	AAAB1392	Amino aci
717	25	75.8	603	8	ADS41604	Bacterial	790	25	75.8	816	6	ADU93248	Plant ful
718	25	75.8	605	8	ADS41604	Bacterial	791	25	75.8	828	6	ABU34281	Protein e
719	25	75.8	605	8	ADS29900	Bacterial	792	25	75.8	829	6	ABJ26402	Aspergill
720	25	75.8	615	3	ADN46225	Thermococ	793	25	75.8	831	6	ABU36664	Protein e
721	25	75.8	616	3	AAB23861	Haemophil	794	25	75.8	834	8	ADR08831	Human pro
722	25	75.8	616	3	AAB29569	Winter wh	795	25	75.8	840	3	AAAB10622	Human Ewi
723	25	75.8	616	8	ADJ49431	Oil-l-aseoc	796	25	75.8	845	2	AAW17890	Photorhab
724	25	75.8	617	3	AAB24788	Plant SDF	797	25	75.8	845	2	AAW56579	Fragment
725	25	75.8	618	5	ABW09169	Methylomo	798	25	75.8	880	2	AAW72093	HSV-2 str
726	25	75.8	618	5	ABG61554	High grow	799	25	75.8	881	2	AAW72002	HSV-2 str
727	25	75.8	618	6	ABU34524	Protein e	800	25	75.8	881	2	AAW72174	HSV-2 str
728	25	75.8	618	6	ABU36899	Protein e	801	25	75.8	882	8	ADG15407	HSV-1 pol
729	25	75.8	621	8	ADN20069	Bacterial	802	25	75.8	883	8	ADM98884	HMG-CoA r
730	25	75.8	622	5	ABB49033	Listeria	803	25	75.8	925	5	ABB97459	Novel hum
731	25	75.8	622	6	ABU33820	Protein e	804	25	75.8	925	7	ADJ69839	Human hea
732	25	75.8	622	6	ABU32854	Protein e	805	25	75.8	936	7	ADJ72226	Methanoba
733	25	75.8	624	7	ABO71744	Human pol	806	25	75.8	937	6	ABP71832	Orthogona
734	25	75.8	624	8	ADL30997	Pseudomon	807	25	75.8	937	9	ADE03193	Orthogona
735	25	75.8	625	6	ABU35993	Protein e	808	25	75.8	937	9	ADM43606	M. thermo
736	25	75.8	625	6	ABU35993	Protein e	809	25	75.8	944	8	ADX95875	Plant ful
737	25	75.8	625	7	ADH39870	H. vulgar	810	25	75.8	969	4	ABB67598	Drosophil
738	25	75.8	625	8	ADJ49268	Oil-l-aseoc	811	25	75.8	993	6	ABM69310	Photorhab
739	25	75.8	625	9	ADW28880	H. vulgare	812	25	75.8	1002	3	ABM23854	Photorhab
740	25	75.8	626	2	AAW2297	Sucrose-f	813	25	75.8	1004	3	AAB23857	Haemophil
741	25	75.8	626	4	AAB31990	Amino aci	814	25	75.8	1017	5	ABB92194	Herbicida
742	25	75.8	626	4	AAG93203	C glutami	815	25	75.8	1024	5	ABB04820	LDL recep
743	25	75.8	631	7	ADH34696	CE7-speci	816	25	75.8	1094	3	AAB23858	Haemophil
744	25	75.8	633	2	AAW56696	CryIIAa. 1	817	25	75.8	1094	6	ABU35459	Protein e
745	25	75.8	633	8	ADR89422	CryIIAa. 1	818	25	75.8	1098	2	AAR99392	Haemophil
746	25	75.8	634	3	AAW94259	Cry2Aa de	819	25	75.8	1104	3	AAB23859	Haemophil
747	25	75.8	635	2	AAW75772	Amino aci	820	25	75.8	1104	3	AAB23856	Haemophil
748	25	75.8	635	3	ABW24787	Plant SDF	821	25	75.8	1105	6	ADL05613	M. catarr
749	25	75.8	635	4	AAU02043	B. thurin	822	25	75.8	1106	6	ABM67225	Photorhab
750	25	75.8	637	4	AAW79357	Corynebac	823	25	75.8	1116	6	ABM69308	Photorhab
751	25	75.8	637	7	ADD13345	C. glutam	824	25	75.8	1131	6	ABM67711	Photorhab
752	25	75.8	639	3	AAB24786	Plant SDF	825	25	75.8	1287	7	ABM87031	Rice abio
753	25	75.8	641	4	AAE05101	Drosophil	826	25	75.8	1332	7	ABM90146	Rice abio
754	25	75.8	648	7	ABO64021	Klebsiell	827	25	75.8	1501	5	ABP69798	Human pol

828	25	75.8	5	ABP30895	Abp30895	Streptococ	901	24	72.7	68	7	ADB92946	Adb92946	Human col
829	25	75.8	5	ABP29894	Abp29894	Streptococ	902	24	72.7	71	8	ADX94907	Adx94907	Plant ful
830	25	75.8	5	ABP30531	Abp30531	Streptococ	903	24	72.7	74	4	AAU52093	Aau52093	Propionib
831	25	75.8	8	ADU69668	Adu69668	S agalact	904	24	72.7	74	6	ABM48612	Abm48612	Propionib
832	25	75.8	8	ADU88224	Adu88224	Streptococ	905	24	72.7	75	7	ADC24844	Adc24844	Human bre
833	25	75.8	8	ADV81649	Adv81649	Streptococ	906	24	72.7	78	8	ADX80478	Adx80478	Plant ful
834	25	75.8	8	ADV79477	Adv79477	Streptococ	907	24	72.7	85	6	ABM64573	Abm64573	Propionib
835	25	75.8	7	ABH80241	Abh80241	CepA. 12/	908	24	72.7	87	4	AAU65405	Aau65405	Propionib
836	25	75.8	6	ABP71293	Abp71293	Group B S	909	24	72.7	87	6	ABM61924	Abm61924	Propionib
837	25	75.8	4	AAE04843	Aae04843	Human SGP	910	24	72.7	89	7	ABO64126	AbO64126	Klebsiell
838	25	75.8	5	ABP28560	Abp28560	Streptococ	911	24	72.7	91	8	ADM99765	Adm99765	L. inter
839	25	75.8	4	ABR60544	Abbr60544	Drosophil	912	24	72.7	94	8	ADM97176	Adm97176	Human IL-
840	25	75.8	8	ADL91596	Adl91596	Drosophil	913	24	72.7	96	7	ABE31064	Abe31064	Human dila
841	25	75.8	1801	ABBS59945	Abbs59945	Drosophil	914	24	72.7	100	3	AAAB40081	AaAB40081	Anti-hiLi
842	25	75.8	2	AAW17900	Aaw17900	Photorhab	915	24	72.7	101	5	ABP07187	Abp07187	Human ORF
843	25	75.8	2	AAW56573	Aaw56573	Toxin Tcd	916	24	72.7	102	8	ADQ65079	AdQ65079	Novel hum
844	25	75.8	1925	AAE37000	Aae37000	Micromono	917	24	72.7	103	4	AAV72557	Aav72557	Eacherich
845	25	75.8	8	ADF83256	Adf83256	Bacterial	918	24	72.7	103	4	ASG04932	Asg04932	Novel hum
846	25	75.8	8	ADL13634	Adl13634	L. kirsch	919	24	72.7	104	3	ABAB41235	AbAB41235	Human ORF
847	25	75.8	8	ADI26358	Adi26358	Wagtaila	920	24	72.7	104	5	ABP02122	Abp02122	Human ORF
848	25	75.8	2261	ABJ18914	Abj18914	Pathogen	921	24	72.7	105	4	AAU65878	Aau65878	Propionib
849	25	75.8	6	ABU16000	Abu16000	Protein e	922	24	72.7	105	5	AAU84330	Aau84330	Protein D
850	25	75.8	6	ABW72734	Abw72734	Staphyloc	923	24	72.7	105	6	ABM62397	Abm62397	Propionib
851	25	75.8	2283	ABP56876	Abp56876	Staphyloc	924	24	72.7	105	8	ADP25037	Adp25037	PRO poly
852	25	75.8	4	AAU37120	Aau37120	Staphyloc	925	24	72.7	106	7	ABO63661	AbO63661	Klebsiell
853	25	75.8	2	AAK99393	Aak99393	Haemophil	926	24	72.7	110	3	AAAB39156	AaAB39156	Human sec
854	25	75.8	4	AAU34139	Aau34139	Staphyloc	927	24	72.7	111	6	ABU44358	Abu44358	Protein e
855	25	75.8	2368	AAU36796	Aau36796	Staphyloc	928	24	72.7	111	8	ADK79529	Adk79529	Plant ful
856	25	75.8	4	ABU42252	Abu42252	Protein e	929	24	72.7	113	8	ADY07770	Ady07770	Plant ful
857	25	75.8	3	ABE23860	AbE23860	Haemophil	930	24	72.7	114	8	ABM81499	Abm81499	Tumour-as
858	25	75.8	4	AAU37374	Aau37374	Staphyloc	931	24	72.7	114	8	AEAL1024	AeAL1024	Human ant
859	25	75.8	4	AAU34320	Aau34320	Staphyloc	932	24	72.7	115	5	ABB07232	Abb07232	Anti-IL-4
860	25	75.8	6	ABJ19002	Abj19002	Pathogen	933	24	72.7	115	9	AEAL1028	AeAL1028	Human ant
861	25	75.8	6	ABM71899	Abm71899	Staphyloc	934	24	72.7	115	9	AEAL1023	AeAL1023	Human ant
862	25	75.8	2481	ABU15838	Abu15838	Protein e	935	24	72.7	115	9	AEAL1022	AeAL1022	Human ant
863	25	75.8	7	ABE62804	AbE62804	Methicill	936	24	72.7	115	9	AEAL1019	AeAL1019	Human ant
864	25	75.8	8	ADU74047	Adu74047	Staphyloc	937	24	72.7	115	9	AEAL1026	AeAL1026	Human ant
865	25	75.8	2	AAH82665	Aah82665	Porcine r	938	24	72.7	115	9	AEA08909	Aea08909	Heavy cha
866	25	75.8	2	AAW17899	Aaw17899	Photorhab	939	24	72.7	115	9	AEA08891	Aea08891	Heavy cha
867	25	75.8	2	AAW56572	Aaw56572	Toxin Tcd	940	24	72.7	115	9	AEA08905	Aea08905	Heavy cha
868	25	75.8	4	ABW72609	Abw72609	Photorhab	941	24	72.7	115	9	AEA08988	Aea08988	Heavy cha
869	25	75.8	5	ABG32851	Abg32851	P. lumine	942	24	72.7	115	9	AEA08983	Aea08983	Heavy cha
870	25	75.8	8	ADP18614	Adp18614	Photorhab	943	24	72.7	115	9	AEA08994	Aea08994	Heavy cha
871	25	75.8	8	ADR21575	Adr21575	Photorhab	944	24	72.7	115	9	AEA08989	Aea08989	Heavy cha
872	25	75.8	9	ADZ72157	Adz72157	P. lumine	945	24	72.7	115	9	AEA08991	Aea08991	Heavy cha
873	25	75.8	4	ABW72611	Abw72611	Modified	946	24	72.7	115	9	AEA08992	Aea08992	Heavy cha
874	25	75.8	2	AAV33729	Aav33729	Photorhab	947	24	72.7	115	9	AEA08995	Aea08995	Heavy cha
875	25	75.8	6	ABW70229	Abw70229	Photorhab	948	24	72.7	115	9	AEA08987	Aea08987	Heavy cha
876	25	75.8	4	ABW72614	Abw72614	TcdA toxi	949	24	72.7	115	9	AEA08993	Aea08993	Heavy cha
877	25	75.8	4	ABB70376	Abb70376	Drosophil	950	24	72.7	115	9	AEA08933	Aea08933	Heavy cha
878	25	75.8	4	AAU37403	Aau37403	Staphyloc	951	24	72.7	115	9	AEA08937	Aea08937	Heavy cha
879	25	75.8	6	ABU15887	Abu15887	Protein e	952	24	72.7	115	9	AEA08990	Aea08990	Heavy cha
880	25	75.8	6	ABW73008	Abw73008	Staphyloc	953	24	72.7	115	9	AEA08897	Aea08897	Heavy cha
881	25	75.8	10431	ABU54861	Abu54861	Human CAl	954	24	72.7	115	9	AEA08985	Aea08985	Heavy cha
882	25	75.8	6	ABU19119	Abu19119	Pathogen	955	24	72.7	115	9	AEA08929	Aea08929	Heavy cha
883	25	75.8	8	ADR72871	Adr72871	Human ova	956	24	72.7	115	9	AEA08929	Aea08929	Heavy cha
884	24	72.7	7	ADF73146	Adf73146	Anti-RELP	957	24	72.7	115	9	AEA08901	Aea08901	Heavy cha
885	24	72.7	16	AAE24164	Aae24164	Human 234	958	24	72.7	115	9	AEA08982	Aea08982	Heavy cha
886	24	72.7	16	AAU82611	Aau82611	Llama CDR	959	24	72.7	115	9	AEA08984	Aea08984	Heavy cha
887	24	72.7	16	ADU05831	Adu05831	Human hyd	960	24	72.7	115	9	AEA08986	Aea08986	Heavy cha
888	24	72.7	17	AEA46259	Aea46259	Apolipop	961	24	72.7	117	2	AAH85857	AaH85857	S. pneumo
889	24	72.7	18	ADM56176	Adm56176	Synthetic	962	24	72.7	117	8	ADK73709	Adk73709	Plant ful
890	24	72.7	8	ADM97729	Adm97729	MNAR frag	963	24	72.7	120	8	ADM97719	Adm97719	Human MNA
891	24	72.7	33	AAH81532	Aah81532	Human ing	964	24	72.7	123	7	ADB64080	AdB64080	Human pro
892	24	72.7	37	AAE08563	Aae08563	Human Bet	965	24	72.7	127	8	ADF73149	Adf73149	Anti-RELP
893	24	72.7	37	AAE08564	Aae08564	Human Bet	966	24	72.7	128	7	ADH85868	Adh85868	Enterococ
894	24	72.7	51	ADC00645	Adc00645	Enterohae	967	24	72.7	129	3	AAAY27233	AaAY27233	Amino aci
895	24	72.7	53	ABP78592	Abp78592	N. gonorr	968	24	72.7	130	3	AAAB42203	AaAB42203	Human ORF
896	24	72.7	54	ABW71885	Abw71885	Protein #	969	24	72.7	130	5	ABG76529	Abg76529	HCV B1 an
897	24	72.7	63	ADA33825	Ada33825	Acinetoba	970	24	72.7	133	2	RAY07279	Ray07279	Bovine sy
898	24	72.7	68	AAW93122	Aaw93122	Human dig	971	24	72.7	133	6	ABM65592	Abm65592	Propionib
899	24	72.7	68	AAW38638	Aaw38638	Human col	972	24	72.7	134	2	AAAY07278	AaAY07278	Human bet
900	24	72.7	68	ABG97690	Abg97690	Human col	973	24	72.7	134	4	AAU51221	Aau51221	Propionib

974 24 72.7 134 6 ABM47740 Propionib
 975 24 72.7 134 8 ADP86572 Human bet
 976 24 72.7 134 8 ADU05019 Amino aci
 977 24 72.7 140 2 AAY07274 Rat synuc
 978 24 72.7 140 3 AAY92220 NACP/alph
 979 24 72.7 140 7 ADE54628 Rat Prote
 980 24 72.7 140 7 ADE54632 Rat Prote
 981 24 72.7 140 7 ADE61796 Rat Prote
 982 24 72.7 140 7 ADD47875 Rat Prote
 983 24 72.7 140 7 ADI62684 Human apo
 984 24 72.7 143 2 AAY07280 Zebrafinc
 985 24 72.7 143 4 AAB64990 Gene 47 h
 986 24 72.7 147 5 ABB48575 Listeria
 987 24 72.7 152 2 AAY07275 Rat synuc
 988 24 72.7 152 5 ABB54439 Lactococ
 989 24 72.7 153 6 ABM70023 Phototrab
 990 24 72.7 154 8 ADK48527 Streptoco
 991 24 72.7 156 5 ABP04112 Human ORF
 992 24 72.7 156 5 ABB49768 Listeria
 993 24 72.7 157 5 ABP03089 Human ORF
 994 24 72.7 158 5 ABB92569 Herbicida
 995 24 72.7 158 6 ABU45399 Protein e
 996 24 72.7 158 8 ADR96024 Novel S.
 997 24 72.7 158 9 AEA59894 Streptoco
 998 24 72.7 159 3 AAB07516 A ketored
 999 24 72.7 159 3 AAG11579 Arabidops
 1000 24 72.7 160 6 ABU31867 Protein e

ALIGNMENTS

RESULT 1
 AAW23434
 ID AAW23434 standard; peptide; 7 AA.
 XX AC
 XX AAW23434;
 DT 23-APR-1998 (first entry)
 XX
 DE CDR-2 of rWI2 light chain.
 XX
 XX Antibody; complementarity determining region; CDR; light chain; rat; CEA;
 KW rWI2; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 XX Rattus sp.
 OS
 XX WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 PF 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Loeman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 FT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 FT stimulate immune response against cancer.
 XX
 XX Claim 4; Page 30; 46pp; English.
 PS
 XX This sequence represents the complementarity determining region-2 (CDR-2)
 CC of the rWI2 light chain. This sequence is used in an antibody of the
 CC invention. The antibody of the invention is a chimeric or humanised anti-
 CC idiotype antibodies (cAb and hAb, respectively) or a fragment which
 CC specifically binds to the idiotype region of an anti-carcinoembryonic

CC antigen (CEA), where: (i) cAb comprises the rWI2 light (L) and heavy (H)
 CC chain variable regions, or silent mutations; and (ii) hAb comprises rWI2
 CC complementarity determining regions (CDR) and humanised framework (FR)
 CC regions. The hAb is used as a vaccine to stimulate an immune response in
 CC a patient against cancers expressing CEA. The hAb, can be used to clear
 CC non-targeted antibody in a method of diagnosis or treatment of a patient
 CC where a CEA antibody is used as a (pre-)targeting or therapy agent. The
 CC cAb is used to detect the presence of an antibody that specifically binds
 CC to CEA in a sample
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 33; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 Db 1 GATNLAA 7
 RESULT 2
 AAW23439
 ID AAW23439 standard; protein; 108 AA.
 XX AC
 XX AAW23439;
 DT 23-APR-1998 (first entry)
 XX
 DE Modified light chain variable region REIW2V2KRS.
 XX
 KW Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rWI2; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.
 XX
 OS Synthetic.
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 4 /note= "L to M mutation"
 FT Misc-difference 9 /note= "A to S mutation"
 FT Misc-difference 12 /note= "P to S mutation"
 FT Misc-difference 15 /note= "L to V mutation"
 FT Region 24..34
 FT Misc-difference 39 /note= "complementarity determining region-1"
 FT Misc-difference 43 /note= "K to T mutation"
 FT Misc-difference 45 /note= "S to A mutation"
 FT Misc-difference 45 /note= "R to K mutation"
 FT Region 50..56
 FT Misc-difference 72 /note= "complementarity determining region-2"
 FT Misc-difference 73 /note= "S to T mutation"
 FT Misc-difference 76 /note= "L to F mutation"
 FT Misc-difference 76 /note= "N to S mutation"
 FT Misc-difference 79 /note= "E to Q mutation"
 FT Misc-difference 80 /note= "S to P mutation"
 FT Misc-difference 83 /note= "M to I mutation"
 FT Misc-difference 85 /note= "I to T mutation"
 FT Region 89..97
 FT /note= "complementarity determining region-3"

FT Misc-difference 105 /note= "E to Q mutation"

FT Misc-difference 106 /note= "R to I mutation"

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Losman MJ, Hansen H;

XX WPI, 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer.

XX Claim 8; Fig 2; 46pp; English.

XX This sequence represents a modified version of the rat rW12 light chain variable region, designated REIWI2VKR. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotypic antibodies (cAb and hAb, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light (L) and heavy (H) chain variable regions, or silent mutations; and (ii) hAb comprises rW12 complementarity determining regions (CDR) and humanised framework (FR) regions. The hAb is used as a vaccine to stimulate an immune response in a patient against cancers expressing CEA. The hAb, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CEA antibody is used as a (pre-)targeting or therapy agent. The cAb is used to detect the presence of an antibody that specifically binds to CEA in a sample

XX Sequence 108 AA;

Query Match 100.0%; Score 33; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7

DB 50 GATNLAA 56

RESULT 3

AAW23440

ID AAW23440 standard; protein; 108 AA.

XX AAW23440;

XX 23-APR-1998 (first entry)

XX Modified light chain variable region REIWI2VK.

XX Antibody; complementarity determining region; heavy chain; rat; CEA;

XX rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;

XX therapy; idiotype region; mutein; variable region.

XX Synthetic.

XX Rattus sp.

XX Key Location/Qualifiers

FT Misc-difference 4 /note= "L to M mutation"

FT Misc-difference 9 /note= "A to S mutation"

FT Misc-difference 12 /note= "P to S mutation"

FT Misc-difference 15 /note= "L to V mutation"

FT Region 24..34

FT /note= "complementarity determining region-1"

FT Misc-difference 39 /note= "K to T mutation"

FT Misc-difference 43 /note= "S to A mutation"

FT Misc-difference 45 /note= "R to K mutation"

FT Region 50..56

FT /note= "complementarity determining region-2"

FT Misc-difference 66 /note= "R to G mutation"

FT Misc-difference 69 /note= "S to T mutation"

FT Misc-difference 72 /note= "S to T mutation"

FT Misc-difference 73 /note= "L to F mutation"

FT Misc-difference 76 /note= "N to S mutation"

FT Misc-difference 79 /note= "E to Q mutation"

FT Misc-difference 80 /note= "S to P mutation"

FT Misc-difference 83 /note= "M to I mutation"

FT Misc-difference 85 /note= "I to T mutation"

FT Region 89..97

FT /note= "complementarity determining region-3"

FT Misc-difference 105 /note= "E to Q mutation"

FT Misc-difference 106 /note= "R to I mutation"

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Losman MJ, Hansen H;

XX WPI, 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic antibodies - useful in detection of anti-CEA antibodies and as vaccine to stimulate immune response against cancer.

XX Claim 8; Fig 2; 46pp; English.

XX This sequence represents a modified version of the rat rW12 light chain variable region, designated REIWI2VK. This sequence is used in an antibody of the invention. The antibody of the invention is a chimeric or humanised anti-idiotypic antibodies (cAb and hAb, respectively) or a fragment which specifically binds to the idiotype region of an anti-carcinoembryonic antigen (CEA), where: (i) cAb comprises the rW12 light (L) and heavy (H) chain variable regions, or silent mutations; and (ii) hAb comprises rW12 complementarity determining regions (CDR) and humanised framework (FR) regions. The hAb is used as a vaccine to stimulate an immune response in a patient against cancers expressing CEA. The hAb, can be used to clear non-targeted antibody in a method of diagnosis or treatment of a patient where a CEA antibody is used as a (pre-)targeting or therapy agent. The cAb is used to detect the presence of an antibody that specifically binds to CEA in a sample

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 33; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 50 GATNLAA 56

RESULT 4

AAW23442
 ID AAW23442 standard; protein; 108 AA.

XX AC AAW23442;
 XX DT 23-APR-1998 (first entry)
 XX DE hWI2 light chain.

XX KW Antibody; complementarity determining region; light chain; human; CEA;
 KW hWI2; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 89..97
 FT /note= "complementarity determining region-3"

XX PN WO9734636-A1.
 XX PD 25-SEP-1997.
 XX PF 19-MAR-1997; 97WO-US004696.
 XX PR 20-MAR-1996; 96US-0013708P.
 XX PA (IMMU-) IMMUNOMEDICS INC.
 XX PI Leung S, Loeman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86304.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.

XX PS Disclosure; Fig 4; 46pp; English.

XX CC This sequence represents the human hWI2 light chain. This sequence is
 CC used in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotype antibodies (cab and hab,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cab
 CC comprises the hWI2 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hab comprises hWI2 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hab is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hab, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cab is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 33; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 50 GATNLAA 56

RESULT 5

AAW23436
 ID AAW23436 standard; protein; 108 AA.

XX AC AAW23436;
 XX DT 23-APR-1998 (first entry)
 XX DE rWI2 light chain.

XX KW Antibody; complementarity determining region; light chain; rat; CEA;
 KW rWI2; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.

XX OS Rattus sp.

XX FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 88..97
 FT /note= "complementarity determining region-3"

XX PN WO9734636-A1.
 XX PD 25-SEP-1997.
 XX PF 19-MAR-1997; 97WO-US004696.
 XX PR 20-MAR-1996; 96US-0013708P.
 XX PA (IMMU-) IMMUNOMEDICS INC.
 XX PI Leung S, Loeman MJ, Hansen H;
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86287.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 PT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 PT stimulate immune response against cancer.

XX PS Claim 6; Fig 7; 46pp; English.

XX CC This sequence represents the rat rWI2 light chain. This sequence is used
 CC in an antibody of the invention. The antibody of the invention is a
 CC chimeric or humanised anti-idiotype antibodies (cab and hab,
 CC respectively) or a fragment which specifically binds to the idiotype
 CC region of an anti-carcinoembryonic antigen (CEA), where: (i) cab
 CC comprises the rWI2 light (L) and heavy (H) chain variable regions, or
 CC silent mutations; and (ii) hab comprises rWI2 complementarity determining
 CC regions (CDR) and humanised framework (FR) regions. The hab is used as a
 CC vaccine to stimulate an immune response in a patient against cancers
 CC expressing CEA. The hab, can be used to clear non-targeted antibody in a
 CC method of diagnosis or treatment of a patient where a CEA antibody is
 CC used as a (pre-)targeting or therapy agent. The cab is used to detect the
 CC presence of an antibody that specifically binds to CEA in a sample

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 33; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
RESULT 8
ADG67279
ID ADG67279 standard; peptide; 13 AA.
XX
XX AC ADG67279;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Human 5G1.1 antibody MHC class II binding peptide #61.
XX
XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
XX KW immunogenicity; MHC class II; antibody.
XX
XX OS Homo sapiens.
XX
XX PN WO200269232-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 18-FEB-2002; 2002WO-EP001688.
XX
XX PP 19-FEB-2001; 2001EP-00103954.
XX
XX PR 08-MAR-2001; 2001EP-00105777.
XX
XX PR 15-MAR-2001; 2001EP-00106536.
XX
XX PR 15-MAR-2001; 2001EP-00106538.
XX
XX PR 20-MAR-2001; 2001EP-00106899.
XX
XX PR 20-MAR-2001; 2001EP-00107012.
XX
XX PR 27-MAR-2001; 2001EP-00107568.
XX
XX PR 25-APR-2001; 2001EP-00110220.
XX
XX PR 30-MAY-2001; 2001EP-00113228.
XX
XX PR 19-OCT-2001; 2001EP-00124965.
XX
XX PR 12-NOV-2001; 2001EP-00126859.
XX
XX PA (MERE ) MERCK PATENT GMBH.
XX
XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
XX WPI; 2002-750424/81.
XX
XX DR Identifying potential T-cell epitope peptides within the amino acid
XX PT sequence of a biological molecule, useful for preparing a biological
XX PT molecule with reduced immunogenicity, comprises determining peptide
XX PT binding to MHC molecules.
XX
XX PS Example 18; Page 57; 85pp; English.
XX
XX CC The invention relates to a novel method for identifying one or more
XX CC potential T-cell epitope peptides within the amino acid sequence of a
XX CC biological molecule by determining the binding of the peptides to major
XX CC histocompatibility complex (MHC) molecules using in vitro or in silico
XX CC techniques or biological assays. The method of the invention is useful
XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX CC their fragments with reduced immunogenicity. The potential T-cell epitope
XX CC peptide within the amino acid sequence of a parent immunogenically non-
XX CC modified biological molecule identified is useful for preparing a
XX CC biological molecule with reduced immunogenicity and having a retained
XX CC desired biological activity, where the T-cell epitope is a 13mer peptide.
XX CC The present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 13 AA;
XX
XX Query Match 87.9%; Score 29; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GATNLA 6
XX Db |||||
XX 4 GATNLA 9
XX
XX RESULT 9
ADG67277
ID ADG67277 standard; peptide; 13 AA.
XX
XX AC ADG67277;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Human 5G1.1 antibody MHC class II binding peptide #59.
XX
XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
XX KW immunogenicity; MHC class II; antibody.
XX
XX OS Homo sapiens.
XX
XX PN WO200269232-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 18-FEB-2002; 2002WO-EP001688.
XX
XX PP 19-FEB-2001; 2001EP-00103954.
XX
XX PR 08-MAR-2001; 2001EP-00105777.
XX
XX PR 15-MAR-2001; 2001EP-00106536.
XX
XX PR 15-MAR-2001; 2001EP-00106538.
XX
XX PR 20-MAR-2001; 2001EP-00106899.
XX
XX PR 20-MAR-2001; 2001EP-00107012.
XX
XX PR 27-MAR-2001; 2001EP-00107568.
XX
XX PR 25-APR-2001; 2001EP-00110220.
XX
XX PR 30-MAY-2001; 2001EP-00113228.
XX
XX PR 19-OCT-2001; 2001EP-00124965.
XX
XX PR 12-NOV-2001; 2001EP-00126859.
XX
XX PA (MERE ) MERCK PATENT GMBH.
XX
XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
XX WPI; 2002-750424/81.
XX
XX DR Identifying potential T-cell epitope peptides within the amino acid
XX PT sequence of a biological molecule, useful for preparing a biological
XX PT molecule with reduced immunogenicity, comprises determining peptide
XX PT binding to MHC molecules.
XX
XX PS Example 18; Page 57; 85pp; English.
XX
XX CC The invention relates to a novel method for identifying one or more
XX CC potential T-cell epitope peptides within the amino acid sequence of a
XX CC biological molecule by determining the binding of the peptides to major
XX CC histocompatibility complex (MHC) molecules using in vitro or in silico
XX CC techniques or biological assays. The method of the invention is useful
XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX CC their fragments with reduced immunogenicity. The potential T-cell epitope
XX CC peptide within the amino acid sequence of a parent immunogenically non-
XX CC modified biological molecule identified is useful for preparing a
XX CC biological molecule with reduced immunogenicity and having a retained
XX CC desired biological activity, where the T-cell epitope is a 13mer peptide.
XX CC The present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 13 AA;
XX
XX Query Match 87.9%; Score 29; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GATNLA 6
XX Db |||||
XX 4 GATNLA 9
XX
XX RESULT 10
AAU40729
ID AAU40729 standard; protein; 93 AA.
XX
XX AC AAU40729;
XX
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ID AD026410 standard; protein; 107 AA.
XX AC
XX AD026410;
XX DT
XX DE 29-JUL-2004 (first entry)
XX KW Murine anti-truncated Nogo-A antibody II-1-8 light chain variable region.
XX KW rat; human; Nogo-A; truncated; affinity; membrane-bound protein; mouse;
XX KW antibody.
XX OS Mus sp.
XX OS Synthetic.
XX PN WO2004039836-A1.
XX PD 13-MAY-2004.
XX PF 31-OCT-2002; 2002WO-EP012210.
XX PR 31-OCT-2002; 2002WO-EP012210.
XX PA (PIER-) PIERIS PROTEOLAB AG.
XX PI Skerra A, Fiedler M;
XX WPI; 2004-376159/35.
XX New isolated truncated Nogo-A polypeptide that corresponds to a truncated
PT form of the Nogo-A protein, useful for identifying a compound having
PT detectable affinity to a Nogo-A protein.
XX Claim 21; Page 60; 80pp; English.
XX The present invention relates to an isolated truncated Nogo-A polypeptide
CC that corresponds to a truncated form of the Nogo-A protein from the rat
CC and from the human. The truncated polypeptide is useful for identifying a
CC compound having detectable affinity to a Nogo-A protein. The present
CC sequence is a fragment of an anti-Nogo-A antibody used in the
CC exemplification of the invention.
XX Sequence 107 AA;
XX Query Match 87.9%; Score 29; DB 8; Length 107;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATNLA 6
DB 50 GATNLA 55
RESULT 13
ADJ78464
ID ADJ78464 standard; protein; 145 AA.
XX AC
XX ADJ78464;
XX DT
XX DE 06-MAY-2004 (first entry)
XX DE Mouse perilipin protein SEQ ID NO:11.
XX perilipin; perilipin inhibitor; antisense oligonucleotide; antidiabetic;
KW anorectic; antiarteriosclerotic; cardiant; metabolic disorder; diabetes;
KW obesity; atherosclerosis; mouse.
XX OS Mus musculus.
XX PN WO2004012745-A1.
XX PD 12-FEB-2004.
XX PF 30-JUL-2003; 2003WO-US023760.
XX
XX 06-AUG-2002; 2002US-00213796.
XX (ISIS-) ISIS PHARM INC.
XX Bhanot S, Freier SM;
XX WPI; 2004-157008/15.
XX N-PSDB; ADJ78303.
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acids encoding perilipin, useful for treating a metabolic
PT disorder e.g. obesity, diabetes or atherosclerosis.
XX Example 13; SEQ ID NO 11; 167pp; English.
XX The present invention describes a compound 8-80 nucleobases in length
CC targeted to, and which specifically hybridises with a nucleic acid
CC molecule encoding perilipin, and inhibits the expression of perilipin.
CC Also described: (1) a compound 8-80 nucleobases in length that
CC specifically hybridises with at least an 8-nucleobase portion of an
CC active site on a nucleic acid molecule encoding perilipin; (2) a
CC composition comprising the compound and a carrier or diluent; (3) a
CC method for inhibiting the expression of perilipin in cells or tissues by
CC contacting the cells or tissues with the compound so that expression of
CC perilipin is inhibited; (4) a method of treating an animal having a
CC disease or condition associated with perilipin by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of perilipin is inhibited; and (5) a method for screening an
CC antisense compound by contacting a preferred target region of a nucleic
CC acid molecule encoding perilipin with one or more candidate antisense
CC compounds comprising at least an 8-nucleobase portion that is
CC complementary to the preferred target region, and selecting for one or
CC more candidate antisense compounds that inhibit the expression of a
CC nucleic acid encoding perilipin. The antisense compounds have
CC antidiabetic, anorectic, antiarteriosclerotic and cardiant activities,
CC and can be used in perilipin inhibitors. The compounds, compositions and
CC methods of the present invention are useful for treating a disease or
CC condition associated with perilipin, such as a metabolic disorder, e.g.
CC diabetes, obesity or atherosclerosis. They are also useful in research
CC and diagnostics for modulating the expression of perilipin. The present
CC sequence represents mouse perilipin, which is used in an example from the
CC present invention.
XX Sequence 145 AA;
XX Query Match 87.9%; Score 29; DB 8; Length 145;
XX Best Local Similarity 85.7%; Pred. No. 1.6e+02;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATNLAA 7
DB 64 GASNLAA 70
RESULT 14
AAB94485
ID AAB94485 standard; protein; 158 AA.
XX AC
XX AAB94485;
XX DT 26-JUN-2001 (first entry)
XX DE Human protein sequence SEQ ID NO:15166.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX PD 07-FEB-2001.
XX

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PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 15166; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 158 AA;
 Query Match 87.9%; Score 29; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GATNLA 6
 Db 62 GATNLA 67
 RESULT 15
 ADG28555
 ID ADG28555 standard; protein; 235 AA.
 XX
 AC ADG28555;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Paramyxovirus vector-related antibody IN-1 light chain protein.
 XX
 KW Paramyxovirus vector; antibody variable region; neuroprotective;
 KW nerve elongation inhibitor; nerve injury; monoclonal antibody drug;
 KW antibody IN-1 light chain.
 XX
 OS Unidentified.
 XX
 PN WO2003102183-A1.

XX 11-DEC-2003.
 PD
 XX
 PF 03-JUN-2003; 2003WO-JP007005.
 XX
 PR 03-JUN-2002; 2002JP-00161964.
 XX
 PA (DNAV-) DNAVEC RES INC.
 XX
 PI Inoue M, Hasegawa M, Hironaka T;
 PI WPI; 2004-043115/04.
 DR N-ESDB; ADG28553.
 XX
 PT Paramyxovirus vectors encoding antibody applicable as gene therapeutic
 PT vectors for in vivo or ex vivo administration against nerve elongation
 PT inhibitor, useful in treating nerve injury.
 XX
 PS Example 1; SEQ ID NO 11; 143pp; Japanese.
 XX
 CC The invention relates to a novel paramyxovirus vector encoding a
 CC polypeptide containing antibody variable regions. The vector of the
 CC invention demonstrates neuroprotective activity and may be applicable as
 CC a gene therapeutic vector for in vivo or ex vivo administration against a
 CC nerve elongation inhibitor and thus may be useful in treating nerve
 CC injury. The vector is capable of localised expression within the vicinity
 CC of the disease locus to reduce side-effects and to minimise the
 CC associated cost when developing monoclonal antibody drugs. Furthermore,
 CC the vector can express an antibody which inhibits immunopotentialiation,
 CC signal transfer thereby enabling the prolonged expression of a gene from
 CC the vector and repeated administrations are possible. The current
 CC sequence is that of the Sendai virus paramyxovirus vector-related
 CC antibody IN-1 light chain protein of the invention.
 XX
 SQ Sequence 235 AA;
 Query Match 87.9%; Score 29; DB 8; Length 235;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GATNLA 6
 Db 71 GATNLA 76
 RESULT 16
 AAR77614
 ID AAR77614 standard; protein; 236 AA.
 XX
 AC AAR77614;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1996 (first entry)
 XX
 DE Humanised 5G1.1 VL + 012.
 XX
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= sig_peptide
 FT 23..236
 FT /label= mat_peptide
 FT 47..57
 FT Region /label= CDR-L1
 FT 73..79
 FT /label= CDR-L2
 FT 112..120
 FT /label= CDR-L3

DR	WPI; 2004-460973/43.
DR	N-PSDB; ADQ16650.
XX	
PT	New immunoglobulin molecule comprising a region, where two
PT	complementarity determining regions (CDRs) are replaced with EPO mimetic
PT	or a TPO mimetic, useful for treating thrombocytopenia.
XX	
PS	Example 4; SEQ ID NO 69; 107pp; English.
XX	
CC	The invention relates to a novel immunoglobulin molecule or its fragment
CC	comprising a region where amino acid residues corresponding to at least a
CC	portion of a two complementarity determining regions (CDRs) are replaced
CC	with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC	a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC	invention has immunosuppressive activity, and may have a use in
CC	immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC	treating thrombocytopenia as a result of chemotherapy, bone marrow
CC	transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC	The present sequence represents an immunoglobulin antibody light chain of
XX	the invention.
XX	
SQ	Sequence 236 AA;
	Query Match 87.9%; Score 29; DB 8; Length 236;
	Best Local Similarity 100.0%; Pred. No. 2.7e+02;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GATNLA 6
DB	72 GATNLA 77
RESULT 19	
ADV44387	
ID	ADV44387 standard; protein; 236 AA.
XX	
AC	ADV44387;
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	SG1.1 light chain with TPO mimetic peptide.
XX	
KW	anti-HIV; cytostatic; gene therapy; antibody engineering; diagnosis;
KW	HIV-infection; anti-HIV; chemotherapy; bone marrow transplantation;
KW	transplant rejection; prophyllaxis; myeloproliferative disorder;
KW	hematological disease.
XX	
OS	Synthetic.
OS	Unidentified.
XX	
PN	WO2004108078-A2.
XX	
PD	16-DEC-2004.
XX	
XX	26-MAY-2004; 2004WO-US016574.
XX	
PR	02-JUN-2003; 2003US-00452590.
XX	
PA	(ALEX-) ALEXION PHARM INC.
XX	
PI	Bowdish KS, Frederickson S, Renshaw M, Orenica C;
XX	
XX	WPI; 2005-031588/03.
DR	N-PSDB; ADV44388.
XX	
XX	New immunoglobulin molecule comprises a region where amino acid residues
PT	corresponding to a portion of complementarity determining region (CDR) is
PT	replaced with a peptide mimetic, useful for treating, e.g. HIV-infected
PT	patients.
XX	
PS	Example 4; SEQ ID NO 69; 139pp; English.
XX	
CC	The invention describes an immunoglobulin molecule or its fragment

comprising a region where amino acid residues corresponding to at least a portion of a complementarity determining regions (CDR) is replaced with a peptide selected from human brain natriuretic protein (hBNP), hBNP mimetics, glycogen phosphorylase (GLP)-1, GLP-1 mimetics, GLP-2, GLP-2 mimetics, exendin, exendin mimetics, glucagons, glucagon mimetics and PACAP-38. Also included are a nucleic acid encoding the immunoglobulin molecule, an expression vector comprising the nucleic acid, a host cell transformed with the expression vector, producing an immunoglobulin molecule (or its fragment, comprising culturing the host cell under conditions suitable for expression of the immunoglobulin or its fragment), a composition comprising an immunoglobulin (or its fragment) and a pharmaceutically acceptable carrier, treating congestive heart failure (comprising administering to the subject an immunoglobulin molecule or fragment comprising a region where amino acid residues corresponding to at least a portion of a CDR is replaced with a peptide selected from hBNP and hBNP mimetics), treating diabetes or obesity (comprising administering to a subject an immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a CDR is replaced with GLP-1), inducing endothelial-dependent relaxation of precontracted pulmonary artery rings (comprising administering to a subject an immunoglobulin molecule or fragment thereof comprising a region where amino acid residues corresponding to at least a portion of a CDR is replaced with GLP-1) and administering to a subject an immunoglobulin molecule or its fragment (comprising a region where amino acid residues corresponding to at least a portion of a complementarity determining regions (CDR) is replaced with a thiazolidinedione derivative), regulating adiponectin expression (comprising administering to a subject an immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a CDR is replaced with a thiazolidinedione derivative). The immunoglobulin is an anti-tetanus toxoid antibody (Tt) where the heavy chain CDR2 and/or CDR3 are fully or partially replaced with a peptide listed above or (as described in the examples) a Thrombopoietin (TPO) mimetic, erythropoietin (EPO) mimetic or ANP (atrial natriuretic peptide). The molecule, composition and methods are useful for treating congestive heart failure, diabetes or obesity. The present sequence represents a light chain of the anti-tetanus toxoid Fab antibody with engrafted TPO mimetic peptides in place of one or more of its CDRs.

Query Match 87.9%; Score 29; DB 9; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 72 GATNLA 77
|||||

RESULT 21
ID AAR77612 standard; protein; 240 AA.
AC AAR77612;
XX AAR77612;

DT 25-MAR-2003 (revised)
DT 15-MAR-1996 (first entry)

XX Humanised 5G1.1 VL + KLV56.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR.
OS Synthetic.

Key Location/Qualifiers
FH Peptide 1. .25
FT /label= sig_peptide
FT Peptide 26. .240
FT /label= mat_peptide
FT Region 51. .61
FT /label= CDR-L1
FT Region 77. .83
FT /label= CDR-L2
FT Region 116. .124
FT /label= CDR-L3

WO9529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95WO-US005688.

XX 02-MAY-1994; 94US-00236208.

PA (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
XX Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;

DR WPI; 1995-392923/50.

DR N-PSDB; AAT08485.

XX Treating glomerulonephritis with antibody against complement C5 component
FT - to inhibit complement induced cell lysis.

XX Example 11; Page 126-128; 181pp; English.

XX A humanised CDR-grafted and framework sequence-altered light chain, 5G1.1
CC VL + KLV56 (AAR77612), includes CDRs derived from mouse anti-C5
CC monoclonal antibody 5G1.1. It can be co-expressed with a humanised Fd
CC (AAR77610) in human 293 EBNA cells using encoding DNAs subcloned into
CC vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain
CC the ability of Mab 5G1.1 to block human complement C5a generation and
CC thus to reduce glomerular inflammation and kidney dysfunction associated
CC with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 240 AA;

Query Match 87.9%; Score 29; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 76 GATNLA 81
|||||

RESULT 22
AAR77613
ID AAR77613 standard; protein; 241 AA.
XX AAR77613;
AC AAR77613;

XX 25-MAR-2003 (revised)
DT 02-APR-1996 (first entry)

XX Humanised 5G1.1 VL + KLV56B.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR.

OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1. .25
FT /label= sig_peptide

FT	Peptide	26. .241	
FT		/label= mat_peptide	
XX			
XX	WO9529697-A1.		
XX			
XX	09-NOV-1995.		
PD			
XX			
PP	01-MAY-1995;	95WO-US005688.	
XX			
PP	02-MAY-1994;	94US-00236208.	
XX			
XX	(ALEX-) ALEXION PHARM INC.		
XX			
PI	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP,		
PI	Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;		
XX			
DR	WPI; 1995-392923/50.		
DR			
DR	N-PSDB; AAT10706.		
XX			
XX	Treating glomerulonephritis with antibody against complement C5 component		
PT	- to inhibit complement induced cell lysis.		
XX			
XX	Claim 42; Page 129-131; 181pp; English.		
XX			
CC	A DNA construct (AAT10706) codes for a humanised CDR-grafted and		
CC	framework sequence-altered light chain, 5G1.1 VL + KLV56B (AAR77613),		
CC	which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.		
CC	The DNA can be subcloned together with DNA (AAT08483) coding for a		
CC	humanised Fd (AAR77610) into vector APEX-3P (AAT08476) for expression of		
CC	humanised antibody in human 293 EBNA cells. Such recombinant antibodies		
CC	retain the ability of Mab 5G1.1 to block human complement C5a generation		
CC	and thus to reduce glomerular inflammation and kidney dysfunction		
CC	associated with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI		
CC	field.)		
XX			
XX			
SQ	Sequence 241 AA;		
	Query Match	87.9%; Score 29; DB 2; Length 241;	
	Best Local Similarity	100.0%; Pred. No. 2.7e+02;	
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 GATNLA 6		
Db	77 GATNLA 82		
	RESULT 23		
	AAR77608		
ID	AAR77608 standard; protein; 241 AA.		
XX			
XX	AAR77608;		
XX			
DT	25-MAR-2003 (revised)		
DT	15-MAR-1996 (first entry)		
XX			
DE	Chimeric light chain 5G1.1M1 VL HuK.		
XX			
XX	Complement C5; haemolysis; kidney; glomerulonephritis;		
KW	monoclonal antibody; antiinflammatory; antibody engineering;		
KW	humanised antibody; complementarity determining region; CDR;		
KW	chimeric antibody; Fab.		
XX			
OS	Synthetic.		
XX			
XX	Key	Location/Qualifiers	
FT	Peptide	1. .25	
FT		/label= sig_peptide	
FT	Peptide	26. .241	
FT		/label= mat_peptide	
XX			
XX	WO9529697-A1.		
XX			
XX	09-NOV-1995.		

PD 09-NOV-1995.
 XX
 PF 01-MAY-1995; 95WO-US005688.
 XX
 PR 02-MAY-1994; 94US-00236208.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
 PI Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
 XX
 DR WPI; 1995-392923/50.
 DR N-PSDB; AAT08479.
 XX
 XX Treating glomerulonephritis with antibody against complement C5 component
 FT - to inhibit complement induced cell lysis.
 XX
 PS Example 11; Page 107-110; 181pp; English.
 XX
 CC Murine scFv 5G1.1M1 (AAR77606) is the product of a DNA construct
 CC (AAT08479) obtd. from DNA of hybridoma ATCC HB 11625, which produces anti
 CC -C5 monoclonal antibody (MAb) 5G1.1. Recombinant scFv 5G1.1M1 is obtd. by
 CC expression of this DNA in Escherichia coli using vector pET Trc S05/N1.
 CC The light and/or heavy chain CDRs of scFv 5G1.1M1 can be combined with
 CC CDRs from other 5G1.1-derived antibodies, Fds and light chains (AAR77607-
 CC 16) in the prodn. of recombinant, including humanised, antibodies that
 CC retain the ability of MAb 5G1.1 to block human complement C5a generation
 CC and thus to reduce glomerular inflammation and kidney dysfunction
 CC associated with glomerulonephritis. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 248 AA;

Query Match 87.9%; Score 29; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLA 6
 Db ||||| 52 GATNLA 57

RESULT 25
 AAR77616
 ID AAR77616 standard; protein; 248 AA.
 XX
 AC AAR77616;
 XX
 XX 25-MAR-2003 (revised)
 DT 15-MAR-1996 (first entry)
 XX
 DE Humanised CDR-grafted 5G1.1 scFv DO12.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW single chain antibody; scFv.

XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Region 26..36
 FT /label= CDR-L1
 FT Region 52..58
 FT /label= CDR-L2
 FT Region 91..99
 FT /label= CDR-L3
 FT Region 152..161
 FT /label= CDR-H1
 FT Region 176..186
 FT /label= CDR-H2
 FT Region 225..237
 FT /label= CDR-H3

XX WO9529697-A1.
 PN
 XX
 PD 09-NOV-1995.
 XX
 PF 01-MAY-1995; 95WO-US005688.
 XX
 PR 02-MAY-1994; 94US-00236208.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
 PI Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
 XX
 DR WPI; 1995-392923/50.
 DR N-PSDB; AAT08488.
 XX
 XX Treating glomerulonephritis with antibody against complement C5 component
 FT - to inhibit complement induced cell lysis.
 XX
 PS Example 11; Page 138-140; 181pp; English.
 XX
 CC A humanised CDR-grafted scFv, designated 5G1.1 scFv DO12 (AAR77616),
 CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
 CC scFv can be expressed in Escherichia coli ME1 cells by subcloning of
 CC encoding DNA (AAT08488) into vector pET Trc S05/N1. This humanised,
 CC recombinant antibody retained the ability of MAb 5G1.1 to block human
 CC complement C5a generation and thus to reduce glomerular inflammation and
 CC kidney dysfunction associated with glomerulonephritis. (Updated on 25-MAR
 CC -2003 to correct PI field.)
 XX
 SQ Sequence 248 AA;

Query Match 87.9%; Score 29; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLA 6
 Db ||||| 52 GATNLA 57

RESULT 26
 AAR77607
 ID AAR77607 standard; protein; 248 AA.
 XX
 AC AAR77607;
 XX
 XX 25-MAR-2003 (revised)
 DT 15-MAR-1996 (first entry)
 XX
 DE Humanised CDR-grafted 5G1.1 scFv CB.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW single chain antibody; scFv.

XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Region 26..36
 FT /label= CDR-L1
 FT Region 52..58
 FT /label= CDR-L2
 FT Region 91..99
 FT /label= CDR-L3
 FT Region 152..161
 FT /label= CDR-H1
 FT Region 176..192
 FT /label= CDR-H2
 FT Region 225..237
 FT /label= CDR-H3

XX WO9529697-A1.
XX
XX
XX PD 09-NOV-1995.
XX
XX PF 01-MAY-1995; 95WO-US005688.
XX
XX PR 02-MAY-1994; 94US-00236208.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
PI Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
XX
XX DR WPI; 1995-392923/50.
XX
XX DR N-PSDB; AAT08480.
XX
XX PT Treating glomerulonephritis with antibody against complement C5 component
XX - to inhibit complement induced cell lysis.
XX
XX PS Example 11; Page 110-113; 181pp; English.
XX
XX CC Humanised CDR-grafted 5G1.1 scFv CB (AAR77607) is the product of a DNA
XX construct (AAT08479) derived from DNA of hybridoma ATCC HB 11625, the
XX producer of anti-C5 monoclonal antibody (MAB) 5G1.1. Recombinant scFv CB
XX is obt'd. by expression of this DNA in Escherichia coli using vector pET
XX Trc SOS/NI. The light and/or heavy chain CDRs of scFv CB can be combined
XX with CDRs from other 5G1.1-derived antibodies, Fds and light chains
XX (AAR77606-16) in the prodn. of recombinant, including humanised,
XX antibodies that retain the ability of MAB 5G1.1 to block human complement
XX C5a generation and thus to reduce glomerular inflammation and kidney
XX dysfunction associated with glomerulonephritis. (Updated on 25-MAR-2003
XX to correct PI field.)
XX
XX SQ Sequence 248 AA;

Query Match 87.9%; Score 29; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 6
Db 52 GATNLAA 57
|||||

RESULT 27
ADM05455
ID ADM05455 standard; protein; 336 AA.
XX
XX AC ADM05455;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human protein of the invention SEQ ID NO:4140.
XX
XX KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX OS Homo sapiens.
XX
XX FN EP1347046-A1.
XX
XX PD 24-SEP-2003.
XX
XX PF 12-APR-2002; 2002EP-00008400.
XX
XX PR 22-MAR-2002; 2002JP-00137785.
XX
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX

DR WPI; 2003-723558/69.
XX N-PSDB; ADM03012.
XX
XX PT New polynucleotides and polypeptides are useful in gene therapy, for
XX developing a diagnostic marker or medicines for regulating their
XX expression and activity, or as a target of gene therapy.
XX
XX PS Claim 1; SEQ ID NO 4140; 305pp; English.
XX
XX CC The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
XX therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
XX as a primer for synthesizing the polynucleotide or as a probe for
XX detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
XX useful in gene therapy, for developing a diagnostic marker or medicines
XX for regulating their expression and activity, or as a target of gene
XX therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX are useful as pharmaceutical agents. The present sequence represents a
XX protein sequence of the invention.
XX
XX SQ Sequence 336 AA;

Query Match 87.9%; Score 29; DB 7; Length 336;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
Db 281 GGTNLAA 287
|||||

RESULT 28
AAW11301
ID AAW11301 standard; protein; 422 AA.
XX
XX AC AAW11301;
XX
XX DT 25-MAR-2003 (revised)
XX 18-MAR-1997 (first entry)
XX
XX DE Perilipin B (NSEQOFPB.RAT).
XX
XX KW Perilipin; human; rat; HUPERI; cAMP-dependent protein kinase; A-kinase;
XX lipid storage droplet; adipocyte.
XX
XX OS Rattus rattus.
XX
XX FN US5585462-A.
XX
XX PD 17-DEC-1996.
XX
XX PF 04-OCT-1993; 93US-00132649.
XX
XX PR 11-JUN-1991; 91US-00712152.
XX
XX PA (USGO) US GOVERNMENT.
XX
XX PI Egan JJ, Kimmel AR, Londres C, Greenberg AS;
XX
XX DR WPI; 1997-051234/05.
XX N-PSDB; AAT51228.
XX
XX PT Perilipin proteins expressed in adipocyte(s) - used to understand lipid
XX metabolism and trafficking.
XX
XX PS Claim 2; Col 43-48; 43pp; English.
XX
XX CC This sequence represents rat perilipin B, which is also known as
XX NSEQOFPB.RAT. Perilipin is the major cAMP-dependent protein kinase
XX substrate in lipids, and is found at the surface of the lipid storage
XX droplets. In rats, there are two forms of perilipin (perilipin A and
XX perilipin B). Perilipin A contains six consensus A-kinase phosphorylation
XX sites, consistent with the number of phosphates added upon activation of

CC A-kinase in the cell. Perilipin B lacks three of these consensus A-kinase
 CC phosphorylation sites. The DNA encoding this sequence was used to isolate
 CC the human perilipin coding sequence from a human adipocyte cDNA library.
 CC The protein encoded by the isolated human sequence (see AAW11299), and
 CC the rat perilipins (this sequence and AAW11300) can be used for studying
 CC proteins and other molecules on the surface of intracellular lipid
 CC droplets in adipocytes, that may be involved in lipid metabolism and
 CC trafficking. The proteins also provide a definitive marker which can be
 CC used to differentiate true adipocytes from non-adipocyte cells which, as
 CC a result of pathophysiological conditions, assume adipocyte
 CC characteristics and become lipid-laden. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 CC
 XX

SQ Sequence 422 AA;
 Query Match 87.9%; Score 29; DB 2; Length 422;
 Best Local Similarity 85.7%; Pred. No. 5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 Db 64 GASNLAA 70
 ||:||||
 ||:||||

RESULT 29
 AAB12394
 ID AAB12394 standard; protein; 422 AA.
 XX
 AC AAB12394;
 XX
 DT 06-NOV-2000 (first entry)
 XX
 DE Rat perilipin B protein.
 XX
 KW Perilipin B; rat; adipocyte.
 XX
 OS Rattus sp.
 XX
 PN US6074842-A.
 XX
 PD 13-JUN-2000.
 XX
 PF 16-DEC-1996; 96US-00767579.
 XX
 PR 11-JUN-1991; 91US-00712152.
 PR 04-OCT-1993; 93US-00132649.
 XX

(USSH) US DEPT HEALTH & HUMAN SERVICES.
 Egan JJ, Kimmel AR, Londres C, Greenberg AS;
 WPI; 2000-430393/37.
 DR N-PSDB; AAA63084.
 XX
 PT New DNA sequences for producing perilipin protein, useful for
 PT differentiating true adipocytes from non-adipocyte cells which, as a
 PT result of pathophysiological conditions, assume adipocyte characteristics
 PT and become lipid-laden.
 XX
 XX Claim 4; Col 47-50; 43pp; English.

XX The present sequence is rat perilipin B protein. The present invention
 CC relates to the DNA encoding this sequence and rat perilipin A and human
 CC perilipin DNA (see AAA63083 and AAA63085). The rat perilipin cDNAs were
 CC isolated by probing a rat adipocyte cDNA library with total and affinity
 CC purified polyclonal antiserum to perilipin. The rat perilipin sequences
 CC were then used as probes to isolate human perilipin cDNA. The isolated
 CC perilipin DNAs are useful for producing or cloning human or rat perilipin
 CC proteins. The perilipin proteins are useful as markers for
 CC differentiating true adipocytes from non-adipocyte cells which, as a
 CC result of pathophysiological conditions, assume adipocyte characteristics
 CC and become lipid-laden
 XX

SQ Sequence 422 AA;
 Query Match 87.9%; Score 29; DB 3; Length 422;
 Best Local Similarity 85.7%; Pred. No. 5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 Db 64 GASNLAA 70
 ||:||||
 ||:||||

RESULT 30
 AAW11300
 ID AAW11300 standard; protein; 517 AA.
 XX
 AC AAW11300;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-MAR-1997 (first entry)
 XX
 DE Perilipin A (NSEQOFA.RAT).
 XX
 KW Perilipin; human; rat; HUPERI; CAMP-dependent protein kinase; A-kinase;
 KW lipid storage droplet; adipocyte.
 XX
 OS Rattus rattus.
 XX
 PN US5585462-A.
 XX
 PD 17-DEC-1996.
 XX
 PF 04-OCT-1993; 93US-00132649.
 XX
 PR 11-JUN-1991; 91US-00712152.
 XX
 XX (USGO) US GOVERNMENT.

Egan JJ, Kimmel AR, Londres C, Greenberg AS;
 WPI; 1997-051234/05.
 DR N-PSDB; AAT51227.
 XX
 PT Perilipin proteins expressed in adipocyte(s) - used to understand lipid
 PT metabolism and trafficking.
 XX
 PS Claim 2; Col 37-42; 43pp; English.

XX This sequence represents rat perilipin A, which is also known as
 CC NSEQOFA.RAT. Perilipin is the major CAMP-dependent protein kinase
 CC substrate in lipids, and is found at the surface of the lipid storage
 CC droplets. In rats, there are two forms of perilipin (perilipin A and
 CC perilipin B). Perilipin A contains six consensus A-kinase phosphorylation
 CC sites, consistent with the number of phosphates added upon activation of
 CC A-kinase in the cell. Perilipin B lacks three of these consensus A-kinase
 CC phosphorylation sites. The DNA encoding this sequence was used to isolate
 CC the human perilipin coding sequence from a human adipocyte cDNA library.
 CC The protein encoded by the isolated human sequence (see AAW11299), and
 CC the rat perilipins (this sequence and AAW11301) can be used for studying
 CC proteins and other molecules on the surface of intracellular lipid
 CC droplets in adipocytes, that may be involved in lipid metabolism and
 CC trafficking. The proteins also provide a definitive marker which can be
 CC used to differentiate true adipocytes from non-adipocyte cells which, as
 CC a result of pathophysiological conditions, assume adipocyte
 CC characteristics and become lipid-laden. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX

SQ Sequence 517 AA;
 Query Match 87.9%; Score 29; DB 2; Length 517;
 Best Local Similarity 85.7%; Pred. No. 6.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7

XX PR 16-JAN-2004; 2004US-0536968P.
 XX PA (FAND/) FANDL J P.
 XX PA (CHEN/) CHEN G.
 XX PA (PAPA/) PAPADOPOULOS N.
 XX PA (ALDR/) ALDRICH T H.
 XX FI Fandl JP, Chen G, Papadopoulos N, Aldrich TH;
 XX DR WPI; 2005-603251/62.
 XX CC New nucleic acid molecule encoding a fusion polypeptide, useful in
 XX PT preparing a composition for treating disorders, e.g., wound, ischemia or
 XX PT diabetes.
 XX XX Disclosure; SEQ ID NO 53; 34pp; English.
 XX CC The invention relates to a nucleic acid molecule which encodes a fusion
 CC polypeptide (A)x-M-(A')y, where A and A' are polypeptides capable of
 CC binding a target receptor; M is a multimerizing component; and x or y is
 CC a number between 1-10. Also described: (1) a nucleic acid molecule
 CC encoding a fusion polypeptide (A)x-M-(A')y; (2) a vector comprising the
 CC nucleic acid sequence; (3) a host-vector system for producing a fusion
 CC protein or polypeptide encoded by the nucleic acid molecule; (4) a dimer
 CC comprising two of the fusion polypeptides; and (6) a pharmaceutical
 CC composition comprising the dimer and a carrier. The nucleic acid molecule
 CC is useful in preparing a composition for treating disorders, e.g., wound,
 CC ischemia or diabetes. The present sequence represents an amino acid
 CC sequence given in the Sequence Listing of the patent, but which does not
 CC appear to be further mentioned within the specification.
 XX SQ Sequence 702 AA;
 Query Match 87.9%; Score 29; DB 9; Length 702;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GATNLA 6
 Db 190 GATNLA 195
 RESULT 34
 AEC08431
 ID AEC08431 standard; protein; 731 AA.
 XX AC AEC08431;
 XX DT 20-OCT-2005 (first entry)
 XX DE ScFv-2-1G3-FC-ScFv-1-1F11 fusion protein SEQ ID NO:51.
 XX KW fusion protein; vulnery; antidiabetic; vasotropic; antibody; ScFv;
 XX KW wound healing; ischemia; diabetes.
 XX OS Synthetic.
 XX FN US2005158829-A1.
 XX PD 21-JUL-2005.
 XX PF 14-JAN-2005; 2005US-00035599.
 XX PR 16-JAN-2004; 2004US-0536968P.
 XX XX (FAND/) FANDL J P.
 XX PA (CHEN/) CHEN G.
 XX PA (PAPA/) PAPADOPOULOS N.
 XX PA (ALDR/) ALDRICH T H.
 XX PI Fandl JP, Chen G, Papadopoulos N, Aldrich TH;

XX DR WPI; 2005-603251/62.
 XX CC New nucleic acid molecule encoding a fusion polypeptide, useful in
 XX PT preparing a composition for treating disorders, e.g., wound, ischemia or
 XX PT diabetes.
 XX XX Example 8; SEQ ID NO 51; 34pp; English.
 XX CC The invention relates to a nucleic acid molecule which encodes a fusion
 CC polypeptide (A)x-M-(A')y, where A and A' are polypeptides capable of
 CC binding a target receptor; M is a multimerizing component; and x or y is
 CC a number between 1-10. Also described: (1) a nucleic acid molecule
 CC encoding a fusion polypeptide (A)x-M-(A')y; (2) a vector comprising the
 CC nucleic acid sequence; (3) a host-vector system for producing a fusion
 CC polypeptide comprising the vector in a suitable host cell; (4) a fusion
 CC protein or polypeptide encoded by the nucleic acid molecule; (5) a dimer
 CC comprising two of the fusion polypeptides; and (6) a pharmaceutical
 CC composition comprising the dimer and a carrier. The nucleic acid molecule
 CC is useful in preparing a composition for treating disorders, e.g., wound,
 CC ischemia or diabetes. The present sequence represents a ScFv-2-1G3-FC-
 CC ScFv-1-1F11 fusion protein, which is used in an example from the present
 CC invention for the construction of monospecific and bispecific activating
 CC dimers.
 XX SQ Sequence 731 AA;
 Query Match 87.9%; Score 29; DB 9; Length 731;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GATNLA 6
 Db 670 GATNLA 675
 RESULT 35
 AEC08430
 ID AEC08430 standard; protein; 734 AA.
 XX AC AEC08430;
 XX DT 20-OCT-2005 (first entry)
 XX DE ScFv-1-1F11-FC-ScFv-1-1F11 fusion protein SEQ ID NO:50.
 XX KW fusion protein; vulnery; antidiabetic; vasotropic; antibody; ScFv;
 XX KW wound healing; ischemia; diabetes.
 XX OS Synthetic.
 XX FN US2005158829-A1.
 XX PD 21-JUL-2005.
 XX PF 14-JAN-2005; 2005US-00035599.
 XX PR 16-JAN-2004; 2004US-0536968P.
 XX XX (FAND/) FANDL J P.
 XX PA (CHEN/) CHEN G.
 XX PA (PAPA/) PAPADOPOULOS N.
 XX PA (ALDR/) ALDRICH T H.
 XX PI Fandl JP, Chen G, Papadopoulos N, Aldrich TH;
 XX DR WPI; 2005-603251/62.
 XX CC New nucleic acid molecule encoding a fusion polypeptide, useful in
 XX PT preparing a composition for treating disorders, e.g., wound, ischemia or
 XX PT diabetes.
 XX XX Example 8; SEQ ID NO 50; 34pp; English.

XX The invention relates to a nucleic acid molecule which encodes a fusion
 CC polypeptide (A)x-M-(A')y, where A and A' are polypeptides capable of
 CC binding a target receptor; M is a multimerizing component; and x or y is
 CC a number between 1-10. Also described: (1) a nucleic acid molecule
 CC encoding a fusion polypeptide (A)x-M-(A')y; (2) a vector comprising the
 CC nucleic acid sequence; (3) a host-vector system for producing a fusion
 CC polypeptide comprising the vector in a suitable host cell; (4) a fusion
 CC protein or polypeptide encoded by the nucleic acid molecule; (5) a dimer
 CC comprising two of the fusion polypeptides; and (6) a pharmaceutical
 CC composition comprising the dimer and a carrier. The nucleic acid molecule
 CC is useful in preparing a composition for treating disorders, e.g., wound,
 CC ischemia or diabetes. The present sequence represents a Scrv-1-1fl1-FC-
 CC Scrv-1-1fl1 fusion protein, which is used in an example from the present
 CC invention for the construction of monospecific and bispecific activating
 CC dimers.
 XX
 SQ Sequence 734 AA;

Query Match 87.9%; Score 29; DB 9; Length 734;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
 Db 190 GATNLA 195
 |||||

RESULT 36
 AAR13793
 ID AAR13793 standard; protein; 878 AA.

XX AAR13793;
 AC
 XX 25-MAR-2003 (revised)
 DT 29-NOV-1991 (first entry)
 XX
 XX Ecdysone receptor.
 XX
 XX Insect steroid receptor; Ecd; hormone; DHR23.
 KW
 XX Drosophila melanogaster.

XX Key Location/Qualifiers
 FH Domain 264..329
 FT /note= "zinc-finger DNA-binding domain C"
 FT Domain 431..651
 FT /note= "hormone-binding domain E"

XX WO9113167-A.
 XX
 XX 05-SEP-1991.
 XX
 XX 26-FEB-1990; 90US-00485749.
 XX
 XX 26-FEB-1990; 90US-00485749.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Hogness DS, Koelle MR, Segraves WA;
 PI WPI; 1991-281480/38.
 DR N-PSDB; AAQ13574.

XX DNA encoding insect steroid receptors - and ligands, for use as benign
 PT inducing factors.
 XX
 XX Claim 24; Page 103; 126pp; English.

XX The amino acid sequence codes for the (20-OH) ecdysone receptor protein
 CC which is part of the insect steroid receptor superfamily. It can be used
 CC to screen for ligands specific for the insect steroid receptors which can
 CC be used as highly specific and highly active pesticides which are

CC biodegradable. See also AAR13791-R13794. (Updated on 25-MAR-2003 to
 CC correct PA field.)

SQ Sequence 878 AA;

Query Match 87.9%; Score 29; DB 2; Length 878;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLA 7
 Db 116 GATNLA 122
 |||||

RESULT 37
 AAR32889
 ID AAR32889 standard; protein; 878 AA.

XX AAR32889;
 AC
 XX 25-MAR-2003 (revised)
 DT 22-JUN-1993 (first entry)
 XX
 XX DHR23alpha protein.

XX
 KW Ecdysteroid; receptor; DHR23alpha; Drosophila; steroid; receptor;
 KW ligand-dependent; transcription factor; mammalian cell; hormone;
 KW ecdysone response element; ecdysone.

XX Drosophila melanogaster.

XX Key Location/Qualifiers
 FH Binding-site 281..330
 FT /note= "Putative DNA-binding domain"

XX WO9303162-A1.

XX 18-FEB-1993.
 XX
 XX 03-AUG-1992; 92WO-US006391.
 XX
 XX 08-AUG-1991; 91US-00742127.

XX (GETH) GENENTECH INC.

XX Godowski PJ;

XX WPI; 1993-076519/09.
 DR N-PSDB; AAQ37556.

XX Ecdysteroid dependent regulation of genes in mammalian cells - for
 PT induced expression of heterologous genes.

XX Disclosure; Fig 1; 45pp; English.

XX This sequence represents an ecdysteroid receptor DHR23alpha. DHR23- alpha
 CC is a Drosophila steroid receptor homologue which can function as a ligand
 CC -dependent transcription factor in mammalian cells when induced by
 CC specific ecdysteroids such as DHR23alpha. The activity of DHR23- alpha is
 CC induced upon administration of certain ecdysteroids but not any of the
 CC mammalian hormones tested. DHR23alpha has been reported to regulate
 CC transcription of genes containing ecdysone response elements in
 CC Drosophila tissue culture cells treated with 20-OH ecdysone. (Updated on
 CC 25-MAR-2003 to correct PN field.)

SQ Sequence 878 AA;

Query Match 87.9%; Score 29; DB 2; Length 878;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLA 7
 |||||

Db	116 GATNLGA 122	
RESULT 39		
ABE53805		
ID	ABE53805 standard; protein; 878 AA.	
XX		
AC	ABE53805;	
XX		
DT	06-OCT-2005 (first entry)	
XX		
DE	Drosophila nuclear receptor #17.	
XX		
KW	Insecticide; pesticide; toxin; nuclear receptor; receptor.	
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO2005069859-A2.	
XX		
PD	04-AUG-2005.	
XX		
PF	13-JAN-2005; 2005WO-US001218.	
XX		
PR	13-JAN-2004; 2004US-0536337P.	
XX		
PA	(UTAH) UNIV UTAH RES FOUND.	
XX		
PI	Thummel CS, King-Jones K, Horner M, Lam G;	
XX		
DR	WPI; 2005-555376/56.	
XX		
DR	N-PSDB; ABE53806.	
XX		
PT	Composition useful for increasing effect of existing toxins to control insects, and for inhibiting insect growth, comprises inhibitor of DHR96 activity, and optionally pesticide.	
XX		
PS	Disclosure; SEQ ID NO 33; 211pp; English.	
XX		
CC	The invention relates to a composition comprising an inhibitor of DHR96 activity and optionally a pesticide. The invention also relates to an insect comprising a gene, where the gene comprises a non-naturally occurring mutation in the DHR96 gene, a method of enhancing the effect a pesticide has on an insect involving administering to the insect an inhibitor of DHR96 activity, a method of identifying an inhibitor of DHR96 activity involving testing compounds for inhibition activity of DHR96 and/or inhibition of xenobiotic activity and comparing the activity of these compounds to known inhibitors of DHR96, a method of producing a composition for inhibiting DHR96 activity involving admixing the inhibitor with a pesticide and a composition produced by the method. The composition and method are useful for enhancing the effect a pesticide has on an insect, for identifying an inhibitor of DHR96 activity, for identifying ligands for DHR96 and for producing a composition for inhibiting DHR96 activity. The composition is useful for regulating DHR96, preferably for inhibiting DHR96 gene expression or activity and for increasing the effect of existing toxins or pesticides e.g., DDT to control insects. The composition is useful for controlling insects e.g., silverfish, Dragonflies, Stoneflies, beetles, fleas, ants, bees, wasps, termites etc. and decreases the resistance exhibited by the insects with respect to toxins or pesticides. This sequence represents a Drosophila nuclear receptor used in the scope of the invention.	
XX		
SQL	Sequence 878 AA;	
Query Match	87.9%; Score 29; DB 9; Length 878;	
Best Local Similarity	85.7%; Pred. No. 1.1e+03;	
Matches	6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 GATNLAA 7	
Db	116 GATNLGA 122	
RESULT 40		
ABE58488		
ID	ABE58488 standard; protein; 881 AA.	
XX		

AC ABB58488;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 2256.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX PA Venter JC, Adams M, Li PWD, Myers EW;
 XX PI WPI; 2001-556860/75.
 XX DR N-PSDB; ABL02591.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 2256; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 881 AA;
 Query Match 87.9%; Score 29; DB 4; Length 881;
 Best Local Similarity 85.7%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GATNLAA 7
 Db 116 GATNLGA 122
 |||||
 RESULT 41
 ABB02406
 ID ABB02406 standard; protein; 945 AA.
 XX AC ABB02406;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #2397.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.
 XX PF 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX PA Drmanac RT, Liu C, Tang YT;
 XX PI WPI; 2001-639362/73.
 XX DR N-PSDB; AAS66593.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PS Claim 20; SEQ ID NO 32765; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABB00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 945 AA;
 Query Match 87.9%; Score 29; DB 4; Length 945;
 Best Local Similarity 85.7%; Pred. No. 1.2e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GATNLAA 7
 Db 284 GGTNLAA 290
 |||||
 RESULT 42
 ADX67119
 ID ADX67119 standard; protein; 226 AA.
 XX AC ADX67119;
 XX DT 21-APR-2005 (first entry)
 XX DE Plant full length insert polypeptide seqid 37962.
 XX KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX OS Unidentified.

XX US2004034888-A1.
 XX 19-FEB-2004.
 XX 28-APR-2003; 2003US-00425114.
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00385678.
 XX (LIUJ//) LIU J.
 XX (ZHOU//) ZHOU Y.
 XX (KOVA//) KOVALIC D K.
 XX (SCRE//) SCREEN S E.
 XX (TABAS//) TABASKA J E.
 XX (CAOY//) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.
 XX Claim 1; SEQ ID NO 37962; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 XX polynucleotide consisting of a sequence encoding an amino acid sequence
 XX available in electronic form from the US patent office at
 XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 XX of the invention are also useful in physical arrays of molecules and as
 XX plant breeding markers. The recombinant DNA construct is useful for
 XX improving plant tolerance to cold, heat, drought, herbicides, extreme
 XX osmotic conditions, pathogens or pests, for manipulating growth rate in
 XX plant cells by modification of the cell cycle pathway, for conferring
 XX increased resistance to plant disease, for producing galactomannan,
 XX lignin or plant growth regulators, for increasing the rate of homologous
 XX recombination in plants, for improving yield by modification of
 XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 XX or by providing improved plant growth and development under at least one
 XX stress condition or for modifying seed oil or protein yield and/or
 XX content. This is the amino acid sequence of a plant full length insert
 XX polypeptide that can be used in the recombinant DNA construct of the
 XX invention.
 XX Sequence 226 AA;
 XX Query Match 84.8%; Score 28; DB 8; Length 226;
 XX Best Local Similarity 85.7%; Pred. No. 4.3e+02;
 XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 DB 158 GETNLAA 164
 RESULT 43
 ABU35172
 ID ABU35172 standard; protein; 233 AA.
 XX AC ABU35172;
 XX 19-JUN-2003 (first entry)
 XX Protein encoded by Prokaryotic essential gene #20699.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Moraxella catarrhalis.
 XX WO200277183-A2.
 XX

XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 XX 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 XX 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 XX N-PSDB; ACA39042.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 XX for homologous nucleic acids required for cellular proliferation to
 XX isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 63096; 1766pp; English.
 XX The invention relates to an isolated nucleic acid comprising any one of
 XX the 6213 antisense sequences given in the specification where expression
 XX of the nucleic acid inhibits proliferation of a cell. Also included are:
 XX (1) a vector comprising a promoter operably linked to the nucleic acid
 XX encoding a polypeptide whose expression is inhibited by the antisense
 XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
 XX polypeptide or its fragment whose expression is inhibited by the
 XX antisense nucleic acid; (4) an antibody capable of specifically binding
 XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 XX proliferation or the activity of a gene in an operon required for
 XX proliferation; (7) identifying a compound that influences the activity of
 XX the gene product or that has an activity against a biological pathway
 XX required for proliferation, or that inhibits cellular proliferation; (8)
 XX identifying a gene required for cellular proliferation or the biological
 XX pathway in which a proliferation-required gene or its gene product lies
 XX on a gene on which the test compound that inhibits proliferation of an
 XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
 XX compound's activity; (11) a culture comprising strains in which the gene
 XX product is overexpressed or underexpressed; (12) determining the extent
 XX to which each of the strains is present in a culture or collection of
 XX strains; or (13) identifying the target of a compound that inhibits the
 XX proliferation of an organism. The antisense nucleic acids are useful for
 XX identifying proteins or screening for homologous nucleic acids required
 XX for cellular proliferation to isolate candidate molecules for rational
 XX drug discovery programs, or for screening homologous nucleic acids
 XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 XX the target prokaryotic essential genes. Note: The sequence data for this
 XX patent did not form part of the printed specification, but was obtained
 XX in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 233 AA;
 XX Query Match 84.8%; Score 28; DB 6; Length 233;
 XX Best Local Similarity 85.7%; Pred. No. 4.5e+02;
 XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 DB 61 GATNLPA 67
 RESULT 44
 ADI42942
 ID ADI42942 standard; protein; 289 AA.
 XX AC ADI42942;
 XX

XX 22-APR-2004 (first entry)
XX Plant transcription factor #491.
XX transgenic; plant; enhanced tolerance to abiotic stress;
KW glyophosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
XX transcription factor; gene; ds.
XX Oryza sativa.
OS US2004019927-A1.
XX 29-JAN-2004.
XX 25-FEB-2003; 2003US-00374780.
XX 18-APR-2001; 2001US-00837944.
XX (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAKE/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PIUG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX WPI; 2004-132245/13.
XX New transgenic plant comprising a recombinant polynucleotide of any one
PT of more than 500 nucleotide sequences, useful in bioinformatic search
PT methods.
XX Claim 1; SEQ ID NO 1405; 435pp; English.
XX The invention describes a transgenic plant comprising a recombinant
CC polynucleotide of any one of more than 500 nucleotide sequences fully
CC defined in the specification or its complement. The method of the
CC invention can be used to produce a plant having altered traits such as:
CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone
CC sensitivity; disease resistance; sugar sensing; early or late flowering;
CC altered flower structure, change in stem bifurcations, altered branching
CC pattern, reduced apical dominance, reduced trichome density; lack of
CC trichomes; reduced ectopic trichome development; altered trichome
CC development; increase in trichome number; altered stem morphology;
CC increased root growth; increased root hairs; altered seed development;
CC altered cell proliferation or cell differentiation; rapid development;
CC premature senescence; increased necrosis; increase in seedling or plant
CC size; decreased plant size; leaf morphology; seed morphology; seed
CC biochemistry; increase in root anthocyanins; increase in plant
CC anthocyanins; or alteration in light response or shade avoidance. The
CC transgenic plant, polynucleotides and polypeptides are useful in
CC bioinformatic search methods. This is the amino acid sequence of a plant
CC transcription factor, and an orthologue of Arabidopsis thaliana
CC transcription factors isolated in the invention, that can be used in the

CC creation of a transgenic plant with altered traits.

XX Sequence 289 AA;

Query Match 84.8%; Score 28; DB 8; Length 289;

Best Local Similarity 85.7%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GATNLAA 7

Db 171 GATSLAA 177

RESULT 45

ADQ16242

ID ADQ16242 standard; protein; 289 AA.

XX AC ADQ16242;

XX DT 23-SEP-2004 (first entry)

XX Rice AT-hook DNA binding protein G3407 #2.

KW Rice; AT-hook domain; DNA binding protein; transcription factor; plant;

KW transgenic plant; biomass; abiotic stress tolerance; osmotic stress;

KW drought; salt stress; heat stress; cold stress.

OS Oryza sativa.

XX US2004128712-A1.

XX 01-JUL-2004.

XX 23-SEP-2003; 2003US-00669824.

XX 17-FEB-2000; 2000US-00506720.

XX 21-MAR-2000; 2000US-00532091.

XX 22-MAR-2000; 2000US-00533029.

XX 22-MAR-2000; 2000US-00533030.

XX 22-MAR-2000; 2000US-00533392.

XX 16-NOV-2000; 2000US-00713994.

XX 30-MAR-2001; 2001US-00823676.

XX 22-AUG-2001; 2001US-00934455.

XX 26-NOV-2001; 2001US-00996140.

XX 09-AUG-2002; 2002US-00225067.

XX 26-SEP-2002; 2002US-00255868.

XX 25-FEB-2003; 2003US-00374780.

XX 10-APR-2003; 2003US-00412699.

XX 23-APR-2003; 2003US-00421138.

XX (JIAN/) JIANG C.

XX (HEAR/) HEARD J E.

XX (RATC/) RATCLIFFE O.

XX (GUTT/) GUTTERSON N I.

XX (HEMP/) HEMPEL F D.

XX (KUMI/) KUMIMOTO R W.

XX (KEDD/) KEDDIE J S.

XX (SHER/) SHERMAN B K.

XX Jiang C, Heard JE, Ratcliffe O, Gutterson NI, Hempel FD;

PI Kumimoto RW, Keddie JS, Sherman BK;

XX WPI; 2004-542563/52.

XX N-PSDB; ADQ16241.

XX New polynucleotides encoding plant transcription factors, useful in

PT producing plants with increased biomass and abiotic stress tolerance.

XX Disclosure; SEQ ID NO 34; 130pp; English.

XX The invention relates to an isolated polynucleotide (ADQ16209, ADQ16211 or

CC ADQ16213) encoding an Arabidopsis thaliana AT-hook domain-containing

PI Guttererson NI, Jiang C, Heard JB, Ratcliffe O, Hempel FD;
 PI Kumimoto RW, Keddle JS, Sherman BK, Libby JM;
 XX WPI; 2005-262952/27.
 DR N-PSDB; ADZ00557.
 XX
 PT New transgenic plant, useful for further producing plants with increased
 PT tolerance to an abiotic stress and/or increased biomass.
 XX
 PS Claim 6; SEQ ID NO 12; 220pp; English.
 XX
 CC This sequence represents a member of the G1073 clade of transcription
 CC factors. The G1073 clade is characterized by having at least two
 CC conserved domains, including an AT-hook domain and a second domain
 CC comprising the sequences ADZ00609ADZ00610. Recombinant nucleotides
 CC encoding the G1073 clade may be used in the generation of a transgenic
 CC plant having increased tolerance to an abiotic stress or having increased
 CC biomass. The transgenic plant comprises a recombinant polynucleotide
 CC encoding a member of the G1073 clade of transcription factor
 CC polypeptides. The recombinant polynucleotide is operably linked to an
 CC inducible or tissue-specific promoter that regulates expression of the
 CC recombinant polynucleotide when the recombinant polynucleotide is
 CC inducible or tissue-specific promoter that regulates expression of the
 CC recombinant polynucleotide when the recombinant polynucleotide is
 CC transformed into a plant, where the tissue-specific promoter is a
 CC vascular, epidermal, leaf, or root promoter, and where the inducible or
 CC tissue specific promoter is a SUC2, a CUT1, an RBCS3, an ARSK1, or an
 CC RD29A promoter. The abiotic stress is cold or an osmotic stress, e.g.
 CC heat, drought, desiccation, freezing, or high salt.
 CC ortholog of G1073. At the seedling stage about half the transformed lines
 CC appeared larger than controls. At later stages of growth, there were no
 CC consistent morphological differences.
 XX
 SQ Sequence 289 AA;
 Query Match 84.8%; Score 28; DB 9; Length 289;
 Best Local Similarity 85.7%; Pred. No. 5.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 Db 171 GATSLAA 177
 |||:||||
 RESULT 48
 ADZ00580
 ID ADZ00580 standard; protein; 289 AA.
 XX
 AC ADZ00580;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE G3407 polypeptide.
 XX
 KW G1073 clade; transcription factor; conserved domain; abiotic stress;
 KW biomass; vascular; epidermal; leaf; root; promoter; cold; osmotic stress;
 KW heat; drought; desiccation; freezing; high salt.
 XX
 OS Oryza sativa.
 XX
 PN WO2005030966-A2.
 XX
 PD 07-APR-2005.
 XX
 PF 17-SEP-2004; 2004WO-US030739.
 XX
 PP 23-SEP-2003; 2003US-00669824.
 PR 26-APR-2004; 2004US-0565948P.
 PR 16-JUN-2004; 2004US-00870198.
 XX
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX
 XX Guttererson NI, Jiang C, Heard JB, Ratcliffe O, Hempel FD;
 PI Kumimoto RW, Keddle JS, Sherman BK, Libby JM;
 XX

DR WPI; 2005-262952/27.
 DR N-PSDB; ADZ00579.
 XX
 PT New transgenic plant, useful for further producing plants with increased
 PT tolerance to an abiotic stress and/or increased biomass.
 XX
 PS Disclosure; SEQ ID NO 34; 220pp; English.
 XX
 CC This sequence represents a member of the G1073 clade of transcription
 CC factors. The G1073 clade is characterized by having at least two
 CC conserved domains, including an AT-hook domain and a second domain
 CC comprising the sequences ADZ00609ADZ00610. Recombinant nucleotides
 CC encoding the G1073 clade may be used in the generation of a transgenic
 CC plant having increased tolerance to an abiotic stress or having increased
 CC biomass. The transgenic plant comprises a recombinant polynucleotide
 CC encoding a member of the G1073 clade of transcription factor
 CC polypeptides. The recombinant polynucleotide is operably linked to an
 CC inducible or tissue-specific promoter that regulates expression of the
 CC recombinant polynucleotide when the recombinant polynucleotide is
 CC transformed into a plant, where the tissue-specific promoter is a
 CC vascular, epidermal, leaf, or root promoter, and where the inducible or
 CC tissue specific promoter is a SUC2, a CUT1, an RBCS3, an ARSK1, or an
 CC RD29A promoter. The abiotic stress is cold or an osmotic stress, e.g.
 CC heat, drought, desiccation, freezing, or high salt.
 XX
 SQ Sequence 289 AA;
 Query Match 84.8%; Score 28; DB 9; Length 289;
 Best Local Similarity 85.7%; Pred. No. 5.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 Db 171 GATSLAA 177
 |||:||||
 RESULT 49
 AEA26513
 ID AEA26513 standard; protein; 289 AA.
 XX
 AC AEA26513;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Stress tolerant plant-related transcription factor protein SeqID354.
 XX
 KW transcription factor; transgenic plant; agriculture; drought resistance;
 KW stress tolerance.
 XX
 OS Oryza sativa.
 XX
 PN WO2005047516-A2.
 XX
 PD 26-MAY-2005.
 XX
 PF 12-NOV-2004; 2004WO-US037584.
 XX
 PR 13-NOV-2003; 2003US-00714887.
 PR 05-DEC-2003; 2003US-0527658P.
 PR 05-FEB-2004; 2004US-0542928P.
 XX
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX
 XX Heard JB, Riechmann JL, Creelman RA, Ratcliffe OJ, Canales RD;
 PI Repetti P, Kumimoto RW, Guttererson NI, Reuber TL, Pineda O;
 PI Sherman BK, Morrison TA, Keddle JS, Jiang C, Century KS, Adam L;
 PI Zhang JZ, Hempel FD, Libby JM;
 XX
 XX WPI; 2005-372386/38.
 DR N-PSDB; AEA26512.
 XX
 PT New transgenic plants for producing commercially or agriculturally useful
 PT plants having improved tolerance to drought, shade and low nitrogen

PT conditions.
 XX Example 8; SEQ ID NO 354; 407pp; English.
 PS
 XX This invention relates to a novel plant transcription factor
 CC polypeptides, the DNA sequences which encode them and their use in
 CC creating transgenic plants. The transgenic plant and methods are useful
 CC for producing commercially or agriculturally useful plants having
 CC improved tolerance to drought, shade and low nitrogen conditions when
 CC compared to wild-type reference plants. The present sequence is that of a
 CC plant transcription factor protein which was used during the development
 CC of the transgenic plants of the invention.
 XX
 XX Sequence 289 AA;
 SQ

Query Match 84.8%; Score 28; DB 9; Length 289;
 Best Local Similarity 85.7%; Pred. No. 5.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GATNLAA 7
 |||||
 Db 171 GATSLAA 177

RESULT 50
 ADA34821
 ID ADA34821 standard; protein; 323 AA.
 XX
 AC ADA34821;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Acinetobacter baumannii protein #1982.
 XX
 KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
 KW plant biocontrol agent.
 XX
 OS Acinetobacter baumannii.
 XX
 FN US6562958-B1.
 XX
 PD 13-MAY-2003.
 XX
 PF 04-JUN-1999; 99US-00328352.
 XX
 PR 09-JUN-1998; 98US-0088701P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton G, Bush D;
 XX
 DR WPI; 2003-576092/54.
 DR N-ESDB; ADA30695.
 XX
 PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
 PT for diagnosing a bacterial disease, as components of antibacterial
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
 PT plants.
 XX
 PS Example; SEQ ID NO 6108; 328pp; English.
 XX
 CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents
 CC for diagnosing a bacterial disease, as components of antibacterial
 CC vaccines, as targets for antibacterial drugs, to detect the presence of
 CC A. baumannii and other Acinetobacter species in a sample, in screening
 CC compounds for the ability to interfere with the A. baumannii life cycle
 CC or to inhibit A. baumannii infection, and as biocontrol agents for
 CC plants. The present sequence represents the amino acid sequence of an A.
 CC baumannii protein.
 XX
 XX Sequence 323 AA;
 SQ

Query Match 84.8%; Score 28; DB 6; Length 323;
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GATNLAA 7
 |||||
 Db 86 GMTNLAA 92

Search completed: May 11, 2006, 16:26:34
 Job time : 104.721 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 10.3279 Seconds
(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-5

Perfect score: 33

Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	321	T50966	hypothetical prote
2	29	87.9	95	S26333	Ig kappa chain v r
3	29	87.9	111	S24217	Ig kappa chain - m
4	29	87.9	114	P70358	Ig kappa chain v r
5	29	87.9	166	A00657	hypothetical prote
6	29	87.9	252	G70629	thiamin biosynthes
7	29	87.9	309	AH2831	ABC transporter, m
8	29	87.9	329	D97609	hypothetical prote
9	29	87.9	517	A49413	perilipin A - rat
10	29	87.9	592	D70863	hypothetical prote
11	29	87.9	619	A13336	potassium/proton a
12	29	87.9	878	A41055	ecdysone receptor
13	28	84.8	237	T26660	hypothetical prote
14	28	84.8	356	B97742	hypothetical prote
15	28	84.8	391	G30266	na(+)/H(+) antiport
16	28	84.8	449	D70726	probable gabra - My
17	28	84.8	508	T29988	hypothetical prote
18	28	84.8	566	S74633	high affinity sulf
19	28	84.8	589	A50076	probable membrane
20	28	84.8	809	G95299	probable adenylate
21	28	84.8	950	D86974	probable amino aci
22	28	84.8	957	D70835	hypothetical glyci
23	28	84.8	1161	G81186	conserved hypotet
24	28	84.8	1161	G81915	hypothetical prote
25	27	81.8	64	S70550	sipa protein - Sal
26	27	81.8	124	A45691	hypothetical prote
27	27	81.8	192	T35904	probable transcrip
28	27	81.8	213	G82723	partition protein
29	27	81.8	235	S70219	sipa protein - Sal

30	27	81.8	274	2	T20248	hypothetical prote
31	27	81.8	286	2	G72625	probable ribosomal
32	27	81.8	286	2	F87146	methyl mycolic aci
33	27	81.8	298	2	S72880	hypothetical prote
34	27	81.8	301	2	C84331	homoserine kinase
35	27	81.8	316	2	AG2977	hypothetical prote
36	27	81.8	319	2	E98305	hypothetical prote
37	27	81.8	395	2	S42680	phosphoserine tran
38	27	81.8	407	2	A71673	probable ATP-depen
39	27	81.8	414	2	D97827	ATP-dependent RNA
40	27	81.8	432	2	A90465	hypothetical prote
41	27	81.8	461	2	S34472	MFH-1 protein - mo
42	27	81.8	504	1	D69417	probable thymidine
43	27	81.8	537	2	C71008	probable proline p
44	27	81.8	557	1	S76051	hypothetical prote
45	27	81.8	581	2	G83189	probable sodium/hy
46	27	81.8	634	2	D71493	probable DNA helic
47	27	81.8	637	2	D97708	cell division prot
48	27	81.8	637	2	C71712	cell division prot
49	27	81.8	644	2	T16136	hypothetical prote
50	27	81.8	685	2	AF0850	hypothetical prote
51	27	81.8	700	2	A84243	phosphoribosylform
52	27	81.8	748	2	D87632	phosphoribosylform
53	27	81.8	755	2	C90439	sensory box/GDEP
54	27	81.8	987	2	AB3075	cation transportin
55	27	81.8	987	2	G98211	sarcosine oxidase
56	27	81.8	1246	2	S60954	hypothetical prote
57	27	81.8	1309	2	P96509	probable membrane
58	27	81.8	1318	2	T05745	protein P27F5.19 I
59	27	81.8	1377	2	I54632	hypothetical prote
60	27	81.8	1402	2	F84480	tsn protein - Esch
61	27	81.8	1418	2	D75281	probable retroelem
62	27	81.8	1433	2	A71444	ribonucleoside-dip
63	27	81.8	1467	2	A75564	probable LTR retro
64	27	81.8	3705	2	AD0123	conserved hypotet
65	26	78.8	147	2	S31444	probable autotrans
66	26	78.8	148	2	S31446	nucleoside-diphosp
67	26	78.8	149	2	T17131	nucleoside-diphosp
68	26	78.8	207	2	AH1190	3-methyladenine DN
69	26	78.8	207	2	AH1548	3-methyladenine DN
70	26	78.8	236	2	F75375	nodulin 21-related
71	26	78.8	266	2	B97686	regulator protein
72	26	78.8	266	2	AD2911	transcription regu
73	26	78.8	292	2	A10422	conserved hypotet
74	26	78.8	295	2	C23750	30K actin-bundling
75	26	78.8	318	2	C84212	immunogenic protei
76	26	78.8	320	2	A40660	outer membrane pro
77	26	78.8	326	1	S44259	sucrose operon reg
78	26	78.8	334	2	T24649	hypothetical prote
79	26	78.8	367	2	C84258	hypothetical prote
80	26	78.8	369	2	AF0966	probable transfera
81	26	78.8	412	2	A59034	oleoyl-[acyl-carri
82	26	78.8	416	2	G69748	conserved hypotet
83	26	78.8	418	2	F83986	transporter BH2694
84	26	78.8	421	2	C85644	hypothetical prote
85	26	78.8	421	2	A90784	hypothetical prote
86	26	78.8	427	2	A11264	N-acetylmuramoyl-L
87	26	78.8	446	2	H71490	hypothetical prote
88	26	78.8	503	2	AE3026	dehydratase (impor
89	26	78.8	503	2	D98258	altronate hydrolas
90	26	78.8	510	1	JC2311	NADH oxidase (hydr
91	26	78.8	558	2	H72565	hypothetical prote
92	26	78.8	577	2	C82582	Na+-dependent symp
93	26	78.8	590	1	S28920	acetolactate synth
94	26	78.8	590	1	S73251	acetohydroxyacid s
95	26	78.8	590	2	E70946	probable PPG prote
96	26	78.8	599	2	S15004	acetolactate synth
97	26	78.8	602	2	H87503	phosphoglucosate d
98	26	78.8	609	2	JC7819	metalloprotease
99	26	78.8	638	2	S22490	acetolactate synth
100	26	78.8	638	2	S22491	acetolactate synth
101	26	78.8	652	2	S29838	acetolactate synth
102	26	78.8	655	2	S17691	acetolactate synth

103	26	78.8	661	1	A69048	ferrous iron trans	176	25	75.8	370	2	G87212	conserved hypochet
104	26	78.8	664	1	YCNT2	acetylactate synth	177	25	75.8	383	2	T48870	muconate cycloisom
105	26	78.8	667	1	YCMT1	acetylactate synth	178	25	75.8	385	2	T46824	muconate cycloisom
106	26	78.8	670	1	YCMU	acetylactate synth	179	25	75.8	386	2	G64494	quinolone resistanc
107	26	78.8	741	2	T48694	probable transcrip	180	25	75.8	394	2	T21752	hypothetical prote
108	26	78.8	742	2	T24755	hypothetical prote	181	25	75.8	395	2	AG2835	sarcosine oxidase
109	26	78.8	772	2	S22660	excision repair pr	182	25	75.8	400	2	B81405	aspartate kinase (
110	26	78.8	774	2	JC7887	alpha, alpha-trehal	183	25	75.8	404	1	S62440	mevalonate kinase
111	26	78.8	879	2	S64755	hypothetical prote	184	25	75.8	410	2	T34717	probable transmemb
112	26	78.8	1072	2	T30846	serine-repeat anti	185	25	75.8	416	2	B75455	N-acetyl-gamma-glu
113	26	78.8	1127	2	D70671	pyruvate carboxyla	186	25	75.8	416	2	C86778	threonine ammonia-
114	26	78.8	1186	2	H88869	protein unc-31 [im	187	25	75.8	417	2	C32185	Fzr CD protein - M
115	26	78.8	1270	2	T28087	hypothetical prote	188	25	75.8	430	2	AE1803	sugar binding prot
116	26	78.8	1297	2	T52065	probable myb-relat	189	25	75.8	430	2	AF1429	sugar binding prot
117	26	78.8	1804	2	H96597	hypothetical prote	190	25	75.8	436	2	H72050	serine-type D-Ala-
118	26	78.8	1891	2	T13594	hypothetical prote	191	25	75.8	436	2	E86574	serine-type D-Ala-
119	26	78.8	1920	2	T13893	gene hindsight pro	192	25	75.8	437	2	B97613	monomeric sarcosin
120	26	78.8	2479	2	F87386	conserved hypochet	193	25	75.8	441	2	S35141	probable threonine
121	25	75.8	111	2	T19094	hypothetical prote	194	25	75.8	442	2	F87345	L-sorbose dehydr
122	25	75.8	121	2	C36790	hypothetical prote	195	25	75.8	444	2	C82981	probable pyridoxal
123	25	75.8	124	2	G85105	hypothetical prote	196	25	75.8	448	2	T32575	hypothetical prote
124	25	75.8	143	2	AG0974	probable secreted	197	25	75.8	449	2	T50409	utrl protein homol
125	25	75.8	150	2	E83769	hypothetical prote	198	25	75.8	457	2	T12399	NADH2 dehydrogenas
126	25	75.8	157	2	A11910	hypothetical prote	199	25	75.8	457	2	T31707	hypothetical prote
127	25	75.8	168	2	A55479	CDK6 inhibitor p18	200	25	75.8	470	1	E64081	probable rhamnulok
128	25	75.8	174	2	T14514	hypothetical prote	201	25	75.8	470	2	C69725	phosphotransferase
129	25	75.8	184	1	D70177	4-methyl-5(b-hydro	202	25	75.8	472	2	AC0863	L-fucose kinase
130	25	75.8	185	2	AG0747	conserved hypochet	203	25	75.8	476	2	T28936	hypothetical prote
131	25	75.8	190	2	S75069	K+-transporting AT	204	25	75.8	479	1	C70664	IMP dehydrogenase
132	25	75.8	195	2	AB0587	potassium-transport	205	25	75.8	482	1	K1ECFK	fucokinase [EC 2.7
133	25	75.8	200	2	S75591	hypothetical prote	206	25	75.8	482	2	A85932	L-fuculokinase [im
134	25	75.8	201	2	AH2069	hypothetical prote	207	25	75.8	482	2	G91086	L-fuculokinase [im
135	25	75.8	202	2	AH2199	potassium-transport	208	25	75.8	494	2	G64382	acetylactate synth
136	25	75.8	210	2	A83440	conserved hypochet	209	25	75.8	495	2	H84359	threonine dehydrat
137	25	75.8	212	2	A11223	precorrin isomerase	210	25	75.8	501	2	AH1852	hypothetical prote
138	25	75.8	215	2	AC1577	precorrin isomerase	211	25	75.8	506	2	T25870	hypothetical prote
139	25	75.8	225	2	AB2374	ABC transporter AT	212	25	75.8	509	2	B86667	alkyl hydroperoxid
140	25	75.8	227	2	C31390	phlB protein - Ser	213	25	75.8	509	2	A71254	probable glu-tRNA
141	25	75.8	248	2	D29525	methyl coenzyme M	214	25	75.8	518	2	AH3616	N-acylmannosamine
142	25	75.8	255	2	AD1159	flagellar biosynth	215	25	75.8	521	1	VHBET4	major capsid prote
143	25	75.8	255	2	AD1518	flagellar biosynth	216	25	75.8	524	2	D87440	2-isopropylmalate
144	25	75.8	265	2	F64089	acetylactate synth	217	25	75.8	527	2	JC5357	laccase [EC 1.10.3
145	25	75.8	275	2	F69402	conserved hypochet	218	25	75.8	530	2	S53392	probable membrane
146	25	75.8	279	2	H84040	sulfate ABC transp	219	25	75.8	537	2	AG3572	oligopeptide-bind
147	25	75.8	279	2	D84185	hypothetical prote	220	25	75.8	541	2	B95320	dextran glucosidas
148	25	75.8	279	2	T34848	probable transcrip	221	25	75.8	541	2	H98083	acetylactate synth
149	25	75.8	280	2	S24986	flagellin B chain	222	25	75.8	547	2	AD2250	dextranase [EC 3.2
150	25	75.8	292	2	F65171	2-dehydro-3-deoxyg	223	25	75.8	547	2	G83123	acetylactate synth
151	25	75.8	292	2	B90823	probable anti-repre	224	25	75.8	548	1	YCEC	probable acetylact
152	25	75.8	292	2	B85682	probable anti-repre	225	25	75.8	548	2	AF0924	acetylactate synth
153	25	75.8	293	1	QBEG1	Hvrf1 protein - hu	226	25	75.8	548	2	A82375	acetylactate synth
154	25	75.8	293	2	T25502	hypothetical prote	227	25	75.8	548	2	AC0475	acetylactate synth
155	25	75.8	299	2	E70570	hypothetical prote	228	25	75.8	548	2	G86062	acetylactate synth
156	25	75.8	300	1	OUBP22	antirepressor prot	229	25	75.8	548	2	F91216	acetylactate synth
157	25	75.8	301	2	S16070	porin - Rhodobacte	230	25	75.8	550	2	AH2837	acetylactate synth
158	25	75.8	303	2	H81395	probable ferredoxel	231	25	75.8	550	2	S75122	probable decarboxy
159	25	75.8	307	2	B86965	probable pyridoxin	232	25	75.8	554	2	B97615	acetylactate synth
160	25	75.8	317	2	AG2209	4-diphosphocytidyl	233	25	75.8	554	2	G97289	acetylactate synth
161	25	75.8	317	2	JC2110	tropomyosin-relate	234	25	75.8	560	2	AF0279	acetylactate synth
162	25	75.8	320	2	JC5727	porin precursor -	235	25	75.8	560	2	F70688	hypothetical prote
163	25	75.8	325	2	T36434	threonine ammonia-	236	25	75.8	562	1	YCEC11	acetylactate synth
164	25	75.8	328	2	G95332	probable protease	237	25	75.8	562	2	AB0963	acetylactate synth
165	25	75.8	339	2	G83900	hypothetical prote	238	25	75.8	562	2	D91205	acetylactate synth
166	25	75.8	342	2	T36477	probable DNA-bind	239	25	75.8	562	2	G75044	hypothetical prote
167	25	75.8	342	2	E96668	protein FIN19.3 [i	240	25	75.8	562	2	F86051	acetylactate synth
168	25	75.8	345	2	T43182	tetrahydrofolylpol	241	25	75.8	563	2	C97348	alpha-acetylactate
169	25	75.8	347	2	T01044	hypothetical prote	242	25	75.8	564	2	AH1696	alpha-acetylactate
170	25	75.8	353	2	S37873	hypothetical prote	243	25	75.8	565	2	AF1325	alpha-acetylactate
171	25	75.8	355	2	G82941	hypothetical prote	244	25	75.8	568	1	S44904	ZK652.9 protein -
172	25	75.8	358	2	F70577	probable lipoprote	245	25	75.8	571	2	H69584	acetylactate synth
173	25	75.8	359	2	S58167	fructose-bisphosph	246	25	75.8	574	2	B69644	acetylactate synth
174	25	75.8	362	2	H84175	hypothetical prote	247	25	75.8	574	2	S01272	regulatory protein
175	25	75.8	367	2	S72924	hypothetical prote	248	25	75.8	575	2	T06353	isocitrate lyase (

249	25	75.8	577	2	C69059	acetolactate synth	322	24	72.7	152	2	C97371	hypothetical prote
250	25	75.8	577	2	F86261	Flk23.7 protein -	323	24	72.7	156	2	AD2745	conserved hypothet
251	25	75.8	579	2	B4857	acetolactate synth	324	24	72.7	156	2	C97526	pB5 protein (U6790
252	25	75.8	582	2	H70588	probable proS prot	325	24	72.7	156	2	AF1784	conserved hypothet
253	25	75.8	585	2	C70341	acetolactate synth	326	24	72.7	156	2	AH1408	conserved hypothet
254	25	75.8	585	2	T11997	acetohydroxyacid s	327	24	72.7	158	2	S26672	peroxidase (EC 1.1
255	25	75.8	591	2	P64334	acetolactate synth	328	24	72.7	158	2	T12958	copper transport p
256	25	75.8	592	2	A75387	acetolactate synth	329	24	72.7	160	2	T40636	glycosylphosphatid
257	25	75.8	594	1	A56684	acetohydroxy acid	330	24	72.7	161	2	AE0709	probable exported
258	25	75.8	606	2	S77654	isocitrate lyase (331	24	72.7	161	2	A99935	spheroplast protei
259	25	75.8	612	2	A44857	acetolactate synth	332	24	72.7	161	2	E85783	hypothetical prote
260	25	75.8	613	2	T35828	acetolactate synth	333	24	72.7	161	2	G64933	Spheroplast protei
261	25	75.8	616	2	JC7905	fructan 6-fructosy	334	24	72.7	162	2	A95006	hypothetical prote
262	25	75.8	618	2	F70855	probable flvB prot	335	24	72.7	173	2	E97878	phosphoribosylamin
263	25	75.8	620	2	T20450	hypothetical prote	336	24	72.7	188	1	YQECF2	F7-2 fimbrial prot
264	25	75.8	619	2	H84416	hypothetical prote	337	24	72.7	192	2	T13106	minor tail protein
265	25	75.8	620	2	H85431	ATPase-like protei	338	24	72.7	192	2	E71830	hypothetical prote
266	25	75.8	620	2	A70525	hypothetical prote	339	24	72.7	195	2	S24997	formate C-acetyltr
267	25	75.8	621	2	S75115	acetohydroxy acid	340	24	72.7	195	2	C95974	hypothetical prote
268	25	75.8	621	2	JC5164	acetolactate synth	341	24	72.7	198	2	T26708	hypothetical prote
269	25	75.8	622	2	AB1090	bacteriophage mino	342	24	72.7	201	2	G02361	small GTP binding
270	25	75.8	622	2	AI1453	bacteriophage mino	343	24	72.7	201	2	S36187	grp-binding protei
271	25	75.8	625	2	T06184	sucrose-fructan 6-	344	24	72.7	201	2	AR2069	hypothetical prote
272	25	75.8	625	2	T45413	acetolactate synth	345	24	72.7	203	2	AI3366	nitrotriacetate
273	25	75.8	626	1	A48648	acetolactate synth	346	24	72.7	205	2	H90532	hypothetical prote
274	25	75.8	628	2	AG3357	peptidylprolyl iso	347	24	72.7	206	1	I40173	orotate phosphorib
275	25	75.8	632	2	AE2382	acetohydroxy acid	348	24	72.7	213	2	A95013	hypothetical prote
276	25	75.8	633	2	C32053	parasporal crystal	349	24	72.7	213	2	E83972	hypothetical prote
277	25	75.8	638	1	XXAV	dihydrolipoamide S	350	24	72.7	213	2	D97884	hypothetical prote
278	25	75.8	660	2	T41580	probable dna-bindi	351	24	72.7	223	2	S32872	regulatory protein
279	25	75.8	681	2	T08085	acetolactate synth	352	24	72.7	225	2	AD3278	nicotinamide-nucie
280	25	75.8	681	2	T07968	acetolactate synth	353	24	72.7	225	2	T36651	probable cation tr
281	25	75.8	683	2	T07941	acetolactate synth	354	24	72.7	226	2	A82019	hypothetical prote
282	25	75.8	683	2	T07912	acetolactate synth	355	24	72.7	226	2	D81001	conserved hypothet
283	25	75.8	709	2	T29692	hypothetical prote	356	24	72.7	227	2	D95367	probable response
284	25	75.8	715	1	TNBE77	77K alpha trans-in	357	24	72.7	233	2	F70668	probable lipoprote
285	25	75.8	718	1	TNBEF6	77K alpha trans-in	358	24	72.7	251	2	A48577	filarial antigen A
286	25	75.8	734	2	F88098	protein F18A12.4 [359	24	72.7	257	2	B83169	probable methyltra
287	25	75.8	739	2	T45891	ABC transporter-li	360	24	72.7	261	2	T44741	thiamin biosynthes
288	25	75.8	749	2	S61643	probable membrane	361	24	72.7	264	2	D83602	thymidylate synth
289	25	75.8	754	2	S61113	VTAG protein - yea	362	24	72.7	273	2	J00418	pyrroline-5-carbox
290	25	75.8	760	2	E64817	probable membrane	363	24	72.7	275	2	D97525	hypothetical prote
291	25	75.8	760	2	E85589	hypothetical prote	364	24	72.7	276	2	A84309	cobalamin biosynth
292	25	75.8	760	2	C90739	hypothetical prote	365	24	72.7	276	2	G82482	hypothetical prote
293	25	75.8	783	1	WMBEHQ	UL5 protein - huma	366	24	72.7	278	2	G65165	DNA-damage-inducib
294	25	75.8	787	2	S53590	hypothetical prote	367	24	72.7	278	2	H91193	DNA-damage-inducib
295	25	75.8	798	2	D87157	isocitrate lyase [368	24	72.7	278	2	A86041	DNA-damage-inducib
296	25	75.8	831	2	E70620	probable pner prot	369	24	72.7	281	2	A84371	ribose phosphate p
297	25	75.8	877	2	T40413	sulfate permease -	370	24	72.7	290	2	T50586	probable membrane
298	25	75.8	882	1	WMBEUS	gene UL5 protein -	371	24	72.7	292	2	H87337	3-hydroxybutyryl-C
299	25	75.8	883	1	A35728	hydroxymethylgluta	372	24	72.7	293	2	D84100	hypothetical prote
300	25	75.8	907	2	S54357	inter-alpha-trypsi	373	24	72.7	294	2	AD0184	cytidine deaminase
301	25	75.8	914	2	JC5574	inter-alpha-trypsi	374	24	72.7	297	2	T39181	hypothetical prote
302	25	75.8	937	2	B69068	leucine-tRNA ligas	375	24	72.7	303	2	AD1367	Erwinia chrysanth
303	25	75.8	1036	2	B69368	hypothetical prote	376	24	72.7	305	2	AE1736	Erwinia chrysanth
304	25	75.8	1507	2	T18544	alpha-2-macroglobu	377	24	72.7	305	2	T28063	hypothetical prote
305	25	75.8	2271	2	F90073	hypothetical prote	378	24	72.7	307	2	AB2807	conserved hypothet
306	25	75.8	2481	2	D90011	FmtB protein limpo	379	24	72.7	317	1	R5FFP0	acidic ribosomal p
307	25	75.8	6713	2	B89921	hypothetical prote	380	24	72.7	320	2	J00183	L-lactate dehydrog
308	24	72.7	51	2	D91246	hypothetical prote	381	24	72.7	325	2	T12852	hypothetical prote
309	24	72.7	124	2	A60218	14K brain-specific	382	24	72.7	325	2	T41658	hypothetical prote
310	24	72.7	124	2	T06427	aminopeptidase - t	383	24	72.7	331	2	T32168	hypothetical prote
311	24	72.7	132	2	D97090	cytidine deaminase	384	24	72.7	333	2	A97586	heptosyltransferas
312	24	72.7	134	2	S44430	synuclein - human	385	24	72.7	333	2	A87659	probable smc22-r p
313	24	72.7	134	2	S39046	phosphonuroprotei	386	24	72.7	334	2	E95869	probable sugar nuc
314	24	72.7	137	2	I56498	phosphonuroprotei	387	24	72.7	334	2	B81272	Y box-binding prot
315	24	72.7	146	2	H75201	hypothetical prote	388	24	72.7	336	1	B38274	LPS biosynthesis p
316	24	72.7	147	2	AB1791	hypothetical prote	389	24	72.7	338	2	H84166	hsp90 protein - Rho
317	24	72.7	147	2	AC1415	hypothetical prote	390	24	72.7	340	2	S32953	hypothetical prote
318	24	72.7	149	2	B43959	synuclein, form 2	391	24	72.7	340	2	AB2224	hypothetical prote
319	24	72.7	151	2	S43727	hypothetical prote	392	24	72.7	340	2	H71479	probable outer mem
320	24	72.7	152	2	C86765	hypothetical prote	393	24	72.7	343	2	AD2448	sulfate adenyliltr
321	24	72.7	152	2	AC2589	conserved hypothet	394	24	72.7	343	2	AC3425	laci-family transc

395	24	72.7	345	2	A42106	acetylserotonin O-
396	24	72.7	346	2	AC0187	probable iron-side
397	24	72.7	348	2	G83976	cytochrome caa3 ox
398	24	72.7	350	2	AF0884	probable ABC-trans
399	24	72.7	351	2	A69808	H+/Ca2+ exchanger
400	24	72.7	351	2	E64524	NADH2 dehydrogenas
401	24	72.7	351	2	G71983	hypothetical prote
402	24	72.7	352	2	B84390	hypothetical prote
403	24	72.7	353	2	AH3099	transcription regu
404	24	72.7	353	2	AH3099	GDEF family prote
405	24	72.7	355	2	A3624	spemidine/putresc
406	24	72.7	356	2	A44869	cell type-specific
407	24	72.7	357	2	S24317	decurin precursor
408	24	72.7	357	2	AG1072	conserved hypotHet
409	24	72.7	357	2	S56601	hypothetical 39.8K
410	24	72.7	357	2	B86137	hypothetical prote
411	24	72.7	357	2	G91295	hypothetical prote
412	24	72.7	362	2	F96541	unknown protein [i
413	24	72.7	363	2	H87277	flagellin modifca
414	24	72.7	364	2	S73516	mannotol-1-phospha
415	24	72.7	372	2	S74859	hypothetical prote
416	24	72.7	375	2	C75201	na+/h+ antiporter
417	24	72.7	378	2	B99995	hypothetical prote
418	24	72.7	378	2	G85840	hypothetical prote
419	24	72.7	378	2	H64979	hypothetical prote
420	24	72.7	385	2	AC2857	conserved hypotHet
421	24	72.7	385	2	A97634	hypothetical prote
422	24	72.7	386	1	PWW16	H+-transporting tw
423	24	72.7	386	2	JC2100	H+-transporting tw
424	24	72.7	387	2	B98187	probable lacI-fami
425	24	72.7	387	2	I51404	cone arrestin - Af
426	24	72.7	389	2	S68175	cone arrestin - bu
427	24	72.7	389	2	S68172	cone arrestin - no
428	24	72.7	394	2	B39436	flagellin flaaB - R
429	24	72.7	394	2	A39436	flagellin flaaB - R
430	24	72.7	398	2	S30901	isopenicillin N ep
431	24	72.7	399	2	T46259	hypothetical prote
432	24	72.7	402	2	E69064	nitrogenase iron-m
433	24	72.7	415	2	F89975	aminopeptidase amp
434	24	72.7	415	2	AG3320	benzoate 1,2-dioxy
435	24	72.7	418	2	A81394	probable sugar tra
436	24	72.7	419	2	A70814	probable integral
437	24	72.7	421	2	F72213	hypothetical prote
438	24	72.7	422	2	S59319	probable membrane
439	24	72.7	422	2	AH1129	a module of peptid
440	24	72.7	422	2	AH1038	probable glutamate
441	24	72.7	423	2	AH0053	conserved hypotHet
442	24	72.7	425	2	S32110	cytochrome P450 PE
443	24	72.7	427	2	AD1490	weakly a module of
444	24	72.7	429	2	A83574	multidrug resistan
445	24	72.7	432	2	A85436	APETALA2 protein [
446	24	72.7	434	2	C71434	probable phosphati
447	24	72.7	436	2	A69777	conserved hypotHet
448	24	72.7	438	2	T39268	hypothetical prote
449	24	72.7	439	2	T36422	probable DEAD-box
450	24	72.7	440	2	AC0962	D-serine dehydrata
451	24	72.7	441	2	E86758	dihydroorotase (EC
452	24	72.7	441	2	T36730	hypothetical prote
453	24	72.7	444	2	T35794	probable 4-aminobu
454	24	72.7	446	2	E85691	probable tail comp
455	24	72.7	459	2	T51558	probable flavonol
456	24	72.7	460	2	F85361	probable aminotran
457	24	72.7	463	2	F85361	hypothetical prote
458	24	72.7	467	1	VMUT7R	variant surface gl
459	24	72.7	467	2	E82567	GumC protein XF236
460	24	72.7	473	2	B84143	Na+/H+ antiporter
461	24	72.7	481	2	S69808	lincomycin resistat
462	24	72.7	488	2	A50001	conserved hypotHet
463	24	72.7	495	2	F95850	probable sulfate p
464	24	72.7	496	2	S61716	ribose-phosphate p
465	24	72.7	498	2	T34592	DEAD-box RNA helic
466	24	72.7	499	2	S51089	ammonium transport
467	24	72.7	502	2	D65057	hypothetical prote
468	24	72.7	504	2	S33191	phase-1 flagellin
469	24	72.7	506	2	S38985	flavonoid 3',5'-hy
470	24	72.7	508	2	S38984	flavonoid 3',5'-hy
471	24	72.7	508	2	S11863	aldehyde dehydroge
472	24	72.7	508	2	F87198	glycerol kinase [i
473	24	72.7	511	2	T34315	hypothetical prote
474	24	72.7	513	2	T01506	probable hexose tr
475	24	72.7	518	2	A55864	flagellin - Woline
476	24	72.7	519	2	C75370	Mg(2+) chelatase f
477	24	72.7	522	2	I67414	nuclear factor kap
478	24	72.7	524	2	F75610	histidine amonia-
479	24	72.7	526	2	S49641	L-galactonolactone
480	24	72.7	526	2	S03600	cell surface antig
481	24	72.7	527	2	S64702	cell surface antig
482	24	72.7	527	2	B87320	conserved hypotHet
483	24	72.7	545	1	RRBPM	RNA-directed RNA p
484	24	72.7	547	2	S91135	probable alkaline
485	24	72.7	547	2	H85980	probable alkaline
486	24	72.7	547	2	H65107	hypothetical 61.6
487	24	72.7	549	2	F70563	probable transmemb
488	24	72.7	555	2	A83327	probable AMP-bindi
489	24	72.7	555	2	A26639	regulatory protein
490	24	72.7	557	2	JC5229	laccase (EC 1.10.3
491	24	72.7	570	2	D97317	membrane associate
492	24	72.7	573	2	C64611	hypothetical prote
493	24	72.7	576	2	T48573	hypothetical prote
494	24	72.7	580	2	D69645	myo-inositol catab
495	24	72.7	581	1	RYEBT	DNA primase (EC 2.
496	24	72.7	581	2	A10892	DNA primase (impor
497	24	72.7	583	2	S34785	catechol oxidase (
498	24	72.7	583	2	S30930	catechol oxidase (
499	24	72.7	584	2	G71676	hypothetical prote
500	24	72.7	584	2	JC7809	sulfakinin recepto
501	24	72.7	585	1	S33544	catechol oxidase (
502	24	72.7	587	1	S33543	catechol oxidase (
503	24	72.7	588	2	S34786	catechol oxidase (
504	24	72.7	588	2	S30929	catechol oxidase (
505	24	72.7	588	2	A39624	probable helicase
506	24	72.7	592	2	T03682	catechol oxidase (
507	24	72.7	595	2	B86798	prophage pi3 prote
508	24	72.7	596	2	B87430	flagellin modifca
509	24	72.7	599	2	G71481	probable phosphoen
510	24	72.7	600	2	E72027	phosphoenolpyruvat
511	24	72.7	600	2	A86597	phosphoenolpyruvat
512	24	72.7	601	2	T35054	probable transport
513	24	72.7	606	2	A70960	probable pcta prot
514	24	72.7	608	2	JQ1462	phosphoenolpyruvat
515	24	72.7	609	2	F87237	phosphoenolpyruvat
516	24	72.7	611	2	C81388	succinate dehydrog
517	24	72.7	614	1	EFEC5B	translation elonga
518	24	72.7	615	2	T15575	hypothetical prote
519	24	72.7	615	2	F82132	probable peptidase
520	24	72.7	618	2	A71364	probable phosphoen
521	24	72.7	619	2	A45625	phosphoenolpyruvat
522	24	72.7	622	1	QYCHGC	phosphoenolpyruvat
523	24	72.7	622	1	QYRTGP	phosphoenolpyruvat
524	24	72.7	631	2	B86233	hypothetical prote
525	24	72.7	640	1	QYCHGM	phosphoenolpyruvat
526	24	72.7	640	2	S69546	phosphoenolpyruvat
527	24	72.7	643	2	G75539	probable drug tran
528	24	72.7	645	2	A47081	triacylglycerol li
529	24	72.7	647	1	QYFFQM	phosphoenolpyruvat
530	24	72.7	651	2	T32875	hypothetical prote
531	24	72.7	653	2	B84386	oligopeptide bindi
532	24	72.7	654	2	T24168	hypothetical prote
533	24	72.7	656	2	AF1040	Vi polysaccharide
534	24	72.7	656	2	A56975	Vi polysaccharide
535	24	72.7	667	2	T40727	probable chloride
536	24	72.7	671	1	UYPV19	noncapsid protein
537	24	72.7	681	2	P69295	acetyl-CoA synthet
538	24	72.7	683	2	B71325	conserved hypotHet
539	24	72.7	685	2	T09159	RNA helicase prn75
540	24	72.7	709	2	F75584	hypothetical prote

541	24	72.7	714	2	C91102	methionylmalonyl-CoA	614	24	72.7	3429	2	T13853	hypothetical prote
542	24	72.7	714	2	G85947	methionylmalonyl-CoA	615	24	72.7	3512	2	T17121	CPY protein - midg
543	24	72.7	714	2	D65076	sbm protein - Esch	616	24	72.7	3716	2	E70969	probable PPS prote
544	24	72.7	719	2	E87543	methionylmalonyl-CoA	617	24	72.7	4385	2	T29042	hypothetical prote
545	24	72.7	719	2	AB1131	hypothetical prote	618	24	72.7	4976	2	T14165	peptide synthetase
546	24	72.7	726	1	UVPS1	noncapsid protein	619	23	69.7	29	2	S28174	heat-shock protein
547	24	72.7	727	2	AC0180	hypothetical prote	620	23	69.7	38	2	E86077	hypothetical prote
548	24	72.7	729	2	AC3517	3-methyl-2-oxobuta	621	23	69.7	54	2	E70787	hypothetical glyci
549	24	72.7	744	2	T27674	hypothetical prote	622	23	69.7	62	2	G81911	hypothetical prote
550	24	72.7	748	2	T04011	hypothetical prote	623	23	69.7	71	2	F28840	IG kappa chain v r
551	24	72.7	757	2	T02884	D-(-)-3-hydroxybut	624	23	69.7	76	2	A45343	gene 17 protein -
552	24	72.7	757	2	A49398	cycloartenol synth	625	23	69.7	77	2	G28840	IG kappa chain v r
553	24	72.7	759	2	H84481	cycloartenol synth	626	23	69.7	78	2	B44884	sex-specific germ
554	24	72.7	770	2	G88445	protein C26E6.2 [l	627	23	69.7	81	2	E28840	IG kappa chain v r
555	24	72.7	776	2	T31210	membrane protein t	628	23	69.7	84	2	E28840	IG kappa chain v r
556	24	72.7	801	2	PC6010	RNA helicase Gu -	629	23	69.7	98	2	JC2403	PMS8 homolog misa
557	24	72.7	802	2	AF1227	phenylalanyl-tRNA	630	23	69.7	105	2	E84331	hypothetical prote
558	24	72.7	802	2	AH1580	phenylalanyl-tRNA	631	23	69.7	105	2	S74781	UDGlucose 4-epime
559	24	72.7	808	2	F84038	phenylalanyl-tRNA	632	23	69.7	109	2	AC1411	hypothetical prote
560	24	72.7	809	1	QBEB34	BBLF4 protein - hu	633	23	69.7	109	2	AB1787	hypothetical prote
561	24	72.7	813	2	T12506	hypothetical prote	634	23	69.7	110	2	B64480	hypothetical prote
562	24	72.7	821	2	AD1507	probable secreted	635	23	69.7	117	2	AD2760	transcription regu
563	24	72.7	837	2	S54624	ROD1 protein - yea	636	23	69.7	117	2	B97541	arar-like protein
564	24	72.7	837	2	T19825	hypothetical prote	637	23	69.7	120	2	I39623	probable adenylate
565	24	72.7	838	2	S61250	DNA helicase/prima	638	23	69.7	122	2	AF1497	hypothetical prote
566	24	72.7	843	2	A40970	undulin 1 - human	639	23	69.7	124	2	AC2522	hypothetical prote
567	24	72.7	849	2	C90834	tail length tape m	640	23	69.7	128	2	A87510	hypothetical prote
568	24	72.7	853	1	TLBPHL	minor tail protein	641	23	69.7	131	2	C75510	hypothetical prote
569	24	72.7	869	2	AB2055	extracellular nucl	642	23	69.7	136	1	HSBY3	histone H3 - yeast
570	24	72.7	879	2	T41059	replication licens	643	23	69.7	136	1	HSVK3L	histone H3 - yeast
571	24	72.7	880	2	T42600	DNA helicase/prima	644	23	69.7	143	2	AI2057	hypothetical prote
572	24	72.7	881	1	WZBEE9	99.5K DNA helicase	645	23	69.7	148	2	T45328	hypothetical prote
573	24	72.7	882	2	F86164	hypothetical prote	646	23	69.7	150	2	G83581	probable transcrip
574	24	72.7	902	2	H87323	hypothetical prote	647	23	69.7	152	2	C71973	hypothetical prote
575	24	72.7	906	2	T18244	conserved hypothet	648	23	69.7	152	2	H97405	hypothetical prote
576	24	72.7	927	2	AH1369	transmembrane prot	649	23	69.7	152	2	AC3598	ebcC protein limpo
577	24	72.7	929	2	A44048	genome polyprotein	650	23	69.7	155	2	AH3277	immunoglobulin-bin
578	24	72.7	964	2	S13329	hypothetical prote	651	23	69.7	159	2	JC2401	PMS6 homolog misa
579	24	72.7	968	2	A37867	transcription fact	652	23	69.7	161	2	JC2402	PMS7 homolog misa
580	24	72.7	970	2	A41944	mitotic control pr	653	23	69.7	162	2	AB2156	hypothetical prote
581	24	72.7	971	2	A35697	transcription fact	654	23	69.7	163	2	G87331	hypothetical prote
582	24	72.7	971	2	T00268	hypothetical prote	655	23	69.7	164	2	AC0537	hypothetical prote
583	24	72.7	985	2	A96777	hypothetical prote	656	23	69.7	170	2	G87153	50S ribosomal prot
584	24	72.7	987	2	D97029	ribonucleotide red	657	23	69.7	170	2	F82437	probable rRNA meth
585	24	72.7	989	2	T15576	hypothetical prote	658	23	69.7	173	2	H83838	hypothetical prote
586	24	72.7	1001	2	S66704	hypothetical prote	659	23	69.7	175	2	H72538	hypothetical prote
587	24	72.7	1025	2	AE2243	hypothetical prote	660	23	69.7	175	2	A70824	hypothetical glyci
588	24	72.7	1033	2	S19247	cell adhesion prot	661	23	69.7	179	2	S49782	MSF1 protein homol
589	24	72.7	1066	2	S50237	TATA box-binding p	662	23	69.7	182	2	AG2180	ribosomal-protein-
590	24	72.7	1076	2	C70007	hypothetical prote	663	23	69.7	183	2	E75435	pyrimidine operon
591	24	72.7	1092	2	T45095	probable arabinosy	664	23	69.7	183	2	A10799	conserved hypothet
592	24	72.7	1094	2	T05472	hypothetical prote	665	23	69.7	186	2	JC2400	PMS5 homolog misa
593	24	72.7	1095	2	AC2059	hypothetical prote	666	23	69.7	189	2	AB3573	conserved hypothet
594	24	72.7	1125	2	H87644	tonB-dependent rec	667	23	69.7	192	2	E82192	conserved hypothet
595	24	72.7	1234	2	T00363	hypothetical prote	668	23	69.7	193	2	E87346	hypothetical prote
596	24	72.7	1242	2	SI4201	probable adenylate	669	23	69.7	194	2	T51927	membrane protein,
597	24	72.7	1321	2	E69129	protoporphyrin IX	670	23	69.7	196	2	B75124	probable imidazole
598	24	72.7	1336	2	T23110	hypothetical prote	671	23	69.7	198	2	E69779	transcription regu
599	24	72.7	1372	2	A34157	insulin receptor p	672	23	69.7	200	2	AB1898	urase accessory p
600	24	72.7	1382	1	INHUR	insulin receptor p	673	23	69.7	203	2	AB2871	urase accessory p
601	24	72.7	1383	2	A36080	insulin receptor p	674	23	69.7	204	2	F36950	urase accessory p
602	24	72.7	1450	2	AB4780	probable ABC trans	675	23	69.7	204	2	H90627	ureG protein (AB00
603	24	72.7	1608	2	A28182	hemolysin A - Serr	676	23	69.7	204	2	H90247	urase accessory p
604	24	72.7	1672	2	T46237	hypothetical prote	677	23	69.7	204	2	T12959	hypothetical prote
605	24	72.7	1731	2	AB3045	ice nucleation pro	678	23	69.7	205	2	T50714	urase accessory p
606	24	72.7	1731	2	B98241	hypothetical prote	679	23	69.7	206	2	S74933	urase accessory p
607	24	72.7	1781	1	A34374	DNA-directed RNA p	680	23	69.7	208	2	AF3538	uracil phosphoribo
608	24	72.7	2422	2	T18201	fatty-acid synthas	681	23	69.7	208	2	AC3458	urase accessory p
609	24	72.7	2703	2	H81193	hemagglutinin/hemo	682	23	69.7	209	2	AC0273	probable exported
610	24	72.7	3125	1	GNVSPP	genome polyprotein	683	23	69.7	211	2	T36373	hypothetical prote
611	24	72.7	3140	1	GNVSRA	genome polyprotein	684	23	69.7	211	2	JC5105	stromal cell deriv
612	24	72.7	3140	2	S47508	genome polyprotein	685	23	69.7	212	2	E75334	ribonuclease H11 -
613	24	72.7	3141	1	GNVSPD	genome polyprotein	686	23	69.7	213	2	E69443	conserved hypothet

hypothetical prote
CPY protein - midg
probable PPS prote
hypothetical prote
peptide synthetase
heat-shock protein
hypothetical prote
hypothetical glyci
hypothetical prote
IG kappa chain v r
gene 17 protein -
IG kappa chain v r
sex-specific germ
IG kappa chain v r
PMS8 homolog misa
hypothetical prote
UDGlucose 4-epime
hypothetical prote
hypothetical prote
hypothetical prote
transcription regu
arar-like protein
probable adenylate
hypothetical prote
hypothetical prote
histone H3 - yeast
histone H3 - yeast
hypothetical prote
probable transcrip
hypothetical prote
hypothetical prote
ebcC protein limpo
immunoglobulin-bin
PMS6 homolog misa
PMS7 homolog misa
hypothetical prote
hypothetical prote
hypothetical prote
50S ribosomal prot
probable rRNA meth
hypothetical prote
hypothetical prote
hypothetical glyci
MSF1 protein homol
ribosomal-protein-
pyrimidine operon
conserved hypothet
PMS5 homolog misa
conserved hypothet
hypothetical prote
membrane protein,
probable imidazole
transcription regu
urase accessory p
urase accessory p
urase accessory p
ureG protein (AB00
urase accessory p
hypothetical prote
urase accessory p
urase accessory p
uracil phosphoribo
urase accessory p
probable exported
hypothetical prote
stromal cell deriv
ribonuclease H11 -
conserved hypothet

687	23	69.7	216	2	C83879	transcription regu	760	23	69.7	282	2	T45307	methylenetetrahydr
688	23	69.7	220	2	H95893	probable amino aci	761	23	69.7	282	2	AC3356	acyl-[acyl-carrier
689	23	69.7	220	2	S43291	FLT3/FLK2 ligand (762	23	69.7	284	2	T41285	hypothetical prote
690	23	69.7	220	2	I58343	flt3 ligand isoform	763	23	69.7	286	2	C82694	ABC transporter su
691	23	69.7	221	2	S60596	transcription regu	764	23	69.7	287	2	C83899	3-hydroxybutyryl-C
692	23	69.7	221	2	I50538	ependymin - northe	765	23	69.7	287	2	E82239	heat shock protein
693	23	69.7	221	2	JC1250	ependymin Om-I pre	766	23	69.7	287	2	T36413	probable ABC-type
694	23	69.7	224	2	T10120	F420-dependent NAD	767	23	69.7	287	2	C29674	phycocyanin linker
695	23	69.7	225	2	D71912	hypothetical prote	768	23	69.7	287	2	C97546	hypothetical prote
696	23	69.7	225	2	S01073	hypothetical prote	769	23	69.7	287	2	AE2765	cytochrome-c oxida
697	23	69.7	226	2	G64599	conserved hypoteth	770	23	69.7	287	2	E95313	cytochrome-c oxida
698	23	69.7	229	2	T34977	ABC transporter At	771	23	69.7	288	2	AD2885	D-alanine aminotra
699	23	69.7	230	2	H64405	tetrahydromethanop	772	23	69.7	288	2	F83708	phosphonates trans
700	23	69.7	230	2	T28851	hypothetical prote	773	23	69.7	289	1	S39991	cytochrome-c oxida
701	23	69.7	231	2	B45239	DNA repair protein	774	23	69.7	289	2	F95344	FixPl Di-heme cyto
702	23	69.7	231	2	A54313	androgen-regulated	775	23	69.7	289	2	A87534	carboxylesterase f
703	23	69.7	233	2	B70897	hypothetical prote	776	23	69.7	290	2	T49631	probable Ni-bindin
704	23	69.7	233	2	A38163	hypothetical prote	777	23	69.7	291	2	D83293	heat shock protein
705	23	69.7	233	2	JH0372	42K surface glycop	778	23	69.7	291	2	AG0907	probable kinase [i
706	23	69.7	234	1	Z1ZM3	19K zein precursor	779	23	69.7	292	2	S35915	beta-lactamase (EC
707	23	69.7	235	2	S48924	hypothetical prote	780	23	69.7	292	2	T22631	hypothetical prote
708	23	69.7	238	2	AC2043	heme oxygenase lim	781	23	69.7	293	2	S44080	beta-lactamase (EC
709	23	69.7	238	2	T29082	probable transcrip	782	23	69.7	294	2	S39486	ribosomal protein
710	23	69.7	239	2	H83123	hypothetical prote	783	23	69.7	294	2	AD1910	hypothetical prote
711	23	69.7	241	2	S71473	endo-1,4-beta-xyla	784	23	69.7	294	2	H87570	3-phosphoserine ph
712	23	69.7	241	2	T12051	3-oxoacyl-[acyl-ca	785	23	69.7	295	2	B86320	3-phosphoserine ph
713	23	69.7	244	2	B70422	hypothetical prote	786	23	69.7	295	2	T51362	hypothetical prote
714	23	69.7	244	2	G90778	probable antirepre	787	23	69.7	296	2	T26723	ribosomal protein
715	23	69.7	246	2	A87457	3-oxoacyl-(acyl-ca	788	23	69.7	296	2	A33823	ribosomal protein
716	23	69.7	246	2	H72219	3-oxoacyl-(acyl ca	789	23	69.7	296	2	B33823	ribosomal protein
717	23	69.7	246	2	H84136	3-oxoacyl-(acyl-ca	790	23	69.7	297	1	RSRTL5	ribosomal protein
718	23	69.7	247	2	T12020	3-oxoacyl-[acyl-ca	791	23	69.7	297	2	JC1308	ribosomal protein
719	23	69.7	247	2	E75609	amino acid ABC tra	792	23	69.7	297	2	S55912	ribosomal protein
720	23	69.7	247	2	C85076	Probable athila tr	793	23	69.7	297	2	T12615	ribosomal protein
721	23	69.7	248	2	D72096	3-oxoacyl-(acyl-ca	794	23	69.7	297	2	H83058	hypothetical prote
722	23	69.7	248	2	B81695	3-oxoacyl-(acyl ca	795	23	69.7	300	2	A75599	myb-related protei
723	23	69.7	248	2	F81971	probable 3-oxoacyl	796	23	69.7	302	1	S31818	cysteine synthase
724	23	69.7	248	2	B81026	3-oxoacyl-(acyl-ca	797	23	69.7	302	2	T43792	hypothetical 30.8
725	23	69.7	248	2	F71538	probable oxoacyl (798	23	69.7	302	2	H65113	probable N-acetyl
726	23	69.7	248	2	H86527	oxoacyl carrier p	799	23	69.7	302	2	G91140	probable NAGC-like
727	23	69.7	250	2	D75343	conserved hypoteth	800	23	69.7	302	2	B85986	probable NAGC-like
728	23	69.7	252	2	JC2399	PMS4 homolog misma	801	23	69.7	303	2	T00969	conserved mitochon
729	23	69.7	252	2	A83376	secretion activato	802	23	69.7	304	1	B69449	conserved hypoteth
730	23	69.7	253	2	AC3390	secretion activato	803	23	69.7	304	2	T46730	citrate (pro-3S)-1
731	23	69.7	254	2	S61987	hypothetical prote	804	23	69.7	305	2	H82702	small conductance
732	23	69.7	254	2	T33280	hypothetical prote	805	23	69.7	305	2	T09166	probable peroxidase
733	23	69.7	255	2	T15987	hypothetical prote	806	23	69.7	309	2	A43865	cell wall-associat
734	23	69.7	256	2	JC2398	PMS3 homolog misma	807	23	69.7	311	2	AD0436	aspartate carbanoy
735	23	69.7	257	2	A86877	hypothetical prote	808	23	69.7	312	2	S13325	peroxidase (EC 1.1
736	23	69.7	260	2	S42806	gag-like polypepte	809	23	69.7	313	2	C95247	conserved hypoteth
737	23	69.7	262	2	A57391	TcSL-2 protein pre	810	23	69.7	313	2	H98111	conserved hypoteth
738	23	69.7	264	2	AH0574	ferric enterobacti	811	23	69.7	314	2	AE0144	hypothetical prote
739	23	69.7	264	2	T31521	hypothetical prote	812	23	69.7	315	2	S74513	hypothetical prote
740	23	69.7	264	2	AG3466	transcription regu	813	23	69.7	316	2	C81097	thioredoxin reduct
741	23	69.7	266	2	B84292	extragenic suppres	814	23	69.7	316	2	R81845	phospholipase C (E
742	23	69.7	266	2	H83008	N-formylglutamate	815	23	69.7	317	2	A37204	thiosphatidylinosit
743	23	69.7	266	2	T43453	hypothetical prote	816	23	69.7	317	2	AB1100	hypothetical prote
744	23	69.7	268	2	S73042	purine nucleoside	817	23	69.7	317	2	AH2053	ferrienterobactin-
745	23	69.7	268	2	B70842	probable deob prot	818	23	69.7	318	2	AD0575	hypothetical prote
746	23	69.7	269	2	G98144	hypothetical prote	819	23	69.7	318	2	G90707	hypothetical prote
747	23	69.7	272	1	S58290	invasion-associate	820	23	69.7	318	2	C85558	hypothetical prote
748	23	69.7	273	2	T01985	zinc-finger protei	821	23	69.7	318	2	JV0045	ferrienterobactin-
749	23	69.7	275	2	T02334	probable urase ac	822	23	69.7	319	2	A97661	D-alanine aminotra
750	23	69.7	275	2	T52333	urease accessory p	823	23	69.7	321	2	C90370	conserved hypoteth
751	23	69.7	277	2	A43783	homeotic protein N	824	23	69.7	321	2	D90353	conserved hypoteth
752	23	69.7	280	2	H70825	probable lpgp prot	825	23	69.7	325	2	H84308	cobalamin biosynth
753	23	69.7	280	2	I64007	hypothetical prote	826	23	69.7	326	2	S36705	UDP diphosphatase
754	23	69.7	281	1	WMECUE	sn-Glycerol-3-phos	827	23	69.7	328	2	A84167	UDP-glucose 4-epim
755	23	69.7	281	2	AF0993	sn-Glycerol-3-phos	828	23	69.7	329	2	S74227	cathepsin K (EC 3.
756	23	69.7	281	2	A86012	hypothetical prote	829	23	69.7	329	2	H64220	membrane protein m
757	23	69.7	281	2	A91166	hypothetical prote	830	23	69.7	329	2	H64143	hypothetical prote
758	23	69.7	281	2	A10461	sn-glycerol-3-phos	831	23	69.7	330	2	T03870	hypothetical prote
759	23	69.7	281	2	T34671	probable [2Fe-2S]	832	23	69.7	330	2	C69648	2-keto-3-deoxygluc

833	23	69.7	330	2	D87393	hypothetical prote	906	23	69.7	395	2	T50392	hypothetical coile
834	23	69.7	332	1	A27187	ubiquinol-cytochro	907	23	69.7	397	2	AC2110	hypothetical prote
835	23	69.7	332	2	C48835	kinin-like prote	908	23	69.7	399	2	C81932	probable porphyrin
836	23	69.7	334	2	S12742	transcription fact	909	23	69.7	399	2	D89797	hypothetical prote
837	23	69.7	334	2	H84138	two-component sens	910	23	69.7	400	2	A87700	threonine dehydrat
838	23	69.7	335	2	G72258	conserved hypothet	911	23	69.7	401	2	A96034	hypothetical membr
839	23	69.7	336	2	C69811	nitric-oxide synth	912	23	69.7	401	2	E70884	probable lipid-tra
840	23	69.7	338	2	A72544	probable agmatinas	913	23	69.7	403	2	T42560	envelope protein 1
841	23	69.7	339	2	A84095	transcription regu	914	23	69.7	405	2	S19355	hypothetical prote
842	23	69.7	340	2	H81742	major outer membra	915	23	69.7	406	2	G71404	probable ribonucle
843	23	69.7	342	2	JQ1952	hypothetical 37.7K	916	23	69.7	406	2	A87107	hypothetical prote
844	23	69.7	343	2	C69019	conserved hypothet	917	23	69.7	407	2	P92323	arginine deiminase
845	23	69.7	343	2	A13085	transcription regu	918	23	69.7	407	2	T40582	hypothetical prote
846	23	69.7	345	2	AG0366	thiosulfate-bindin	919	23	69.7	407	2	T50505	hypothetical prote
847	23	69.7	347	2	C87321	arginine N-succiny	920	23	69.7	408	2	B91129	hypothetical prote
848	23	69.7	348	2	AD0638	dihydroorotase (EC	921	23	69.7	408	2	JQ0614	yhaD protein - Eec
849	23	69.7	348	2	E84299	hypothetical prote	922	23	69.7	408	2	AC0961	probable ATP/GTP-B
850	23	69.7	349	2	T23626	probable alcohol d	923	23	69.7	409	2	S60988	hypothetical prote
851	23	69.7	350	2	T48275	hypothetical prote	924	23	69.7	409	2	S72438	phosphatidylserine
852	23	69.7	351	2	T23625	probable alcohol d	925	23	69.7	410	2	G81393	transmembrane tran
853	23	69.7	351	2	I64030	hypothetical prote	926	23	69.7	411	2	T21758	hypothetical prote
854	23	69.7	352	2	T22874	hypothetical prote	927	23	69.7	411	2	H84495	probable retroelem
855	23	69.7	354	2	A87242	probable secreted	928	23	69.7	411	2	G83353	conserved hypothet
856	23	69.7	355	2	S16047	nitrogenase cofact	929	23	69.7	414	2	B82408	hypothetical prote
857	23	69.7	356	2	AG0993	sn-Glycerol-3-phos	930	23	69.7	416	2	AG0125	N-acetyluramoyl-L
858	23	69.7	357	2	AH0461	sn-glycerol-3-phos	931	23	69.7	417	2	S77042	hypothetical prote
859	23	69.7	358	2	A96164	gepIA protein (Ari	932	23	69.7	417	2	AG0864	N-acetylmuramoyl-L
860	23	69.7	358	2	AF3123	sugar nucleotide e	933	23	69.7	418	2	P70940	hypothetical prote
861	23	69.7	358	2	S75659	gene At103 protein	934	23	69.7	419	2	T44308	glutamate dehydrog
862	23	69.7	358	2	B83808	hypothetical prote	935	23	69.7	419	2	AG1660	multidrug resistan
863	23	69.7	360	2	A87419	fatty acid/phospho	936	23	69.7	419	2	AH1288	multidrug resistan
864	23	69.7	360	2	H75375	hypothetical prote	937	23	69.7	420	1	JN0854	glutamate dehydrog
865	23	69.7	363	2	H98200	probable transcrip	938	23	69.7	420	2	A47410	glutamate dehydrog
866	23	69.7	363	2	E83970	UDP-N-acetylglucos	939	23	69.7	420	2	D75176	glutamate dehydrog
867	23	69.7	363	2	AC1329	peptidoglycan synt	940	23	69.7	420	2	I51692	glycogen synthase
868	23	69.7	363	2	AC1700	peptidoglycan synt	941	23	69.7	420	2	I51425	intracellular kina
869	23	69.7	363	2	AH2050	hypothetical prote	942	23	69.7	421	2	T30814	calmodulin-binding
870	23	69.7	365	2	F70988	hypothetical prote	943	23	69.7	422	2	C89953	isocitrate dehydrog
871	23	69.7	366	2	G83752	nitric oxide synth	944	23	69.7	423	2	AG0451	maltoporin (import
872	23	69.7	367	2	T24058	hypothetical prote	945	23	69.7	423	2	AB1862	hypothetical prote
873	23	69.7	369	1	QREUC	sn-Glycerol-3-phos	946	23	69.7	424	2	I60373	uKATP-1 - rat
874	23	69.7	369	2	H91165	hypothetical prote	947	23	69.7	425	2	E97172	flagellin (importe
875	23	69.7	369	2	H82404	hypothetical prote	948	23	69.7	426	2	A30212	alpha-factor recep
876	23	69.7	369	2	H86011	hypothetical prote	949	23	69.7	427	2	I51580	XPKH2 protein - Af
877	23	69.7	370	2	AH1485	fructose-specific	950	23	69.7	428	2	T06290	hypothetical prote
878	23	69.7	370	2	A11124	fructose-specific	951	23	69.7	429	1	T38146	dihydrofolate redu
879	23	69.7	375	1	DERZA2	alcohol dehydrogen	952	23	69.7	429	2	A84511	probable aspartate
880	23	69.7	375	2	JX0131	cellulase (EC 3.2.	953	23	69.7	430	2	D89063	conserved hypothet
881	23	69.7	377	2	B64428	formate hydrogenly	954	23	69.7	431	2	T36319	probable aminotran
882	23	69.7	378	2	H83019	probable glycosyl	955	23	69.7	431	2	S56228	alpha-factor recep
883	23	69.7	378	2	AD1188	membrane proteins	956	23	69.7	432	2	S62461	probable AAA-famil
884	23	69.7	378	2	AD1546	membrane protein h	957	23	69.7	433	1	ITHUC	alpha-1-anticymot
885	23	69.7	381	2	AH0152	acid phosphatase (958	23	69.7	435	2	H72379	ammonium transport
886	23	69.7	383	2	AF3503	benzoate membrane	959	23	69.7	436	2	A70923	hypothetical prote
887	23	69.7	384	2	F84675	hypothetical prote	960	23	69.7	437	2	AH0151	conserved hypothet
888	23	69.7	384	2	T32756	hypothetical prote	961	23	69.7	437	2	T39592	phosphatidylserine
889	23	69.7	384	2	T38544	probable exopolyp	962	23	69.7	437	2	S59831	END13 protein - ye
890	23	69.7	385	2	T04148	Pramp3 protein - r	963	23	69.7	438	2	T30600	probable transamin
891	23	69.7	386	1	JH0610	acid phosphatase (964	23	69.7	441	2	F86708	citrate (si)-synth
892	23	69.7	387	2	B59974	hypothetical prote	965	23	69.7	442	2	T03172	helicase homolog 0
893	23	69.7	387	2	T49598	hypothetical prote	966	23	69.7	444	2	AB1986	nitrogenase olybde
894	23	69.7	388	2	D69468	ammonium transport	967	23	69.7	444	2	S48696	probable ABC-trans
895	23	69.7	388	2	B65054	hypothetical prote	968	23	69.7	445	2	B87087	probable amidase [
896	23	69.7	389	2	C70926	hypothetical prote	969	23	69.7	447	2	B65064	probable amidase [
897	23	69.7	389	2	C82130	conserved hypothet	970	23	69.7	447	2	B81088	probable amidase [
898	23	69.7	389	2	A70172	methyl-accepting c	971	23	69.7	447	2	D85933	probable amidase Z
899	23	69.7	390	1	QBET9	protein UL33 - hum	972	23	69.7	448	2	B55548	crtn protein - Sta
900	23	69.7	391	2	E81172	oxygen-independent	973	23	69.7	449	2	A69643	serine proteinase
901	23	69.7	392	2	S37905	H+-exporting ATPas	974	23	69.7	450	2	AB1420	PTS cellobiose-spe
902	23	69.7	394	2	G82992	ubiH protein PA522	975	23	69.7	450	2	AC1795	probable dolichyl-
903	23	69.7	394	2	D81819	hypothetical prote	976	23	69.7	450	2	T38465	probable dolichyl-
904	23	69.7	394	2	H69412	D-arabino 3-hexulo	977	23	69.7	450	2	AD3117	polygalacturonase
905	23	69.7	394	2	D71379	probable sensory t	978	23	69.7	452	2	C72295	hypothetical prote

979 23 69.7 453 2 S76600
 980 23 69.7 453 2 A98170
 981 23 69.7 455 2 T43583
 982 23 69.7 459 2 G86278
 983 23 69.7 459 2 JC7931
 984 23 69.7 460 2 T30397
 985 23 69.7 461 2 T47782
 986 23 69.7 461 2 T31961
 987 23 69.7 462 1 COBY10
 988 23 69.7 464 2 A96987
 989 23 69.7 464 2 T50734
 990 23 69.7 464 2 H90279
 991 23 69.7 466 2 H90028
 992 23 69.7 467 2 A80082
 993 23 69.7 468 2 A94568
 994 23 69.7 470 2 A54232
 995 23 69.7 470 2 F96806
 996 23 69.7 470 2 C70554
 997 23 69.7 472 2 A70951
 998 23 69.7 474 2 A83022
 999 23 69.7 475 1 A69149
 1000 23 69.7 478 2 AF3288

ALIGNMENTS

RESULT 1
 T50966
 hypothetical protein B24P7.210 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C:Accession: T50966
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: T50966
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-321 <SCH>
 A:Cross-references: UNIPROT:Q9F3R4; UNIPARC:UPI000006C45D; EMBL:AL389890; GSPDB:GN00116;
 A:Experimental source: BAC clone B24P7; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B24P7.210
 A:Map position: 6
 A:Introns: 208/3

Query Match 90.9%; Score 30; DB 2; Length 321;
 Best Local Similarity 85.7%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 78 GATNLAS 84

RESULT 2
 S26333
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: S26333
 R;Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26333
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <STA>
 A:Cross-references: UNIPARC:UPI0000176D6D; EMBL:X59181; NID:G52312; PID:ig1334061
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F;6-80/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 40 GATNLAA 45

RESULT 3
 S24217
 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S24217
 R;Shimizu, T.; Iwasato, T.; Yamagishi, H.
 J. Exp. Med. 173, 1065-1072, 1991
 A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excis
 A:Reference number: S24214; MUID:91217618; PMID:1902500
 A:Accession: S24217
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-111 <SHI>
 A:Cross-references: UNIPARC:UPI000011378E; EMBL:X58219; NID:G53721; PIDN:CAA41183.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;21-95/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 55 GATNLAA 60

RESULT 4
 PT0358
 Ig kappa chain V region (7D2.G12) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
 C:Accession: PT0358
 R;Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
 J. Exp. Med. 173, 287-296, 1991
 A:Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
 A:Reference number: PT0352; MUID:91108325; PMID:1988536
 A:Accession: PT0358
 A:Molecule type: mRNA
 A:Residues: 1-114 <SHE>
 A:Cross-references: UNIPARC:UPI0000176B04
 A:Experimental source: strain BALB/c
 C:Comment: This protein is an anti-double-stranded DNA antibody.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;20-94/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 54 GATNLAA 59

RESULT 5
 AD0657
 hypothetical protein STY1360 [imported] - Salmonella enterica subsp. enterica serovar Ty.
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AD0657
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium DT104
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AD0657
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-166 <PAR>
 A;Cross-references: UNIPARC:UPI0000059F29; GB:AL513382; PIDN:CAD01629.1; PID:gl6502483;
 C;Genetics:
 A;Gene: STY1360

Query Match 87.9%; Score 29; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 27 GATNLAA 32

RESULT 6
 G70629
 thiamin biosynthesis protein thiG - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: G70629
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: G70629
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-252 <COL>
 A;Cross-references: UNIPROT:P96263; UNIPARC:UPI0000136DP5; GB:Z84724; GB:AL123456; NID:9
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: thiG
 C;Superfamily: thiamin biosynthesis protein thiG

Query Match 87.9%; Score 29; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 23 GATNLAA 28

RESULT 7
 AH2831
 ABC transporter, membrane spanning protein Atu2079 [imported] - *Agrobacterium tumefaciens*
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AH2831
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AH2831
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-309 <KUR>
 A;Cross-references: UNIPROT:Q8UDP2; UNIPARC:UPI00001646A4; GB:AE008688; PIDN:AAL43070.1
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu2079
 A;Map position: circular chromosome
 C;Superfamily: hypothetical protein ydeD

Query Match 87.9%; Score 29; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 247 GATNLAA 252

RESULT 8
 D97609
 hypothetical protein AGR_C_3767 [imported] - *Agrobacterium tumefaciens* (strain C58, Cera)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004
 C;Accession: D97609
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C58
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: D97609
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-329 <KUR>
 A;Cross-references: UNIPROT:Q8UDP2; UNIPARC:UPI00000D1D92; GB:AE007869; PIDN:AAK87829.1
 C;Genetics:
 A;Gene: AGR_C_3767
 A;Map position: circular chromosome
 C;Superfamily: hypothetical protein ydeD

Query Match 87.9%; Score 29; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
 |||||
 Db 267 GATNLAA 272

RESULT 9
 A49413
 perillipin A - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49413
 R;Greenberg, A.S.; Egan, J.J.; Wek, S.A.; Moos Jr., M.C.; Londres, C.; Kimmel, A.R.; Proc. Natl. Acad. Sci. U.S.A. 90, 12035-12039, 1993
 A;Title: Isolation of cDNAs for perillipins A and B: sequence and expression of lipid droplet-associated protein perillipin A
 A;Reference number: A49413; MUID:94089764; PMID:7505452
 A;Accession: A49413
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 1-517 <GRE>
 A;Cross-references: UNIPROT:P43884; UNIPARC:UPI0000131BF7; GB:IL26043; NID:9457373; PIDN:
 A;Experimental source: adipocytes
 A;Note: sequence extracted from NCBI backbone (NCBIN:141050, NCBIP:141051)

Query Match 87.9%; Score 29; DB 2; Length 517;
 Best Local Similarity 85.7%; Pred. No. 67;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 64 GASNLAA 70

RESULT 10
D70863
hypothetical protein RV2264c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70863
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A: Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: D70863
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-592 <COL>
A: Cross-references: UNIPROT: O53538; UNIPARC: UPI00000D11AF; GB: AL021925; GB: AL123456; NID
A: Experimental source: strain H37RV
C: Genetics:
A: Gene: RV2264c

Query Match 87.9%; Score 29; DB 2; Length 592;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 14 GVTNLAA 20

RESULT 11
AI3336
potassium/proton antiporter rosb [imported] - Brucella melitensis (strain 16M)
C: Species: Brucella melitensis
C: Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C: Accession: AI3336
R: DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A: Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A: Reference number: AD3252; PMID: 11756688
A: Accession: AI3336
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-619 <KUR>
A: Cross-references: UNIPROT: Q8YHW7; UNIPARC: UPI0000057D91; GB: AE008917; PIDN: AAL51860.1;
A: Experimental source: strain 16M
C: Genetics:
A: Gene: BMEI0679
A: Map position: I
C: Superfamily: glutathione-regulated potassium efflux system protein kefc

Query Match 87.9%; Score 29; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 408 GATNLTA 414

RESULT 12
A41055
ecdysone receptor - fruit fly (Drosophila melanogaster)
C: Species: Drosophila melanogaster
C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C: Accession: A41055
R: Koelle, M.R.; Talbot, W.S.; Segraves, W.A.; Bender, M.T.; Cherbas, P.; Hogness, D.S. Cell 67, 59-77, 1991
A: Title: The Drosophila Ecr gene encodes an ecdysone receptor, a new member of the steroid

A: Reference number: A41055; MUID: 92005697; PMID: 1913820
A: Accession: A41055
A: Molecule type: mRNA
A: Residues: 1-878 <KOE>
A: Cross-references: UNIPROT: P34021; UNIPARC: UPI00001246E6; GB: M74078; NID: g157317; PIDN:
A: Note: the authors also sequenced genomic exon boundaries
C: Comment: mRNA for this receptor is heavily expressed at the end of the third larval in
C: Genetics:
A: Gene: FlyBase: Ecr
A: Cross-references: FlyBase: FBgn0000546
A: Introns: 227/1; 398/3; 446/3; 497/3
C: Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; z1;
P: 262-572/domain: erba transforming protein homology <ERBA>
Query Match 87.9%; Score 29; DB 2; Length 878;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 116 GATNLGA 122

RESULT 13
T26660
hypothetical protein Y38E10A.j - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C: Accession: T26660
R: Wallis, J.
submitted to the EMBL Data Library, September 1999
A: Reference number: Z20252
A: Accession: T26660
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-237 <WIL>
A: Cross-references: UNIPROT: Q9NAK1; UNIPARC: UPI0000079396; EMBL: AL110484; PIDN: CAB54401.
A: Experimental source: clone Y38E10A
C: Genetics:
A: Gene: CESP: Y38E10A.j
A: Introns: 62/2; 104/1; 131/1; 171/2; 212/3
Query Match 84.8%; Score 28; DB 2; Length 237;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 71 GATNTAA 77

RESULT 14
B97742
hypothetical protein RC0338 [imported] - Rickettsia conorii (strain Malish 7)
C: Species: Rickettsia conorii
C: Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C: Accession: B97742
R: Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A: Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A: Reference number: A97700; MUID: 21442074; PMID: 11557893
A: Accession: B97742
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-356 <KUR>
A: Cross-references: UNIPROT: Q92IT2; UNIPARC: UPI000000CBD56; GB: AE006914; PIDN: AAL02876.1;
C: Genetics:
A: Gene: RC0338

Query Match 84.8%; Score 28; DB 2; Length 356;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 || || || || ||
 Db 157 GAANLAA 163

RESULT 15

G90266
 na(+)/H(+) antiporter [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: G90266
 R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
 arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: G90266
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <KUR>
 A:Cross-references: UNIPROT:Q97208; UNIPARC:UPI0000064372; GB:AE006641; NID:gl3814326; F
 C:Genetics:
 A:Gene: SSO1138

Query Match 84.8%; Score 28; DB 2; Length 391;
 Best Local Similarity 85.7%; Pred. No. 87;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 || || || || ||
 Db 134 GATSLAA 140

RESULT 16

D70726
 probable gabT - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: D70726
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Jandreem, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: D70726
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-449 <COL>
 A:Cross-references: UNIPROT:Q50632; UNIPARC:UPI000012APBD; GB:Z77724; GB:AL123456; NID:G
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: gabT
 C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 84.8%; Score 28; DB 2; Length 449;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 || || || || ||
 Db 219 GANLAA 225

RESULT 17

T29988
 hypothetical protein R105.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29988
 R:Le, T.T.; Gattung, S.

submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid R105.
 A:Reference number: Z20716
 A:Accession: T29988
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-508 <LET>
 A:Cross-references: UNIPROT:Q21897; UNIPARC:UPI0000078978; EMBL:US3334; PIDN:AAA96168.1
 A:Experimental source: strain Bristol N2; clone R105
 C:Genetics:
 A:Gene: CESP:R105.1
 A:Map position: 4
 A:Introns: 69/1; 142/1; 164/1; 235/1; 268/3; 359/1; 435/2; 466/3

Query Match 84.8%; Score 28; DB 2; Length 508;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 || || || || ||
 Db 211 GITNLAA 217

RESULT 18

S74633
 high affinity sulfate transporter - Synechocystis sp. (strain PCC 6803)
 N:Alternate names: hypothetical protein slr1776
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S74633
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud.
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S74633
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-566 <KAN>
 A:Cross-references: UNIPROT:P72770; UNIPARC:UPI00000D3478; EMBL:D50900; GB:AB001339; NFI
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: integral membrane protein HP0228

Query Match 84.8%; Score 28; DB 2; Length 566;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
 || || || || ||
 Db 292 GAANLAA 298

RESULT 19

AE0076
 probable membrane protein YPO0618 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AE0076
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AE0076
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-589 <KUR>
 A:Cross-references: UNIPROT:Q82193; UNIPARC:UPI00000CD6F8; GB:AL590842; PIDN:CAC89472.1.

C:Genetics:
A:Gene: YP00618

Query Match 84.8%; Score 28; DB 2; Length 589;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||
Db 461 GLTNLAA 467

RESULT 20

G95299
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95299
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 99, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: G95299
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-809 <KUR>
A:Cross-references: UNIPROT:Q922Z5; UNIPARC:UPI00000CB057; GB:AE006469; PIDN:AAK64961.1;
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA0579
A:Genome: plasmid

Query Match 84.8%; Score 28; DB 2; Length 809;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||
Db 705 GAVNLAA 711

RESULT 21

D86974
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 04-Aug-2003
C:Accession: D86974
R:Coile, S.T.; Eigilmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.N.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D86974
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-950 <STO>
A:Cross-references: UNIPARC:UPI000000C6CD7; GB:AL450380; NID:gl3092734; PIDN:CAC30032.1;
C:Genetics:
A:Gene: adi
C:Superfamily: ornithine/lysine/arginine decarboxylase

Query Match 84.8%; Score 28; DB 2; Length 950;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||
Db 75 GAANLAA 81

RESULT 22

D70835
C:Species: Mycobacterium tuberculosis (strain H37RV)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70835
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70835
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-957 <COL>
A:Cross-references: UNIPROT:P56877; UNIPARC:UPI00000139568; GB:AL021930; GB:AL123456; NID
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0278c
C:Superfamily: elastin

Query Match 84.8%; Score 28; DB 2; Length 957;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||
Db 583 GATNTAA 589

RESULT 23

G81186
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81186
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81186
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1161 <YET>
A:Cross-references: UNIPROT:Q9K0P1; UNIPARC:UPI000000C44EC; GB:AE002410; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0545
C:Superfamily: chromosome segregation protein SMC1

Query Match 84.8%; Score 28; DB 2; Length 1161;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||
Db 958 GAVNLAA 964

A;Contents: annotation
C;Genetics:
A;Gene: XF1084

Query Match 81.8%; Score 27; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
| | | | |
Db 19 ATNLAA 24

RESULT 29
S70219
sipA protein - Salmonella typhi (fragment)
C;Species: Salmonella typhi
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S70219
R;Hermant, D.; Menard, R.; Arricau, N.; Parsot, C.; Popoff, M.Y.
Mol. Microbiol. 17, 781-789, 1995
A;Title: Functional conservation of the Salmonella and Shigella effectors of entry into
A;Reference number: S70215; MUID:96111497; PMID:8801431
A;Accession: S70219
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-235 <HER>
A;Cross-references: UNIPROT:Q56137; UNIPARC:UPI00000B0BD8; EMBL:X82670; NID:g1009001; PI
C;Genetics:
A;Gene: sipA

Query Match 81.8%; Score 27; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
| | | | |
Db 24 ATNLAA 29

RESULT 30
T20248
hypothetical protein C55A1.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T20248
R;Lloyd, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19242
A;Accession: T20248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-274 <WIL>
A;Cross-references: UNIPARC:UPI0000060F7E; EMBL:Z81489; PIDN:CAB04007.1; GSPDB:GN00023;
A;Experimental source: clone C55A1
C;Genetics:
A;Gene: CESP:C55A1.10
A;Map position: 5
A;Introns: 102/3; 141/3; 177/3; 216/1
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 81.8%; Score 27; DB 2; Length 274;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
| | | | |
Db 218 GATNLA 223

RESULT 31
G72625
probable ribosomal protein S6, modification protein APE1463 - Aeropyrum pernix (strain M

C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72625
R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72625
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <KAW>
A;Cross-references: UNIPROT:Q9YBY7; UNIPARC:UPI000005DF6A; DDBJ:AP000061; NID:g5104821;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1463
C;Superfamily: ribosomal protein S6-glutamic acid ligase

Query Match 81.8%; Score 27; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
| | | | |
Db 203 ATNLAA 208

RESULT 32
F87146
methyl mycolic acid synthase 1 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87146
R;Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F87146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <STO>
A;Cross-references: UNIPROT:Q9CBK4; UNIPARC:UPI00000C6504; GB:AL450380; NID:g13093569; P
C;Genetics:
A;Gene: mmaA1

Query Match 81.8%; Score 27; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
| | | | |
Db 239 ATNLAA 244

RESULT 33
S72880
hypothetical protein B2126_F3_142 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72880
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2126.
A;Reference number: S72585
A;Accession: S72880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <SMI>
A;Cross-references: UNIPROT:Q49806; UNIPARC:UPI00000B7A2B; EMBL:U00017; NID:g466994; PID
C;Genetics:

A;Start codon: GTG

Query Match 81.8%; Score 27; DB 2; Length 298;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||
Db 182 GATTLAA 188

RESULT 34

C84331
homoserine kinase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Aug-2004
C;Accession: C84331
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <STO>
A;Cross-references: UNIPROT:Q9HP55; UNIPARC:UPI000012DE1C; GB:AE004437; NID:G10581249; F
C;Genetics:
A;Gene: thrB
C;Superfamily: Homoserine kinase

Query Match 81.8%; Score 27; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||
Db 288 GATTLAA 294

RESULT 35

AG2977
hypothetical protein Atu3424 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG2977
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
sner, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG2977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <KUR>
A;Cross-references: UNIPROT:Q8UAF0; UNIPARC:UPI0000164801; GB:AE008689; PIDN:AA144237.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:

A;Gene: Atu3424

A;Map position: linear chromosome
Query Match 81.8%; Score 27; DB 2; Length 316;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||
Db 201 GAENLAA 207

RESULT 36

E98305
hypothetical protein AGR_L_2799 [imported] - Agrobacterium tumefaciens (strain C58, Cer
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E98305
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E98305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q8UAF0; UNIPARC:UPI000002D1D0; GB:AE007870; PIDN:AAK89967.1;
C;Genetics:
A;Gene: AGR_L_2799
A;Map position: linear chromosome

Query Match 81.8%; Score 27; DB 2; Length 319;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||
Db 204 GAENLAA 210

RESULT 37

S42680
phosphoserine transaminase (EC 2.6.1.52) - Yeast (Saccharomyces cerevisiae)
N;Alternate names: 3-phosphoserine aminotransferase; protein O4731; protein YOR184W
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42680; S67076; S55926; S71156
R;Belhumeur, P.; Fortin, N.; Clark, M.W.
Yeast 10, 385-389, 1994
A;Title: A gene from Saccharomyces cerevisiae which codes for a protein with significant
A;Reference number: S42680; MUID:94287715; PMID:8017107
A;Accession: S42680
A;Molecule type: DNA
A;Residues: 1-395 <BEL>
A;Cross-references: UNIPROT:P33330; UNIPARC:UPI000013588A; EMBL:L20917; NID:G311152; PI
R;Hughes, B.; Pohl, T.M. Sequence Database, July 1996
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67076
A;Molecule type: DNA
A;Residues: 1-395 <HUG>

A;Cross-references: UNIPARC:UPI000013588A; EMBL:Z75092; NID:G1420442; PIDN:CAA99393.1; F
A;Experimental source: strain S288C
R;Melcher, K.; Rose, M.; Kuenzler, M.; Braus, G.H.; Entian, K.D.
Curr. Genet. 27, 501-508, 1995
A;Title: Molecular analysis of the yeast SER1 gene encoding 3-phosphoserine aminotransfe
A;Reference number: S55926; MUID:96031704; PMID:7553933
A;Accession: S55926
A;Molecule type: DNA
A;Residues: 1-395 <MEI>
A;Cross-references: UNIPARC:UPI000013588A; EMBL:U19714
R;Melcher, K.
submitted to the EMBL Data Library, January 1995
A;Reference number: S71156
A;Accession: S71156
A;Molecule type: DNA
A;Residues: 1-257, 'LH', 260-395 <MEW>
A;Cross-references: UNIPARC:UPI00001689FD; EMBL:U19714; NID:G640052; PIDN:AAA85703.1; PI
C;Genetics:
A;Gene: SGD:SER1; SERC
A;Cross-references: SGD:S0005710; MIPS:YOR184W
A;Map position: 15R

C:Function:

A:Description: aminotransferase
 A:Pathway: serine biosynthesis
 C:Superfamily: phosphoserine aminotransferase
 C:Keywords: aminotransferase; serine biosynthesis

Query Match 81.8%; Score 27; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
 |||||
 Db 88 ATNLAA 93

RESULT 38

A:Residues: 1-407 <AND>
 A:Cross-references: UNIPROT:Q9ZCQ0; UNIPARC:UPI00000D37DB; GB:AJ2325272; GB:AJ2325269; NID: A71673
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 R:Accession: A71673
 R:Anderson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alemark, U.
 Nature 396, 133-140, 1998
 A:Title: The Genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: A71673
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-407 <AND>
 A:Cross-references: UNIPROT:Q9ZCQ0; UNIPARC:UPI00000D37DB; GB:AJ2325272; GB:AJ2325269; NID: A71673
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: rhlE; RP669
 C:Superfamily: translation initiation factor eIF-4A

Query Match 81.8%; Score 27; DB 2; Length 407;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 201 GATNKAA 207

RESULT 39

D97827
 ATP-dependent RNA helicase RhlE [imported] - Rickettsia conorii (strain Malish 7)
 C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: D97827
 R:Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R.
 Science 293, 2093-2098, 2001
 A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A37700; MUID:21442074; PMID:11557893
 A:Accession: D97827
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-414 <KUR>
 A:Cross-references: UNIPROT:Q92GV2; UNIPARC:UPI00000CBF89; GB:AE006914; PIDN:AAL03558.1;
 C:Genetics:
 A:Gene: rhlE
 C:Superfamily: translation initiation factor eIF-4A

Query Match 81.8%; Score 27; DB 2; Length 414;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 205 GATNKAA 211

RESULT 40

A90465

hypothetical protein SSO2869 [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
 C:Accession: A90465
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: A90465
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-432 <KUR>
 A:Cross-references: UNIPROT:Q97UX2; UNIPARC:UPI0000068811; GB:AE006641; NID:gl3816230; P
 C:Genetics:
 C:Superfamily: malic enzyme

Query Match 81.8%; Score 27; DB 2; Length 432;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 195 GASNLAA 201

RESULT 41

S34472
 MFH-1 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
 C:Accession: S34472
 R:Miura, N.; Wanaka, A.; Tohyama, M.; Tanaka, K.
 FEBS Lett. 326, 171-176, 1993
 A:Title: MFH-1, a new member of the fork head domain family, is expressed in developing
 A:Reference number: S34472; MUID:93314779; PMID:8325367
 A:Accession: S34472
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <MIU>
 A:Cross-references: UNIPROT:Q61850; UNIPARC:UPI0000170C66; GB:S63607; NID:g386637; PIDN:
 C:Genetics:
 A:Gene: MFH-1
 F:38-129/Domain: fork head DNA-binding domain homology <FHD>

Query Match 81.8%; Score 27; DB 2; Length 461;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 336 GATNLAA 342

RESULT 42

D69417
 Probable thymidine phosphorylase (EC 2.4.2.4) 1 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 05-Oct-2004
 C:Accession: D69417
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.;
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69417
 A:Status: nucleic acid sequence not shown; translation not shown

Query Match 81.8%; Score 27; DB 2; Length 414;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 |||||
 Db 205 GATNKAA 211

A:Molecule type: DNA
A:Residues: 1-504 <KLE>
A:Cross-references: UNIPARC:UPI000056D77; GB:AE001011; GB:AE000782; NID:g2689334; PIDN:
C:Superfamily: thymidine phosphorylase/pyrimidine-nucleoside phosphorylase
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 81.8%; Score 27; DB 1; Length 504;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 6
||| |||
236 GATNLAA 241

Db

RESULT 43
C71008
probable proline permease - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: C71008
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71008
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-537 <KAN>
A:Cross-references: UNIPROT:O59086; UNIPARC:UPI00006685F; GB:AP000006; NID:g3236133; PI
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1361

Query Match 81.8%; Score 27; DB 2; Length 537;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||
229 GATGLAA 235

Db

RESULT 44
S76051
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S76051
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76051
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-557 <KAN>
A:Cross-references: UNIPROT:Q55534; UNIPARC:UPI00000D35A5; EMBL:D63999; GB:AB001339; NID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG
C:Superfamily: sfuB protein

Query Match 81.8%; Score 27; DB 1; Length 557;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7

Db 249 GATQLAA 255
||| |||

RESULT 45

G83189
probable sodium/hydrogen antiporter PA3660 [imported] - *Pseudomonas aeruginosa* (strain F
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83189
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83189
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-581 <STO>
A:Cross-references: UNIPROT:Q9HXX9; UNIPARC:UPI00000C5AA7; GB:AE004785; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3660
C:Superfamily: hypothetical protein yvgP

Query Match 81.8%; Score 27; DB 2; Length 581;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||

Db 43 GATRLAA 49
||| |||

RESULT 46

D71493
probable DNA helicase - *Chlamydia trachomatis* (serotype D, strain UW3/Cx)
C:Species: *Chlamydia trachomatis*
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: D71493
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A>Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trac*
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: D71493
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-634 <ARN>
A:Cross-references: UNIPROT:O84614; UNIPARC:UPI00000D3370; GB:AE001331; GB:AE001273; NID
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: uvrD
C:Superfamily: helicase II

Query Match 81.8%; Score 27; DB 2; Length 634;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||| |||

Db 413 GATTLAA 419
||| |||

RESULT 47

D97708
cell division protein ftsh (SC 3.4.24.-) [imported] - *Rickettsia conorii* (strain Malish
C:Species: *Rickettsia conorii*
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: D97708
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A>Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.

A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97708
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-637 <KUR>
A;Cross-references: UNIPROT:Q92JJ9; UNIPARC:UPI000012ACD9; GB:AE006914; PIDN:AAL02606.1;
C;Genetics:
C;Superfamily: cell division protein ftsh; Ftsh/SEC18/CDC48-type ATP-binding domain homology
C;Keywords: hydrolase; metalloproteinase

Query Match 81.8%; Score 27; DB 2; Length 637;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
|||||
Db 498 GATNIA 503

RESULT 48
C71712
cell division protein ftsh (ftsh) RP043 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: C71712
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: C71712
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-637 <AND>
A;Cross-references: UNIPROT:Q9ZBA2; UNIPARC:UPI000012ACDA; GB:AJ235270; GB:AJ235269; NID:
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: ftsh; RP043
C;Superfamily: cell division protein ftsh; Ftsh/SEC18/CDC48-type ATP-binding domain homology

Query Match 81.8%; Score 27; DB 2; Length 637;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
|||||
Db 498 GATNIA 503

RESULT 49
T16136
hypothetical protein F22D3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16136
R;Leimbach, D.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F22D3.
A;Reference number: Z18465
A;Accession: T16136
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-644 <LEI>
A;Cross-references: UNIPARC:UPI000017B91E; EMBL:U28993; NID:g861377; PID:g861383; PIDN:A
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F22D3.1
A;Introns: 13/2; 117/2; 151/3; 257/1; 419/2; 499/3; 528/3

Query Match 81.8%; Score 27; DB 2; Length 644;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 637 GATKLAA 643

RESULT 50
AF0850
hypothetical protein sipA [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0850
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-685 <PAR>
A;Cross-references: UNIPARC:UPI000005A369; GB:AL513382; PIDN:CAD05989.1; PID:g16503960;
C;Genetics:
A;Gene: sipA

Query Match 81.8%; Score 27; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATNLAA 7
|||||
Db 24 ATNLAA 29

Search completed: May 11, 2006, 16:37:25
Job time : 34.3279 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 64.7213 Seconds
(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-5

Perfect score: 33

Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	555	2 Q73YE4_MYCPA	Q73ye4 mycobacteri
2	33	100.0	1070	2 Q858F5_9CAUD	Q858f5 enterobacte
3	31	93.9	473	2 Q8KN42_SPHCR	Q8kn42 sphingobium
4	31	93.9	535	2 Q4K428_PSEF5	Q4k428 pseudomonas
5	30	90.9	321	2 Q9P3R4_NEUCR	Q9p3r4 neuropept
6	30	90.9	606	2 Q7NCF3_GLOVI	Q7ncf3 gloebacter
7	30	90.9	666	2 Q4MIJ6_BACCE	Q4mij6 bacillus ce
8	30	90.9	666	2 Q72XPI_BACCL	Q72xpi bacillus ce
9	30	90.9	983	2 Q88X96_LACPL	Q88x96 lactobacill
10	29	87.9	136	2 Q80UR2_MESAU	Q80ur2 mesocricetu
11	29	87.9	166	2 Q51T81_MAGGR	Q51t81 magnaporthe
12	29	87.9	166	2 Q69MC6_ORYSA	Q69mc6 oryza sativ
13	29	87.9	166	2 Q8Z7C0_SALTI	Q8z7c0 salmonella
14	29	87.9	252	1 THIG_MYCBO	P59948 mycobacteri
15	29	87.9	252	1 THIG_MYCBO	P59948 mycobacteri
16	29	87.9	258	2 Q32397_ERYLO	Q32397 erythroba
17	29	87.9	268	2 Q7Q7D3_ANGA	Q7q7d3 anopheles g
18	29	87.9	281	2 Q6S9M2_LEPBO	Q6s9m2 leptospira
19	29	87.9	282	2 Q87GM7_VIBPA	Q87gm7 vibrio para
20	29	87.9	294	2 Q5P193_SALPA	Q5p193 salmonella
21	29	87.9	303	2 Q5V2S2_HALMA	Q5v2s2 haloarcula
22	29	87.9	309	2 Q965J1_CAEEL	Q965j1 caenorhabdi
23	29	87.9	309	2 Q8UDP2_AGRF5	Q8udp2 agrobacteri
24	29	87.9	329	2 Q7CX55_AGRF5	Q7cxs5 agrobacteri
25	29	87.9	341	2 Q89J14_BRAJA	Q89j14 bradyrhizob
26	29	87.9	416	2 Q54SD6_DICDI	Q54sd6 dictyosteli
27	29	87.9	419	2 Q53TX6_HUMAN	Q53tx6 homo sapien
28	29	87.9	460	2 Q8SYJ6_DROME	Q8syj6 drosophila
29	29	87.9	462	2 Q88AS9_TETHA	Q88as9 tetragenoco
30	29	87.9	477	2 Q5Z9X3_ORYSA	Q5z9x3 oryza sativ
31	29	87.9	481	2 Q6Y9B4_BORHE	Q6y9b4 borrelia he

32	29	87.9	517	1 PLIN_MOUSE	Q8cgn5 mus musculu
33	29	87.9	517	1 PLIN_MOUSE	P43884 rattus norv
34	29	87.9	517	2 Q8COF5_MOUSE	Q8cof5 mus musculu
35	29	87.9	525	2 Q4V9U2_MOUSE	Q4v9u2 mus musculu
36	29	87.9	525	2 Q414F3_GIBZE	Q414f3 gibberella
37	29	87.9	529	2 Q4HWP9_GIBZE	Q4hwp9 gibberella
38	29	87.9	530	2 Q8IXS8_HUMAN	Q8ixs8 homo sapien
39	29	87.9	530	2 Q5R977_PONPY	Q5r977 pongo pygma
40	29	87.9	530	2 Q8C729_MOUSE	Q8c729 mus musculu
41	29	87.9	530	2 Q6NV64_MOUSE	Q6nv64 mus musculu
42	29	87.9	563	2 Q4JSM7_CORJK	Q4jsm7 corynebacte
43	29	87.9	592	2 Q7VEM4_MYCBO	Q7vem4 mycobacteri
44	29	87.9	592	2 Q53538_MYCTU	Q53538 mycobacteri
45	29	87.9	619	2 Q57CH5_BRUAB	Q57ch5 brucella ab
46	29	87.9	619	2 Q8FZ25_BRUSU	Q8fz25 brucella su
47	29	87.9	619	2 Q8YHW7_BRUME	Q8yhw7 brucella me
48	29	87.9	745	2 Q6GV25_WHEAT	Q6gv25 triticum ae
49	29	87.9	828	2 Q6CAV1_YARLI	Q6cay1 yarrowia li
50	29	87.9	845	2 Q7QS38_GIALA	Q7qes38 giardia lam
51	29	87.9	878	1 ECR_DROME	P34021 drosophila
52	29	87.9	878	2 Q6AWL4_DROME	Q6awl4 drosophila
53	29	87.9	1002	2 Q8GM78_HABIN	Q8gm78 haemophilus
54	29	87.9	1210	2 Q6NHB1_CORDI	Q6nhb1 corynebacte
55	28	84.8	150	2 Q7QNT7_GIALA	Q7qnt7 giardia lam
56	28	84.8	152	2 Q9D4Z2_MOUSE	Q9d4z2 mus musculu
57	28	84.8	165	2 Q89VNO_BRAJA	Q89vn0 bradyrhizob
58	28	84.8	181	2 Q4UNN6_XANCP	Q4unn6 xanthomonas
59	28	84.8	181	2 Q8P365_XANCP	Q8p365 xanthomonas
60	28	84.8	195	2 Q7PYX5_ANGOA	Q7pyx5 anopheles g
61	28	84.8	197	2 Q7R0J0_GIALA	Q7r0j0 giardia lam
62	28	84.8	200	2 Q7QZL9_GIALA	Q7qz19 giardia lam
63	28	84.8	209	2 Q7Q033_ANGOA	Q7q033 anopheles g
64	28	84.8	217	2 Q6FM83_CANGA	Q6fm83 candida gla
65	28	84.8	233	2 Q4FQH0_9GAMM	Q4fqh0 psychrobact
66	28	84.8	235	2 Q4LY14_9BURK	Q4ly14 burkholderi
67	28	84.8	237	2 Q9NAK1_CABEL	Q9nak1 caenorhabdi
68	28	84.8	243	2 Q89BW6_BRAJA	Q89bw6 bradyrhizob
69	28	84.8	247	2 Q5NW77_AZOSE	Q5nw77 azotarcus sp
70	28	84.8	270	2 Q82X95_NITEU	Q82x95 nitrosomona
71	28	84.8	289	2 Q84UQ4_ORYSA	Q84uq4 oryza sativ
72	28	84.8	318	2 Q742U8_MYCPA	Q742u8 mycobacteri
73	28	84.8	333	2 Q4NK16_9MICC	Q4nk16 arthrobacte
74	28	84.8	347	2 Q52624_ORYSA	Q52624 oryza sativ
75	28	84.8	356	2 Q921T2_RICCN	Q921t2 rickettsia
76	28	84.8	386	2 Q974C4_SULTO	Q974c4 sulfolobus
77	28	84.8	391	2 Q97Z08_SULTO	Q97z08 sulfolobus
78	28	84.8	391	2 Q95JV8_WACPA	Q95jv8 macaca fasc
79	28	84.8	399	2 Q9SVY9_DROME	Q9svy9 drosophila
80	28	84.8	406	2 Q5QYJ2_IDILO	Q5qyj2 idiomarina
81	28	84.8	409	2 Q5LLQ7_SILPO	Q5llq7 silicibacte
82	28	84.8	414	2 Q6PY21_OSTTA	Q6py21 ostreococcu
83	28	84.8	420	2 Q89P20_BRAJA	Q89p20 bradyrhizob
84	28	84.8	437	2 Q4TV53_CORJK	Q4tv53 corynebacte
85	28	84.8	449	1 GABT_MYCBO	P63505 m 4-aminobu
86	28	84.8	449	1 GABT_MYCBO	P63504 m 4-aminobu
87	28	84.8	462	2 Q4LQ80_9BURK	Q4lq80 burkholderi
88	28	84.8	488	2 Q7MJ13_VIBVY	Q7mj13 vibrio vuln
89	28	84.8	497	2 Q51IB6_MAGGR	Q51ib6 magnaporthe
90	28	84.8	508	2 Q21897_CAEEL	Q21897 caenorhabdi
91	28	84.8	516	2 Q73U03_MYCPA	Q73u03 mycobacteri
92	28	84.8	529	2 Q63TRS_BURPS	Q63trs burkholderi
93	28	84.8	551	2 Q88W76_LACPL	Q88w76 lactobacill
94	28	84.8	566	2 P72770_SYNY3	P72770 synechocyst
95	28	84.8	573	2 Q82GM7_STRAW	Q82gm7 streptomyce
96	28	84.8	579	2 Q5APB2_CANAL	Q5apb2 candida alb
97	28	84.8	587	2 Q82MY9_STRAW	Q82my9 streptomyce
98	28	84.8	589	2 Q8Z193_YERPE	Q8z193 yersinia pe
99	28	84.8	602	2 Q6MG12_NEUCR	Q6mg12 neuropept
100	28	84.8	608	2 Q7SDR2_NEUCR	Q7sdr2 neuropept
101	28	84.8	612	2 Q6APJ5_DESPS	Q6apj5 deaulfotale
102	28	84.8	633	2 Q8CKF3_YERPE	Q8ckf3 yersinia pe
103	28	84.8	633	2 Q665S4_YERPS	Q665s4 yersinia ps
104	28	84.8	663	2 Q60AH8_METCA	Q60ah8 methylococc

105	28	84.8	665	1	BFSPI_HUMAN	Q12934	homo sapien	178	27	81.8	286	2	Q9YBY7	aeropyrum p
106	28	84.8	671	2	Q6BQNO_DEBHA	Q6bqno	debaromyce	179	27	81.8	286	2	Q9CBK4	mycobacteri
107	28	84.8	731	2	Q76MGA_MOUSE	Q76mga	mus musculus	180	27	81.8	291	2	Q8FFP9	ecoliarichia
108	28	84.8	790	2	Q7WJEZ_BORBR	Q7wjez	mus musculus	181	27	81.8	291	2	Q83BE7	coxiella bu
109	28	84.8	809	2	Q92Z25_RHIME	Q92z25	rhizobium m	182	27	81.8	292	2	Q6ASP6	propionibac
110	28	84.8	833	2	Q4J0N9_AZOTB	Q4j0n9	azotobacter	183	27	81.8	293	2	Q61JF0	caenorhabdi
111	28	84.8	868	2	Q7U2D8_MYCBO	Q7u2d8	mycobacteri	184	27	81.8	296	2	Q7VV42	borderella
112	28	84.8	891	2	Q84TH7_ARATH	Q84th7	arabidopsi	185	27	81.8	298	2	Q49806	mycobacteri
113	28	84.8	896	2	Q9FV29_ARATH	Q9fv29	arabidopsi	186	27	81.8	301	1	Q9HSP5	halobacteri
114	28	84.8	896	2	Q9FV30_ARATH	Q9fv30	arabidopsi	187	27	81.8	302	2	Q4NZV4	anaeromyxob
115	28	84.8	907	2	Q9SS78_ARATH	Q9ss78	arabidopsi	188	27	81.8	302	2	Q63VK0	burkholderi
116	28	84.8	914	2	Q581B5_9TRYP	Q581b5	trypanosoma	189	27	81.8	302	2	Q7WBE0	borderella
117	28	84.8	950	2	Q9CCR8_MYCLE	Q9ccr8	mycobacteri	190	27	81.8	302	2	Q7WMM0	borderella
118	28	84.8	957	1	PG03_MYCTU	P56877	mycobacteri	191	27	81.8	305	2	Q9ZX68	mycobacteri
119	28	84.8	1149	2	Q5FDN2_ACIAD	Q5fdn2	acinobact	192	27	81.8	308	2	Q7W0U4	borderella
120	28	84.8	1161	2	Q5F6V2_NEIGI	Q5f6v2	neisseria g	193	27	81.8	308	2	Q7WNG2	borderella
121	28	84.8	1161	2	Q9K0P1_NEIMB	Q9k0p1	neisseria m	194	27	81.8	312	2	Q7QXP9	giardia lam
122	28	84.8	1161	2	Q9JVR9_NEIMA	Q9jvr9	neisseria m	195	27	81.8	314	2	Q522V3	magnaporth
123	28	84.8	1162	2	Q7NR76_CHRVO	Q7nr76	chromobacte	196	27	81.8	315	2	Q82ID2	streptomyce
124	28	84.8	1167	2	Q841X1_CAMPE	Q841x1	campylobact	197	27	81.8	316	2	Q8UAF0	agrobacteri
125	28	84.8	1248	2	Q4P321_USTMA	Q4p321	ustilago ma	198	27	81.8	319	2	Q7CSF6	agrobacteri
126	28	84.8	1307	2	Q4FUX1_9GAMM	Q4fux1	psychrobact	199	27	81.8	321	2	Q41LO4	gibberella
127	28	84.8	1355	2	Q701A0_9RICK	Q701a0	rickettsia	200	27	81.8	322	2	Q7UQR5	rhodopirell
128	28	84.8	1578	2	Q687B5_9RICK	Q687b5	rickettsia	201	27	81.8	333	2	Q9U3G2	caenorhabdi
129	28	84.8	1578	2	Q687B6_9RICK	Q687b6	rickettsia	202	27	81.8	335	2	Q7VUX9	borderella
130	28	84.8	1585	2	Q687B8_9RICK	Q687b8	rickettsia	203	27	81.8	340	2	Q7F9M1	oryza sativ
131	28	84.8	1587	2	Q687B7_9RICK	Q687b7	rickettsia	204	27	81.8	347	2	Q57P26	salmonella
132	28	84.8	2656	2	Q4QDAO_LEIMA	Q4qdao	leishmania	205	27	81.8	353	2	Q4UMJ3	rickettsia
133	28	84.8	4876	2	Q9VH01_DROME	Q9vh01	drosophila	206	27	81.8	354	2	Q4FKG6	trypanosoma
134	28	84.8	5017	2	Q6GBX6_POLCB	Q6gbx6	polylangium	207	27	81.8	356	2	Q8H3Y5	oryza sativ
135	27	81.8	103	2	Q63LW7_BURPS	Q63lw7	burkholderi	208	27	81.8	363	2	Q82BN3	streptomyce
136	27	81.8	113	2	Q6UVN5_9CHLO	Q6uvt5	pseudodocli	209	27	81.8	363	2	Q6NV41	brachydanio
137	27	81.8	124	1	VSP1_BFLIH	Q4765	lactococcus	210	27	81.8	367	2	Q5YNS4	nocardia fa
138	27	81.8	135	2	Q60EQ5_ORYSA	Q60eq5	oryza sativ	211	27	81.8	371	2	Q41NA2	gibberella
139	27	81.8	142	2	Q855M2_9CAUD	Q855m2	mycobacteri	212	27	81.8	373	2	Q6LEG6	lactococcus
140	27	81.8	155	2	Q98CH1_RHILO	Q98ch1	rhizobium l	213	27	81.8	373	2	Q8FQ05	corynebacte
141	27	81.8	166	2	Q6XCA0_9CHON	Q6xca0	mustelus m	214	27	81.8	376	2	Q8NR32	corynebacte
142	27	81.8	176	2	Q4LS29_9BURK	Q4lsz9	burkholderi	215	27	81.8	377	2	Q4NPM3	anaeromyxob
143	27	81.8	192	1	A16_ANOGA	Q93118	anopheles g	216	27	81.8	378	2	Q6NHQ9	corynebacte
144	27	81.8	192	2	Q606X7_METCA	Q606x7	methylococc	217	27	81.8	379	2	Q62H96	burkholderi
145	27	81.8	192	2	Q92551_STRCO	Q92551	streptomyce	218	27	81.8	379	2	Q63QY7	burkholderi
146	27	81.8	207	2	Q680Y8_ARATH	Q680y8	arabidopsi	219	27	81.8	381	2	Q7U7J0	synechococc
147	27	81.8	210	2	Q4V0A3_XANCP	Q4v0a3	xanthomonas	220	27	81.8	387	1	DXR_WOLPM	wolbachia p
148	27	81.8	210	2	Q8PE09_XANCP	Q8pe09	xanthomonas	221	27	81.8	388	2	Q6FWR6	candida gla
149	27	81.8	210	2	Q8PQK7_XANAC	Q8pqk7	xanthomonas	222	27	81.8	393	2	Q742P7	mycobacteri
150	27	81.8	213	2	Q87ED2_XYLFT	Q87ed2	xyliella fas	223	27	81.8	395	1	SERC_YEAST	saccharomyc
151	27	81.8	213	2	Q9PEB4_XYLFA	Q9pee4	xyliella fas	224	27	81.8	399	2	Q6D928	erwinia car
152	27	81.8	215	2	Q7NTY0_CHRVO	Q7nty0	chromobacte	225	27	81.8	400	2	Q9KHK9	streptomyce
153	27	81.8	224	2	Q5HX36_GLUOX	Q5hx36	gluconobact	226	27	81.8	405	2	Q94K46	arabidopsi
154	27	81.8	225	2	Q5V0G4_HALMA	Q5v0g4	haloarcula	227	27	81.8	407	2	Q9ZCQ0	rickettsia
155	27	81.8	233	2	Q41MW7_GIBZE	Q41mn7	gibberella	228	27	81.8	407	2	Q68W70	rickettsia
156	27	81.8	238	1	Y1180_MYCMO	Q6kih2	mycoplasma	229	27	81.8	408	1	HISZ_SYNEL	synechococc
157	27	81.8	242	2	Q4ZLG3_PSESY	Q4zlg3	pseudomonas	230	27	81.8	408	2	Q4JUL4	corynebacte
158	27	81.8	244	1	TRUA_GEOSL	P60350	geobacter s	231	27	81.8	408	2	Q5FU38	gluconobact
159	27	81.8	249	2	Q6FW56_CANGA	Q6fw56	candida gla	232	27	81.8	410	2	Q7P9E5	rickettsia
160	27	81.8	253	2	Q88F23_PSEPK	Q88f23	pseudomonas	233	27	81.8	413	2	Q55QN7	cryne
161	27	81.8	254	2	Q6G195_BARQU	Q6g195	bartonella	234	27	81.8	414	2	Q92GV2	rickettsia
162	27	81.8	256	2	Q5P4P7_AZOSE	Q5p4p7	azocarcus sp	235	27	81.8	423	2	Q7S2M1	neurospora
163	27	81.8	259	2	Q8PEP7_XANAC	Q8pep7	xanthomonas	236	27	81.8	431	2	Q95Q16	caenorhabdi
164	27	81.8	266	2	Q5GU68_XANOR	Q5gu68	xanthomonas	237	27	81.8	432	2	Q7UXK2	sulfolobus
165	27	81.8	269	2	Q4KGX3_PSEF5	Q4kgx3	pseudomonas	238	27	81.8	437	2	Q7MG47	vibrio vuln
166	27	81.8	269	2	Q63N28_BURPS	Q63nz8	burkholderi	239	27	81.8	439	2	Q82NH7	streptomyce
167	27	81.8	269	2	Q82A18_BURMA	Q82a18	burkholderi	240	27	81.8	442	2	Q8WZJ5	aspergillus
168	27	81.8	271	2	Q4UNT7_XANCP	Q4unt7	xanthomonas	241	27	81.8	445	2	Q6AEY3	leifsonia x
169	27	81.8	271	2	Q8P3B5_XANCP	Q8p3b5	xanthomonas	242	27	81.8	445	2	Q7UMF3	rhodopirell
170	27	81.8	275	2	Q4M0H2_9BURK	Q4m0h2	burkholderi	243	27	81.8	462	2	Q5YZ15	nocardia fa
171	27	81.8	277	2	Q7VYN6_BORPE	Q7vyn6	borderella	244	27	81.8	465	1	PHYA_ASPFU	aspergillus
172	27	81.8	277	2	Q7W6G9_BORPA	Q7w6g9	borderella	245	27	81.8	465	2	Q5XNQ9	aspfufu
173	27	81.8	277	2	Q7W1E0_BORBR	Q7wie0	borderella	246	27	81.8	465	2	Q4WPA8	aspergillus
174	27	81.8	278	1	CHIS_NOCSP	P48846	nocardioide	247	27	81.8	467	1	NORM_RHIME	rhizobium m
175	27	81.8	278	2	Q8B1L2_MOUSE	Q8b1l2	mus musculoid	248	27	81.8	474	2	Q8Y308	raiconia s
176	27	81.8	279	2	Q62IR6_BURMA	Q62ir6	burkholderi	249	27	81.8	475	2	Q7XBS1	oryza sativ
177	27	81.8	282	2	Q856N4_9CAUD	Q856n4	mycobacteri	250	27	81.8	475	2	Q9FRN5	oryza sativ

251	27	81.8	480	2	Q63S65_BURPS	Q63a65	burkholderi	324	27	81.8	1088	2	Q9C7C9_ARATH	Q9c7c9	arabidopsis
252	27	81.8	480	2	Q62LV9_BURMA	Q62lv9	burkholderi	325	27	81.8	1088	2	Q62N46_BURMA	Q62n46	burkholderi
253	27	81.8	488	2	Q63VY9_BURPS	Q63vy9	burkholderi	326	27	81.8	1094	2	Q63XB5_BURPS	Q63xb5	burkholderi
254	27	81.8	488	2	Q62IE8_BURMA	Q62ie8	burkholderi	327	27	81.8	1145	2	Q72AJ7_SHEON	Q72aj7	shewanella
255	27	81.8	494	1	FOX2C_MOUSE	Q61850	mus musculus	328	27	81.8	1152	2	Q5QUJ9_IDILO	Q5quj9	idiomarina
256	27	81.8	494	2	Q8C694_MOUSE	Q8c694	mus musculus	329	27	81.8	1162	2	Q4ZVP8_PSESY	Q4zvf8	pseudomonas
257	27	81.8	495	2	Q4ISRA_AZOVI	Q4isra4	azotobacter	330	27	81.8	1162	2	Q4J2D2_AZOVI	Q4j2d2	azotobacter
258	27	81.8	504	1	TYPHI_ARCFU	Q28928	archaeoglob	331	27	81.8	1162	2	Q4KPH3_PSEPM	Q4kfh3	pseudomonas
259	27	81.8	506	1	TYPHI_METAC	Q8101	methanosarc	332	27	81.8	1162	2	Q87YV4_PSESM	Q87yv4	pseudomonas
260	27	81.8	507	1	TYPHI_METWA	Q8Q0P9	methanosarc	333	27	81.8	1162	2	Q88F23_PSEPK	Q88f23	pseudomonas
261	27	81.8	512	2	Q7M8U4_WOLSU	Q7m8u4	wolinella s	334	27	81.8	1164	2	Q5WT11_LSGPL	Q5wt11	legionella
262	27	81.8	523	2	Q56WR7_ARATH	Q56wr7	arabidopsis	335	27	81.8	1164	2	Q5X1S0_LSGPL	Q5x1s0	legionella
263	27	81.8	537	2	Q5S086_PYRHO	Q5s086	pyrococcus	336	27	81.8	1164	2	Q5ZS99_LSGPH	Q5zsr99	legionella
264	27	81.8	544	2	Q6H2K3_MYCVN	Q6h2k3	mycobacteri	337	27	81.8	1246	2	Q12276_YEAST	Q12276	saccharomyc
265	27	81.8	544	2	Q88PG8_PSEPK	Q88pg8	pseudomonas	338	27	81.8	1261	2	Q5B1N2_EMENI	Q5b1n2	aspergillus
266	27	81.8	546	2	Q5YEQ9_CHLS6	Q5yeq9	chlorarachn	339	27	81.8	1269	2	Q6CEW6_YARLI	Q6cew6	yarrowia li
267	27	81.8	547	2	Q5TX35_ANOGA	Q5tx35	anopheles g	340	27	81.8	1309	2	Q9MAJ8_ARATH	Q9maj8	arabidopsis
268	27	81.8	549	1	ACTP_PHOLL	Q7na72	photorhabdu	341	27	81.8	1318	2	Q81824_ARATH	Q81824	arabidopsis
269	27	81.8	552	2	Q8TGL9_DROME	Q8tgl9	drosophila	342	27	81.8	1363	2	Q4LIW7_9BURK	Q4liw7	burkholderi
270	27	81.8	553	2	Q8MTC6_DROME	Q8mtc6	drosophila	343	27	81.8	1377	1	TSH_ECOLI	Q47692	escherichia
271	27	81.8	557	2	Q55534_SYNY3	Q55534	synecocyst	344	27	81.8	1377	2	Q88093_ECOLI	Q88093	escherichia
272	27	81.8	558	2	Q9U1J2_DROME	Q9u1j2	drosophila	345	27	81.8	1402	2	Q9SLL4_ARATH	Q9sll4	arabidopsis
273	27	81.8	558	2	Q8T4C6_DROME	Q8t4c6	drosophila	346	27	81.8	1418	2	Q9RRW1_DEIRA	Q9rrw1	deinococcus
274	27	81.8	562	2	Q6NDL8_RHOPA	Q6ndl8	rhodospseudo	347	27	81.8	1433	2	Q23588_ARATH	Q23588	arabidopsis
275	27	81.8	581	2	Q9Z9H1_PSEAE	Q9z9h1	pseudomonas	348	27	81.8	1436	2	Q9LF16_ARATH	Q9lf16	arabidopsis
276	27	81.8	581	2	Q9HXX9_PSEAE	Q9hxx9	pseudomonas	349	27	81.8	1467	2	Q9RY75_DEIRA	Q9ry75	deinococcus
277	27	81.8	588	2	Q62F76_BURMA	Q62f76	burkholderi	350	27	81.8	1467	2	Q72F24_DESVH	Q72f24	desulfovibr
278	27	81.8	589	2	Q4LP98_9BURK	Q4lp98	burkholderi	351	27	81.8	1577	2	Q5K116_CRYNE	Q5k116	cryptococcu
279	27	81.8	590	2	Q63XPI_BURPS	Q63xpi1	burkholderi	352	27	81.8	1577	2	Q55UC9_CRYNE	Q55uc9	cryptococcu
280	27	81.8	593	2	Q9N5J5_CAEEL	Q9n5j5	caenorhabdi	353	27	81.8	1609	2	Q9C1C5_TRIVE	Q9c1c5	trichoderma
281	27	81.8	596	2	Q9V8M4_DROME	Q9v8m4	drosophila	354	27	81.8	1677	2	Q4FX65_LEIMA	Q4fx65	leishmania
282	27	81.8	598	2	Q9GTC9_CAEEL	Q9gtc9	caenorhabdi	355	27	81.8	1686	2	Q7RZB6_NEUCR	Q7rzb6	neurospora
283	27	81.8	600	2	Q86BE1_DROME	Q86be1	drosophila	356	27	81.8	1709	2	Q7R4H3_GIALA	Q7r4h3	giardia lam
284	27	81.8	601	2	Q8DID6_SYNEL	Q8did6	synecococc	357	27	81.8	1800	2	Q72GB8_THET2	Q72gb8	thermus the
285	27	81.8	603	2	Q7KRC4_DROME	Q7krc4	drosophila	358	27	81.8	1806	2	Q62N48_BURMA	Q62n48	burkholderi
286	27	81.8	619	2	Q59R29_CANAL	Q59r29	candida alb	359	27	81.8	1824	2	Q4QPD2_LEIMA	Q4qpd2	leishmania
287	27	81.8	619	2	Q4UI87_THEAN	Q4ui87	theileria a	360	27	81.8	2001	2	Q6KCM6_ECOLI	Q6kcm6	escherichia
288	27	81.8	621	2	Q61ZG7_CAEBR	Q61zg7	caenorhabdi	361	27	81.8	2031	2	Q63XB6_BURPS	Q63xb6	burkholderi
289	27	81.8	631	2	Q7PTC2_ANOGA	Q7ptc2	anopheles g	362	27	81.8	2049	2	Q6W5P8_9ACTO	Q6w5p8	streptomyce
290	27	81.8	634	2	Q84614_CHLTR	Q84614	chlamydia t	363	27	81.8	2202	2	Q5SM68_THET8	Q5sm68	thermus the
291	27	81.8	635	2	Q4UN68_RICFE	Q4un68	rickettsia	364	27	81.8	2619	2	Q56K16_MICAE	Q56k16	microcystis
292	27	81.8	637	1	FTSH_RICCN	Q92fj9	rickettsia	365	27	81.8	2631	2	Q9RN85_MICAE	Q9rn85	microcystis
293	27	81.8	637	1	FTSH_RICPR	Q9zeaz	rickettsia	366	27	81.8	2632	2	Q9FDR8_MICAE	Q9fdr8	microcystis
294	27	81.8	637	2	Q7PAH4_RICSI	Q7pah4	rickettsia	367	27	81.8	3705	2	Q9F285_YERPE	Q9f285	yersinia pe
295	27	81.8	637	2	Q68XR9_RICTY	Q68xr9	rickettsia	368	27	81.8	3705	2	Q8ZHA1_YERPE	Q8zha1	yersinia pe
296	27	81.8	638	2	Q6COC9_KLULA	Q6cqc9	kluveromyc	369	27	81.8	3710	2	Q74QP7_YERPE	Q74qp7	yersinia pe
297	27	81.8	641	1	HK38_CAEEL	Q19720	caenorhabdi	370	27	81.8	3710	2	Q8CZU2_YERPE	Q8czu2	yersinia pe
298	27	81.8	645	2	Q8FP48_COREP	Q8fp48	caenorhabdi	371	27	81.8	4042	2	Q8KT64_PHOLU	Q8kt64	photorhabdu
299	27	81.8	648	2	Q8KE27_CHLTE	Q8ke27	corynebacte	372	27	81.8	4080	2	Q56PC8_TRIVE	Q56pc8	trichoderma
300	27	81.8	678	2	Q9VJS8_DROME	Q9vj8	drosophila	373	27	81.8	4224	2	Q57VL9_9TRYP	Q57vl9	trypanosoma
301	27	81.8	685	1	SIPA_SALEN	Q8vqb5	salmonella	374	27	81.8	20925	2	Q8NJX1_TRIVE	Q8njx1	trichoderma
302	27	81.8	685	1	SIPA_SALTI	P74849	salmonella	375	26	78.8	58	2	Q67V08_ORYSA	Q67vq8	oryza sativ
303	27	81.8	685	1	SIPA_SALTY	Q56027	salmonella	376	26	78.8	63	2	Q4HR59_CAMUP	Q4hr59	campylobact
304	27	81.8	685	2	Q57KP2_SALCH	Q57kp2	salmonella	377	26	78.8	85	2	Q5ZDU4_ORYSA	Q5zdu4	oryza sativ
305	27	81.8	685	2	Q5PEC3_SALPA	Q5pec3	salmonella	378	26	78.8	92	2	Q5FFJ7_EHRRG	Q5ffj7	ehrlichia r
306	27	81.8	694	2	Q6NSN0_RHOPA	Q6nsn0	rhodospseudo	379	26	78.8	92	2	Q5HBV9_EHRRG	Q5hbv9	ehrlichia r
307	27	81.8	700	1	PURL_HALSA	Q9hr49	halobacteri	380	26	78.8	97	2	Q4J415_AZOVI	Q4j415	azotobacter
308	27	81.8	748	2	Q9A3V7_CAUCR	Q9a3v7	caulobacter	381	26	78.8	98	2	Q7X9G2_USEUD	Q7x9g2	papaver rho
309	27	81.8	755	2	Q97VH4_SULSO	Q97vh4	sulfolobus	382	26	78.8	98	2	Q7X9G3_USEUD	Q7x9g3	papaver rho
310	27	81.8	784	2	Q9FLG1_ARATH	Q9flg1	arabidopsis	383	26	78.8	103	2	Q8RVP9_AMARE	Q8rvp9	amaranthus
311	27	81.8	784	2	Q7KT93_DROME	Q7kt93	drosophila	384	26	78.8	103	2	Q8RVQ0_AWARE	Q8rvq0	amaranthus
312	27	81.8	824	2	Q5NR17_ZYMOU	Q5nr17	zymomonas m	385	26	78.8	104	2	Q8GRH5_AMABL	Q8grh5	amaranthus
313	27	81.8	830	2	Q6UYJ1_9CAUD	Q6uyj1	burkholderi	386	26	78.8	104	2	Q8H244_AMABL	Q8h244	amaranthus
314	27	81.8	875	2	Q5BGV0_EMENI	Q5bgv0	aspergillus	387	26	78.8	106	2	Q49810_BRATO	Q49810	brassica to
315	27	81.8	886	2	Q5B5B5_EMENI	Q5b5b5	aspergillus	388	26	78.8	107	2	Q4J6B0_AMAHY	Q4j6b0	amaranthus
316	27	81.8	933	2	Q4FKH6_9TRYP	Q4fkh6	trypanosoma	389	26	78.8	116	2	Q8KUN6_SNP7	Q8kun6	synecococc
317	27	81.8	987	2	Q8U877_AGRTS	Q8u877	agrobacteri	390	26	78.8	143	2	Q94UY5_ARATH	Q94uy5	arabidopsis
318	27	81.8	1010	2	Q4HBIA_9DEIO	Q4hb14	deinococcus	391	26	78.8	148	2	Q8RUX2_BRACM	Q8rux2	brassica ca
319	27	81.8	1013	2	Q93ZS5_ARATH	Q93zes5	arabidopsis	392	26	78.8	148	2	Q6L8H5_9ASTR	Q6l8h5	codonopsis
320	27	81.8	1013	2	Q9LKZ3_ARATH	Q9lkz3	arabidopsis	393	26	78.8	149	1	NDK1_ARATH	P39207	arabidopsis
321	27	81.8	1021	2	Q9LH8E_ARATH	Q9lhb8	arabidopsis	394	26	78.8	149	2	Q83AX7_COXBU	Q83ax7	coxiella bu
322	27	81.8	1072	2	Q4NFW7_9MICC	Q4nfw7	arthrobacte	395	26	78.8	152	2	Q8UJ05_9CAUD	Q8uj05	burkholderi
323	27	81.8	1073	2	Q5YU47_NOCPA	Q5yu47	nocardia fa	396	26	78.8	156	2	Q4H5S3_9DSIO	Q4h5s3	deinococcus

397	26	78.8	173	2	Q6UKC5_9CAUD	Q6ukc5_burkholderi	470	26	78.8	320	2	Q6S9K4_9LEPT	Q6s9k4_leptospira
398	26	78.8	173	2	Q6HAN3_9CAUD	Q6han3_burkholderi	471	26	78.8	320	2	Q6S9L0_LEPIN	Q6s9l0_leptospira
399	26	78.8	173	2	Q66ML7_LEPIN	Q66ml7_leptospira	472	26	78.8	320	2	Q6S9L2_LEPIN	Q6s9l2_leptospira
400	26	78.8	177	2	Q4H673_DEINOCOCCUS	Q4h673_deinococcus	473	26	78.8	320	2	Q6KHS4_LEPIN	Q6khs4_leptospira
401	26	78.8	182	2	Q46379_CHLTR	Q46379_chlamydia t	474	26	78.8	320	2	Q72TP4_LEPIC	Q72tp4_leptospira
402	26	78.8	186	2	Q6MHF3_BDEBA	Q6mfh3_bdellovibri	475	26	78.8	326	1	SCRR_PDEPE	P43472_pediococcus
403	26	78.8	191	2	Q5GSL3_WOLTR	Q5gsl3_wolbachia s	476	26	78.8	326	2	Q88ZV7_LACPL	Q88zv7_lactobacill
404	26	78.8	192	1	Y1045_WOLPM	Q73gb4_wolbachia p	477	26	78.8	327	1	Y3208_DESVH	Q72665_desulfovibr
405	26	78.8	201	2	QANP86_9DELT	Qanp86_aeaeomyxob	478	26	78.8	327	2	Q4KJW4_PSEFV	Q4kjw4_pseudomonas
406	26	78.8	207	1	3MGH_LISNF	Q92d89_listeria in	479	26	78.8	331	2	Q4IJR2_GIBZE	Q4ijr2_gibberella
407	26	78.8	207	1	3MGH_LISNF	Q72ln6_listeria mo	480	26	78.8	334	2	Q6C092_YARLI	Q6c092_yarrowia li
408	26	78.8	207	1	3MGH_LISNF	P8621_listeria mo	481	26	78.8	334	2	Q22297_CABEL	Q22297_caenorhabdi
409	26	78.8	210	2	Q4LX87_9BURK	Q4lx87_burkholderi	482	26	78.8	335	2	Q5XH52_XENLA	Q5xh52_xenopus lae
410	26	78.8	212	2	Q85033_9RALS	Q85033_ralstonia s	483	26	78.8	337	2	Q8F1J7_LEPIN	Q8f1j7_leptospira
411	26	78.8	233	2	Q8FD07_ACID	Q8fd07_acinetobact	484	26	78.8	340	2	Q5AXQ8_EMENI	Q5axq8_aspergillus s
412	26	78.8	236	2	Q8RTZ6_DEIRA	Q8rtz6_deinococcus	485	26	78.8	341	2	Q923X3_9RALS	Q923x3_ralstonia s
413	26	78.8	238	2	Q98804_RHILO	Q98804_rhizobium l	486	26	78.8	343	2	P72467_STRLI	P72467_streptomyce
414	26	78.8	240	2	Q94RR3_USEUD	Q94rr3_papaver rho	487	26	78.8	343	2	Q9RD85_STROO	Q9rd85_streptomyce
415	26	78.8	240	2	Q94RR4_USEUD	Q94rr4_papaver rho	488	26	78.8	344	2	Q6DT50_ARALY	Q6dt50_arabidopsis
416	26	78.8	241	2	Q84PPI_BIDPI	Q84ppi_bidens pilo	489	26	78.8	345	2	Q6RCI5_USTWA	Q6rci5_ustilago ma
417	26	78.8	242	2	Q84PPO_9CARY	Q84ppo_amaranthus	490	26	78.8	355	2	Q5YX31_NOCFA	Q5yx31_nocardia fa
418	26	78.8	242	2	Q8S600_ORISA	Q8s600_oryza sativ	491	26	78.8	358	2	Q5YYI3_NOCFA	Q5yyi3_nocardia fa
419	26	78.8	252	2	Q8LPPE_9MAPO	Q8lppe_amaranthus	492	26	78.8	360	2	Q8GDP1_HELMO	Q8gdp1_heliobacill
420	26	78.8	252	2	Q8XQF9_RALSO	Q8xqf9_ralstonia s	493	26	78.8	362	2	Q5PP51_ARATH	Q5pp51_arabidopsis
421	26	78.8	254	2	Q8PGJ0_XANAC	Q8pgj0_xanthomonas s	494	26	78.8	364	2	Q805B4_XENLA	Q805b4_xenopus lae
422	26	78.8	261	2	Q5DYI3_ECOLI	Q5dyi3_escherichia	495	26	78.8	366	2	Q5Z8X1_ORYSA	Q5z8x1_oryza sativ
423	26	78.8	261	2	Q5JYI6_BACLD	Q5jy16_bacillus li	496	26	78.8	367	2	Q9HQT2_HALSA	Q9hqt2_halobacteri
424	26	78.8	266	2	Q8UBX4_AGR15	Q8ubx4_agrobacteri	497	26	78.8	369	2	Q5PC49_SALFA	Q5pc49_salmonella
425	26	78.8	278	2	Q65X47_ORYSA	Q65x47_oryza sativ	498	26	78.8	369	2	Q8Z2J6_SALTI	Q8z2j6_salmonella
426	26	78.8	280	2	Q6S9K9_LEPIN	Q6s9k9_leptospira	499	26	78.8	373	2	Q8KBM8_CHLTE	Q8kbm8_chlorobium
427	26	78.8	281	2	Q6S9K2_9LEPT	Q6s9k2_leptospira	500	26	78.8	384	2	Q5V0G0_HALWA	Q5v0g0_haloarcula
428	26	78.8	281	2	Q6S9K3_9LEPT	Q6s9k3_leptospira	501	26	78.8	402	2	Q836Z9_ENTFA	Q836z9_enterococcu
429	26	78.8	281	2	Q6S9L5_LEPIN	Q6s9l5_leptospira	502	26	78.8	408	2	Q5WKB7_BACSK	Q5wkb7_bacillus cl
430	26	78.8	281	2	Q6S9I7_LEPIN	Q6s9i7_leptospira	503	26	78.8	412	2	Q42558_ARATH	Q42558_arabidopsis
431	26	78.8	282	2	Q6S9K5_9LEPT	Q6s9k5_leptospira	504	26	78.8	412	2	Q9SJE2_ARATH	Q9sj2_arabidopsis
432	26	78.8	283	2	Q5H4V6_XANOR	Q5h4v6_xanthomonas	505	26	78.8	412	2	Q42562_ARATH	Q42562_arabidopsis
433	26	78.8	284	2	QANP99_9DELT	Qanp99_aeaeomyxob	506	26	78.8	415	1	LEU2_PYRAE	LEU2_pyrobaculum
434	26	78.8	285	2	Q6F8B5_ACID	Q6f8b5_acinetobact	507	26	78.8	415	2	Q703X6_THETE	Q703x6_thermoprote
435	26	78.8	288	2	Q4N391_THEPA	Q4n391_theileria p	508	26	78.8	416	2	Q31444_BACSU	Q31444_bacillus su
436	26	78.8	292	2	Q8ZBD6_YERPE	Q8zbd6_yersinia pe	509	26	78.8	418	2	Q9K9F3_BACHD	Q9k9f3_bacillus ha
437	26	78.8	292	2	Q66F46_YERPS	Q66f46_yersinia ps	510	26	78.8	421	2	Q776N0_BPV72	Q776n0_bacteriopa
438	26	78.8	292	2	Q6D998_ERWCT	Q6d998_erwinia car	511	26	78.8	421	2	Q7Y2T3_9CAUD	Q7y2t3_stx2 conver
439	26	78.8	295	1	ACTB_DICDI	P24005_dictyosteli	512	26	78.8	421	2	Q7Y394_9CAUD	Q7y394_stx1 conver
440	26	78.8	295	2	Q4AX35_DICDI	Q4axa5_dictyosteli	513	26	78.8	421	2	Q8SC87_9CAUD	Q8sc87_stx2 conver
441	26	78.8	296	2	Q5DM12_BPT5	Q5dm12_bacteriopa	514	26	78.8	421	2	Q9XDM0_EP933	Q9xjmo_bacteriopa
442	26	78.8	296	2	Q66LU4_BPT5	Q66lu4_bacteriopa	515	26	78.8	421	2	Q9KXA7_ECO57	Q9kxa7_escherichia
443	26	78.8	296	2	Q6QG36_BPT5	Q6qg36_bacteriopa	516	26	78.8	425	2	Q5LSP6_SILPO	Q5lsp6_silicibacte
444	26	78.8	298	2	Q6CGK6_YARLI	Q6cgk6_yarrowia li	517	26	78.8	427	2	Q71ZE9_LISMF	Q71ze9_listeria mo
445	26	78.8	299	2	Q8D1C9_YERPE	Q8dlc9_yersinia pe	518	26	78.8	427	2	Q8Y707_LISMO	Q8y707_listeria mo
446	26	78.8	300	2	Q8S9I4_LEPIN	Q8s9i4_leptospira	519	26	78.8	432	2	Q846Z8_CHLTR	Q846z8_chlamydia t
447	26	78.8	300	2	Q89359_RHOER	Q89359_rhodococcus	520	26	78.8	442	2	Q6L0G0_PICTO	Q6l0g0_picrophilus
448	26	78.8	300	2	Q8XUW2_RALSO	Q8xum2_ralstonia s	521	26	78.8	443	2	Q5I690_9BACT	Q5i690_symbiont ba
449	26	78.8	302	2	Q6S9I3_LEPIN	Q6s9i3_leptospira	522	26	78.8	444	2	Q8VXQ5_CHLS6	Q8vxq5_chlorarachn
450	26	78.8	303	2	Q6S9K1_9LEPT	Q6s9k1_leptospira	523	26	78.8	449	2	Q4UAF4_THEAN	Q4uaf4_theileria a
451	26	78.8	303	2	Q6S9K7_9LEPT	Q6s9k7_leptospira	524	26	78.8	451	2	Q7YAM9_THEVO	Q7yam9_thermoplasm
452	26	78.8	303	2	Q6S9K8_9LEPT	Q6s9k8_leptospira	525	26	78.8	459	2	Q8UJF5_PYRTO	Q8ujf5_pyrococcus
453	26	78.8	303	2	Q6S9I6_LEPIN	Q6s9i6_leptospira	526	26	78.8	462	2	Q5NWL9_AZOSE	Q5nwl9_aeaeoccus sp
454	26	78.8	303	2	Q6S9I8_LEPIN	Q6s9i8_leptospira	527	26	78.8	463	2	Q7XYJ5_CHLS6	Q7xyj5_chlorarachn
455	26	78.8	304	2	Q6S9K6_9LEPT	Q6s9k6_leptospira	528	26	78.8	467	2	Q9HKY7_THEAC	Q9hky7_thermoplasm
456	26	78.8	316	2	Q5X0X8_LEGPA	Q5x0x8_legionella	529	26	78.8	467	2	Q4UUG7_XANCP	Q4uug7_xanthomonas
457	26	78.8	318	2	Q9HRU5_HALSA	Q9hrus_halobacteri	530	26	78.8	467	2	Q8P9D0_XANCP	Q8p9d0_xanthomonas
458	26	78.8	320	2	Q48546_9LEPT	Q48546_leptospira	531	26	78.8	470	2	Q51PL2_MAGGR	Q51pl2_magnaporthe
459	26	78.8	320	2	Q6GXD3_9LEPT	Q6gxd3_leptospira	532	26	78.8	472	2	Q50I45_9VIRU	Q50i45_acidianus r
460	26	78.8	320	2	Q6GXD4_9LEPT	Q6gxd4_leptospira	533	26	78.8	474	2	Q8SR35_ENCCU	Q8sr35_encephalito
461	26	78.8	320	2	Q6GXD5_LEPIN	Q6gxd5_leptospira	534	26	78.8	475	2	Q6G2I3_BARHE	Q6g2i3_bartonella
462	26	78.8	320	2	Q6GXD6_LEPIN	Q6gxd6_leptospira	535	26	78.8	479	2	Q4QQY9_XENLA	Q4qqy9_xenopus lae
463	26	78.8	320	2	Q6GXD7_LEPIN	Q6gxd7_leptospira	536	26	78.8	482	2	Q5BCQ7_EMENI	Q5bcq7_aspergillus
464	26	78.8	320	2	Q6GXD8_LEPIN	Q6gxd8_leptospira	537	26	78.8	495	2	Q5XGN1_XENLA	Q5xgn1_xenopus lae
465	26	78.8	320	2	Q6GXD9_LEPIN	Q6gxd9_leptospira	538	26	78.8	503	2	Q8U9B1_AGR15	Q8u9b1_agrobacteri
466	26	78.8	320	2	Q6GXE0_LEPIN	Q6gxe0_leptospira	539	26	78.8	507	2	Q6NUV2_CORDI	Q6nuv2_corynebacte
467	26	78.8	320	2	Q6GXE1_LEPIN	Q6gxe1_leptospira	540	26	78.8	507	2	Q5CCT3_RUTRI	Q5ccct3_rutillus rut
468	26	78.8	320	2	Q6GXE2_LEPIN	Q6gxe2_leptospira	541	26	78.8	510	2	Q6ZGM2_ORYSA	Q6zgm2_oryza sativ
469	26	78.8	320	2	Q6GXE3_LEPIN	Q6gxe3_leptospira	542	26	78.8	510	2	Q54469_STRMU	Q54469_streptococc

543	26	78.8	510	2	066266_STRMU	066266	streptococc	616	26	78.8	648	2	Q5VB43_HELAN	Q5vb43 helianthus
544	26	78.8	525	1	ALO_KLULA	07c5y3	kluyveromyc	617	26	78.8	648	2	Q41716_9ASTR	Q41716 xanthum sp
545	26	78.8	528	2	Q7YTF8_CABEL	Q7ytf8	caenorhabdi	618	26	78.8	648	2	Q41717_9ASTR	Q41717 xanthum sp
546	26	78.8	529	2	Q68HC2_9EURO	Q68hc2	penicillium	619	26	78.8	649	2	P71134_CHLAB	P71134 chlamydomo
547	26	78.8	529	2	Q4UBP9_THEAN	Q4ubf9	theileria a	620	26	78.8	652	1	ILV3_BRANA	ILV3 brassica na
548	26	78.8	533	2	Q893G9_CLOTE	Q893g9	clostridium	621	26	78.8	652	2	Q5VB45_HELAN	Q5vb45 helianthus
549	26	78.8	541	2	Q65305_HORVU	Q65305	hordeum vul	622	26	78.8	652	2	Q5VB46_HELAN	Q5vb46 helianthus
550	26	78.8	548	2	Q9YAY5_AERPE	Q9yay5	aeropyrum p	623	26	78.8	652	2	Q6MJU2_BDEBA	Q6mju2 bdellovibr
551	26	78.8	561	2	Q8PF12_XANAC	Q8pf12	xanthomonas	624	26	78.8	654	2	Q5VB48_HELAN	Q5vb48 helianthus
552	26	78.8	565	2	Q4UP38_XANCP	Q4up38	xanthomonas	625	26	78.8	655	1	ILV1_BRANA	ILV1 brassica na
553	26	78.8	565	2	Q8P3L4_XANCP	Q8p3l4	xanthomonas	626	26	78.8	655	2	Q5VB49_HELAN	Q5vb49 helianthus
554	26	78.8	567	2	Q9FPQ7_SOLAN	Q9fpq7	solanum pty	627	26	78.8	657	2	Q7Q2V1_ANOGA	Q7q2y1 anopheles g
555	26	78.8	567	2	Q9FEB8_9SOLN	Q9feb8	solanum pty	628	26	78.8	658	2	Q5VB47_HELAN	Q5vb47 helianthus
556	26	78.8	567	2	Q67SD2_SYMTN	Q67sd2	syndyobacte	629	26	78.8	659	2	Q42767_GOSHI	Q42767 gossypium h
557	26	78.8	569	2	Q7URR7_RHOBA	Q7urr7	rhodopirell	630	26	78.8	659	2	Q42768_GOSHI	Q42768 gossypium h
558	26	78.8	570	2	Q8W631_9CAUD	Q8w631	bacterioph	631	26	78.8	661	2	Q27414_METHTH	Q27414 methanobact
559	26	78.8	570	2	Q8W6U9_9CAUD	Q8w6u9	bacterioph	632	26	78.8	662	2	Q520Q2_MAGGR	Q520q2 magnaporthe
560	26	78.8	571	2	Q6JIN0_9CAUD	Q6jino	bacterioph	633	26	78.8	662	2	Q7X9G4_USEUD	Q7x9g4 papaver rho
561	26	78.8	574	2	Q87C02_XYLPF	Q87c02	xyella fas	634	26	78.8	663	2	Q7XKQ8_ORYZA	Q7xkq8 oryza sativ
562	26	78.8	575	2	Q5GU21_XANOR	Q5gu21	xanthomonas	635	26	78.8	663	2	Q631D4_BACCC	Q631d4 bacillus ce
563	26	78.8	577	2	Q9PB93_XYLFA	Q9pb93	xyella fas	636	26	78.8	664	1	ILV2_TOBAC	ILV2 nicotiana t
564	26	78.8	578	2	Q55LM3_CRYNE	Q55lm3	cryptococc	637	26	78.8	665	2	Q6T858_9BRAS	Q6t858 camelina m
565	26	78.8	578	2	Q41N5_GIBRELLA	Q41n5	gibberella	638	26	78.8	665	2	Q38795_9CARY	Q38795 amaranthus
566	26	78.8	578	2	Q5XD62_CRYNE	Q5xd62	cryptococc	639	26	78.8	666	2	Q9ZSU3_KOCCS	Q9zsu3 kochia scop
567	26	78.8	583	2	Q8S3D0_BROTE	Q8s3d0	bromus tect	640	26	78.8	667	1	ILV1_TOBAC	ILV1 nicotiana t
568	26	78.8	583	2	Q8S3J0_BROTE	Q8s3j0	bromus tect	641	26	78.8	668	2	Q6T859_9BRAS	Q6t859 camelina m
569	26	78.8	584	2	Q4MHE8_BACCE	Q4mhe8	bacillus ce	642	26	78.8	668	2	Q6T860_9BRAS	Q6t860 camelina m
570	26	78.8	584	2	Q63BD4_BACCK	Q63bd4	bacillus ce	643	26	78.8	669	2	Q93XN5_AMAPO	Q93xn5 amaranthus
571	26	78.8	584	2	Q6HIR4_BACHK	Q6hir4	bachillus th	644	26	78.8	669	2	Q93XN6_AMARE	Q93xn6 amaranthus
572	26	78.8	584	2	Q738C1_BACCL	Q738c1	bacillus ce	645	26	78.8	670	1	ILVB_ARATH	ILV597 arabidopsis
573	26	78.8	584	2	Q81DN3_BACCR	Q81dn3	bacillus ce	646	26	78.8	670	2	Q8L7Y7_ARATH	Q8l7y7 arabidopsis
574	26	78.8	584	2	Q81Q12_BACAN	Q81q12	bacillus an	647	26	78.8	670	2	Q94B64_ARATH	Q94b64 arabidopsis
575	26	78.8	585	2	Q816E1_9BRAS	Q816e1	raphanus ra	648	26	78.8	671	2	Q5FV34_ARATH	Q5fv34 arabidopsis
576	26	78.8	585	2	Q816E2_9BRAS	Q816e2	raphanus ra	649	26	78.8	671	2	Q4QAC4_LEIMA	Q4qac4 leishmania
577	26	78.8	585	2	Q816D6_9BRAS	Q816d6	raphanus ra	650	26	78.8	674	2	Q4WF25_ASPFU	Q4wf25 aspergillus
578	26	78.8	585	2	Q816E3_9BRAS	Q816e3	raphanus ra	651	26	78.8	685	2	Q6Q097_CABBR	Q6q097 caenorhabdi
579	26	78.8	585	2	Q816D9_9BRAS	Q816d9	raphanus ra	652	26	78.8	701	2	Q6CEM3_YARLI	Q6cem3 yarrowia li
580	26	78.8	585	2	Q816D5_9BRAS	Q816d5	raphanus ra	653	26	78.8	734	2	Q88SA4_LACPL	Q88sa4 lactobacill
581	26	78.8	585	2	Q816E2_9BRAS	Q816e2	raphanus ra	654	26	78.8	741	1	NP2L1_MOUSE	NP2L1 mus musculu
582	26	78.8	585	2	Q816D8_9BRAS	Q816d8	raphanus ra	655	26	78.8	741	2	Q6GTN8_MOUSE	Q6gtne8 mus musculu
583	26	78.8	585	2	Q816E4_9BRAS	Q816e4	raphanus ra	656	26	78.8	749	2	Q9Z2B8_MOUSE	Q9z2e8 mus musculu
584	26	78.8	585	2	Q816D7_9BRAS	Q816d7	raphanus ra	657	26	78.8	767	2	Q6KAM4_MOUSE	Q6kam4 mus musculu
585	26	78.8	585	2	Q816E0_9BRAS	Q816e0	raphanus ra	658	26	78.8	772	1	RAD15_SCHPO	R21659 schizosacch
586	26	78.8	589	2	Q77X53_MYCBO	Q77x53	mycobacteri	659	26	78.8	774	2	Q8L164_THEBR	Q8l164 thermoanaer
587	26	78.8	590	1	ILVB_FORUM	P69683	porphyra pu	660	26	78.8	781	2	Q8RKB9_THETN	Q8rbk9 rhodospirell
588	26	78.8	590	1	ILVB_FORUM	P69684	porphyra um	661	26	78.8	824	2	Q7UR09_RHOBA	Q7ur09 rhodospirell
589	26	78.8	590	2	Q6MX04_MYCTU	Q6mx04	mycobacteri	662	26	78.8	831	2	Q5B9P4_EMENI	Q5b9p4 aspergillus
590	26	78.8	596	2	Q6S8Z2_GRATL	Q6s8z2	gracilaria	663	26	78.8	863	2	Q13400_UMTMA	Q13400 ustilago ma
591	26	78.8	598	2	Q84U05_WHEAT	Q84u05	tritium ae	664	26	78.8	872	2	Q3R0E1_IDILO	Q3r0e1 idiomarina
592	26	78.8	598	2	Q84U06_WHEAT	Q84u06	tritium ae	665	26	78.8	879	1	PUF3_YEAST	PUF3 desulfovibr
593	26	78.8	598	2	Q84U07_WHEAT	Q84u07	tritium ae	666	26	78.8	932	2	Q72BZ4_DESVH	Q72bz4 desulfovibr
594	26	78.8	598	2	Q84U08_WHEAT	Q84u08	tritium ae	667	26	78.8	972	2	Q7XRVT_ORYZA	Q7xrv7 oryza sativ
595	26	78.8	599	2	Q5767_BRANA	Q5767	brassica na	668	26	78.8	992	2	Q9VM91_DROME	Q9vm91 drosophila
596	26	78.8	602	2	Q9A6N2_CAUCR	Q9a6n2	caulobacter	669	26	78.8	998	2	Q6J331_PYPY	Q6j331 pyrus pyrif
597	26	78.8	603	2	Q8VJ66_MYCTU	Q8vj66	mycobacteri	670	26	78.8	998	2	Q6J332_PYPY	Q6j332 pyrus pyrif
598	26	78.8	609	2	Q8VUS4_ALTSO	Q8vus4	alteromonas	671	26	78.8	1001	2	Q64M78_ORYZA	Q64m78 oryza sativ
599	26	78.8	609	2	Q4ST49_TETNG	Q4st49	tetradodon n	672	26	78.8	1047	2	Q529U2_MAGGR	Q529u2 magnaporthe
600	26	78.8	612	2	Q4TAP2_GIBBEZ	Q4tap2	gibberella	673	26	78.8	1050	2	Q95VZ3_DICDI	Q95vz3 dictyosteli
601	26	78.8	612	2	Q65XM7_ORYZA	Q65xm7	oryza sativ	674	26	78.8	1072	2	Q26157_PLAVI	Q26157 plasmodium
602	26	78.8	616	2	Q7QD05_ANOGA	Q7qd05	anopheles g	675	26	78.8	1079	2	Q75BR6_ASHGO	Q75br6 ashbya gos
603	26	78.8	634	2	Q5S8D7_9TRYTP	Q5s8d7	trypanosoma	676	26	78.8	1079	2	Q4J5N9_CORJK	Q4jen9 corynebacte
604	26	78.8	638	2	Q41768_MAIZE	Q41768	zea mays (m	677	26	78.8	1093	2	Q4M0G2_9BURK	Q4m0g2 burkholderi
605	26	78.8	638	2	Q41769_MAIZE	Q41769	zea mays (m	678	26	78.8	1098	2	Q6MKX6_BDBBA	Q6mkx6 bdellovibr
606	26	78.8	640	2	Q9FUD0_LOLMU	Q9fud0	lolium mult	679	26	78.8	1127	2	Q7TXJ1_MYCBO	Q7txj1 mycobacteri
607	26	78.8	644	2	Q5D6B1_ORYZA	Q5d6b1	oryza sativ	680	26	78.8	1127	2	Q95127_MYCTU	Q95127 mycobacteri
608	26	78.8	644	2	Q5D6B2_ORYZA	Q5d6b2	oryza sativ	681	26	78.8	1162	2	Q754X1_ASHGO	Q754x1 ashbya gos
609	26	78.8	644	2	Q5D6B3_ORYZA	Q5d6b3	oryza sativ	682	26	78.8	1170	2	Q63T05_BURPS	Q63t05 burkholderi
610	26	78.8	644	2	Q6K2E8_ORYZA	Q6k2e8	oryza sativ	683	26	78.8	1191	2	Q8RL60_PSEFL	Q8rl60 pseudomonas
611	26	78.8	644	2	Q9FRV2_ORYZA	Q9frv2	oryza sativ	684	26	78.8	1211	2	Q60PC0_CABBR	Q60pc0 caenorhabdi
612	26	78.8	644	2	Q9FRV3_ORYZA	Q9frv3	oryza sativ	685	26	78.8	1260	2	Q23658_CABBL	Q23658 caenorhabdi
613	26	78.8	645	2	Q9NFY7_PENVA	Q9nfy7	penaeus van	686	26	78.8	1276	2	Q4LQ08_9BURK	Q4lq08 burkholderi
614	26	78.8	646	2	Q5VB42_HELAN	Q5vb42	helianthus	687	26	78.8	1291	2	Q41978_MHV68	Q41978 murid herpe
615	26	78.8	646	2	Q5VB44_HELAN	Q5vb44	helianthus	688	26	78.8	1297	2	Q9XEM9_ORYZA	Q9xem9 oryza sativ

689	26	78.8	1310	2	O41976	MHV68	O41976	murid herpes	762	25	75.8	171	2	Q86111	DICD1	Q86111 dictyosteli
690	26	78.8	1378	2	Q5L6J2	CHLAB	Q5l6j2 chlamydophi	763	25	75.8	171	2	Q9I881	CHICK	Q9I881 gallus gall	
691	26	78.8	1379	2	Q4S1M5	TETNG	Q4s1m5 tetraodon n	764	25	75.8	172	2	Q4WEFO	ASPTU	Q4wefo aspergillus	
692	26	78.8	1481	2	Q693A4	YEREN	Q693a4 yersinia en	765	25	75.8	173	2	O15585	ENTHI	O15585 entamoeba h	
693	26	78.8	1804	2	Q9ZVVO	ARATH	Q9zvv0 arabidopsis	766	25	75.8	174	2	O6BXP1	DEBHA	O6bxf1 debaryomyce	
694	26	78.8	1875	2	Q8FGB1	ECOL6	Q8fgb1 escherichia	767	25	75.8	174	2	Q9SW61	ARATH	Q9sw61 arabidopsis	
695	26	78.8	1891	2	Q772V5	DROME	Q772v5 drosophila	768	25	75.8	174	2	Q98PD3	RHILO	Q98pd3 rhizobium l	
696	26	78.8	1893	2	Q7K3V3	DROME	Q7k3v3 drosophila	769	25	75.8	176	2	Q9V9L3	DROME	Q9v9l3 drosophila	
697	26	78.8	1894	2	Q9W4J1	DROME	Q9w4j1 drosophila	770	25	75.8	177	2	O5JL76	ORYSA	O5jl76 oryza sativ	
698	26	78.8	1920	2	Q4G205	DROME	Q4g205 drosophila	771	25	75.8	181	2	Q58GF6	PSEAB	Q58gf6 pseudomonas	
699	26	78.8	1940	2	Q6GPD0	XENLA	Q6gpd0 xenopus lae	772	25	75.8	183	2	Q6AN80	DESPS	Q6an80 desulfotale	
700	26	78.8	2053	2	Q54EQ8	DICD1	Q54eq8 dictyosteli	773	25	75.8	184	2	Q68GZ8	RUMHA	Q68gz8 ruminococcu	
701	26	78.8	2221	2	Q4P825	USTMA	Q4p825 ustilago ma	774	25	75.8	184	2	O51566	BORBU	O51566 borrelia bu	
702	26	78.8	2472	2	Q5B768	EMENI	Q5b768 aspergillus	775	25	75.8	184	2	Q660Q1	BORGA	Q660q1 borrelia ga	
703	26	78.8	2476	2	Q5EG07	EMENI	Q5eg07 aspergillus	776	25	75.8	185	2	Q57N68	SALCH	Q57n68 salmonella	
704	26	78.8	2479	2	Q9A988	CAUCR	Q9a988 caulobacter	777	25	75.8	185	2	Q5PMX1	SALFA	Q5pmx1 salmonella	
705	26	78.8	2691	2	Q8XP01	RALSO	Q8xp01 ralstonia s	778	25	75.8	185	2	Q8ZNU7	SALTY	Q8znu7 salmonella	
706	26	78.8	2732	2	Q5H087	XANOR	Q5h087 xanthomonas	779	25	75.8	185	2	Q8ZSU2	SALTY	Q8zsu2 salmonella	
707	26	78.8	3240	2	Q87PB5	VIBPA	Q87pb5 vibrio para	780	25	75.8	188	2	Q893Q5	CLOTE	Q893q5 clostridium	
708	26	78.8	3989	2	Q9PYB2	9FLAV	Q9pyb2 peptivirug	781	25	75.8	188	2	Q982V0	RHILO	Q982v0 rhizobium l	
709	25	75.8	41	2	Q7QY04	GIALA	Q7qy04 giardia lam	782	25	75.8	188	2	Q8CC11	MOUSE	Q8cc11 mus musculu	
710	25	75.8	74	2	Q6J2C1	PSEYM	Q6j2c1 pseudomonas	783	25	75.8	190	1	ATKC	SYNY3	ATKC_SYNY3	
711	25	75.8	84	2	Q54YM1	DICD1	Q54ym1 dictyosteli	784	25	75.8	191	2	Q9Z9R7	BACHD	Q9z9r7 bacillus ha	
712	25	75.8	86	2	Q7TMI4	MOUSE	Q7tmi4 mus musculu	785	25	75.8	191	2	Q6D7I5	ERWCT	Q6d7i5 erwinia car	
713	25	75.8	92	2	Q75ID7	ORYSA	Q75id7 oryza sativ	786	25	75.8	193	2	Q8XIP8	CLOPE	Q8xip8 clostridium	
714	25	75.8	95	2	Q4ZAB6	9VIRU	Q4zab6 bacterioph	787	25	75.8	194	1	ATKC	SALTY	ATKC_SALTY	
715	25	75.8	95	2	Q4ZAJ0	9VIRU	Q4zaj0 bacterioph	788	25	75.8	194	1	ATKC	SALTY	ATKC_SALTY	
716	25	75.8	95	2	Q4ZBK2	9VIRU	Q4zbk2 bacterioph	789	25	75.8	194	2	Q57RNI	SALCH	Q57rni salmonella	
717	25	75.8	101	1	REV	SIVGB	P23379 simian immu	790	25	75.8	195	2	Q5PCU6	SALFA	Q5pcu6 salmonella	
718	25	75.8	103	2	Q4JXN3	CORJK	Q4jxn3 corynebacte	791	25	75.8	199	2	Q60ER8	ORYSA	Q60er8 oryza sativ	
719	25	75.8	103	2	Q4SLD6	TETNG	Q4sl6 tetraodon n	792	25	75.8	199	2	Q8PGV5	XANAC	Q8pgv5 xanthomonas	
720	25	75.8	105	2	Q6A5L4	PROAC	Q6a5l4 propionibac	793	25	75.8	200	1	GRPE	MYCMS	GRPE_MYCMS	
721	25	75.8	111	2	O62053	CABEL	O62053 caenorhabdi	794	25	75.8	200	1	WRBA	ZYMMO	WRBA_ZYMMO	
722	25	75.8	115	2	Q5PBA8	ANAMM	Q5pba8 anaplasma m	795	25	75.8	200	2	P74074	SYNY3	P74074 synochocyst	
723	25	75.8	118	2	Q944W0	PHYIN	Q944w0 phytophthor	796	25	75.8	201	2	Q6ABK8	PROAC	Q6abk8 proptonibac	
724	25	75.8	119	2	Q82KM3	STRAW	Q82km3 streptomyc	797	25	75.8	201	2	Q8YV71	ANASP	Q8yv71 anabaena sp	
725	25	75.8	121	1	VG38	ICHV1	Q00144 ictaluriid h	798	25	75.8	202	1	ATKCI	ANASP	ATKCI_ANASP	
726	25	75.8	124	2	Q278T6	METTH	Q278t6 methanobact	799	25	75.8	202	2	O5XLH1	ANASL	O5xlh1 anabaena sp	
727	25	75.8	126	2	Q81W87	BACAN	Q81w87 bacillus an	800	25	75.8	202	2	O6LBA3	OLICA	O6lba3 oligotropha	
728	25	75.8	126	2	Q8NR84	CORGL	Q8nr84 corynebacte	801	25	75.8	202	2	Q9I381	PSEAB	Q9i381 pseudomonas	
729	25	75.8	127	2	Q77419	9CAUD	Q77419 pseudomonas	802	25	75.8	204	2	Q4KRS0	9HYME	Q4krs0 euglossa cr	
730	25	75.8	133	2	Q4V619	DROME	Q4v619 drosophila	803	25	75.8	204	2	Q69ST3	ORYSA	Q69st3 oryza sativ	
731	25	75.8	133	2	O6A993	PROAC	Q6a993 propionibac	804	25	75.8	205	2	O5PBR3	ANAMM	O5pbr3 anaplasma m	
732	25	75.8	134	2	Q7NOK3	CHRVO	Q7nqk3 chromobacte	805	25	75.8	206	2	Q4X0F0	ASPTU	Q4x0f0 aspergillus	
733	25	75.8	137	2	Q5ANP2	EMENI	Q5awf2 aspergillus	806	25	75.8	208	2	Q4QMF9	HAEL8	Q4qmf9 haemophilus	
734	25	75.8	143	2	Q9V733	DROME	Q9v733 drosophila	807	25	75.8	210	2	Q72ON6	LISMF	Q72on6 listeria mo	
735	25	75.8	143	2	Q57ID0	SALCH	Q57id0 salmonella	808	25	75.8	210	2	Q8Y7S8	LISMO	Q8y7s8 listeria mo	
736	25	75.8	143	2	Q7CPH6	SALTY	Q7cph6 salmonella	809	25	75.8	210	2	Q92CL5	LISIN	Q92cl5 listeria in	
737	25	75.8	143	2	Q5PBZ3	SALPA	Q5pbz3 salmonella	810	25	75.8	214	2	Q529X9	MAGGR	Q529x9 magnaporthe	
738	25	75.8	143	2	Q8XK1	SALTY	Q8kex1 salmonella	811	25	75.8	218	2	Q74G32	GEOSL	Q74g32 geobacter s	
739	25	75.8	144	1	TRPX	TRVBB	Q77404 trypanosoma	812	25	75.8	219	2	Q9UUI1	SCHPO	Q9uui1 schistosacch	
740	25	75.8	144	2	Q57WB2	9TRYP	Q57wb2 trypanosoma	813	25	75.8	219	2	Q5IWI3	PROMI	Q5iwi3 prototheca	
741	25	75.8	144	2	Q57WB4	9TRYP	Q57wb4 trypanosoma	814	25	75.8	220	2	Q7V599	PROMM	Q7v599 prochloroco	
742	25	75.8	144	2	Q73VG6	MYCPA	Q73vg6 mycobacteri	815	25	75.8	225	2	Q8YNL8	ANASP	Q8ynl8 anabaena sp	
743	25	75.8	148	2	Q7PYD7	ANOAG	Q7pyd7 anopheles g	816	25	75.8	226	2	Q70LK6	LAMPA	Q70lk6 lama guanac	
744	25	75.8	150	2	Q9KE39	BACHD	Q9ke39 bacillus ha	817	25	75.8	226	2	Q9MEI5	LAMPA	Q9mei5 lama guanac	
745	25	75.8	151	2	Q9VHB2	DROME	Q9vnb2 drosophila	818	25	75.8	227	1	PHLB	SERLI	PHLB_SERLI	
746	25	75.8	152	2	Q8D622	VIBVU	Q8d622 vibrio vuln	819	25	75.8	227	2	Q5EGE7	LACRE	Q5ege7 lactobacill	
747	25	75.8	157	2	Q8YIL3	ANASP	Q8yil3 anabaena sp	820	25	75.8	229	2	Q7NLY3	GLOVI	Q7nly3 gloeobacter	
748	25	75.8	158	2	Q7MD43	VIBVY	Q7md43 vibrio vuln	821	25	75.8	230	2	Q62HH2	BURMA	Q62hh2 burkholderi	
749	25	75.8	160	2	Q8VW85	NARPS	Q8vws5 narciassus p	822	25	75.8	231	2	Q8XY37	RALSO	Q8xy37 ralstonia s	
750	25	75.8	160	2	Q8VW85	NARPS	Q8vws5 narciassus p	823	25	75.8	232	2	Q63R87	BURPS	Q63r87 burkholderi	
751	25	75.8	160	2	Q4LUD8	9URUK	Q4lud8 burkholderi	824	25	75.8	234	2	Q8VNP5	9VIRU	Q8vnp5 bacterioph	
752	25	75.8	160	2	Q65WK1	MANSM	Q65wk1 manheimia	825	25	75.8	235	2	Q5IYX9	MAGGR	Q5ixy9 magnaporthe	
753	25	75.8	163	2	Q6AS06	DESPS	Q6as06 desulfotale	826	25	75.8	235	2	Q7XZ20	GRIFA	Q7xz20 griffithsia	
754	25	75.8	165	2	Q84YQ5	ORYSA	Q84yq5 oryza sativ	827	25	75.8	237	2	Q6ZZY3	BIDPI	Q6zzz3 bidens pilo	
755	25	75.8	168	1	CDN2C	HUMAN	P42773 homo sapien	828	25	75.8	237	2	Q6ZZY5	BIDPI	Q6zzz5 bidens pilo	
756	25	75.8	168	2	Q6ICV4	HUMAN	Q6icv4 homo sapien	829	25	75.8	237	2	Q89GU5	BRADA	Q89gu5 bradyrhizob	
757	25	75.8	169	2	Q5WV71	LEGPL	Q5wv71 legionella	830	25	75.8	240	2	Q5GSE6	WOLTR	Q5gse6 wolbachia s	
758	25	75.8	169	2	Q5X6R6	LEGPA	Q5x6r6 legionella	831	25	75.8	240	2	Q73GK1	WOLPM	Q73gk1 wolbachia p	
759	25	75.8	169	2	Q5ZX95	LEGPH	Q5zx95 legionella	832	25	75.8	240	2	Q63F92	BACCC	Q63f92 bacillus ce	
760	25	75.8	170	2	Q6LGS2	PHOPR	Q6lgs2 photobacter	833	25	75.8	243	2	Q9HHA9	METBA	Q9hha9 methanobarc	
761	25	75.8	171	2	Q6IED1	DICD1	Q6ied1 dictyosteli	834	25	75.8	243	2	Q4FS78	9GAMM	Q4fs78 psychrobact	

835	25	75.8	245	2	Q6Z645_ORYSA	Q6Z645	oryza sativ	908	25	75.8	292	2	Q8FBW2_ECOL6	Q8FBW2	escherichia
836	25	75.8	247	1	MCKG_METBA	P07964	methanosarc	909	25	75.8	292	2	Q8ZK20_SALTY	Q8ZK20	salmonella
837	25	75.8	249	2	Q81FD3_BACCR	P07964	bacillus ce	910	25	75.8	292	2	Q83126_SHIFL	Q83126	shigella fl
838	25	75.8	251	2	Q8RKT8_SERMA	Q8-kt8	serratia ma	911	25	75.8	293	1	Q8X797_ECO57	Q8X797	escherichia
839	25	75.8	251	2	Q8X9D9_9ENTR	Q8x9d9	serratia sp	912	25	75.8	293	1	US17_HGWA	US17	human cytom
840	25	75.8	252	2	Q6HMP7_BACHK	Q6hmp7	bacillus th	913	25	75.8	293	2	Q6RXA8_HCMV	Q6RXA8	human cytom
841	25	75.8	252	2	Q7NUL6_CHRVO	Q7nul6	chromobacte	914	25	75.8	293	2	Q6SVY9_HCMV	Q6SVY9	human cytom
842	25	75.8	253	1	UBIG_RHOA	Q6nc69	rhodospseudo	915	25	75.8	294	2	Q7QR20_GIALA	Q7QR20	giardia lam
843	25	75.8	254	2	Q5ORD0_ENTHI	Q5ord0	entamoeba h	916	25	75.8	295	2	Q7VTG6_BORPE	Q7VTG6	bordeitella
844	25	75.8	255	2	Q8Y958_LISMO	Q8y958	listeria ma	917	25	75.8	295	2	Q7WSF4_BORPA	Q7WSF4	bordeitella
845	25	75.8	255	2	Q82DX7_LISIN	Q82dx7	listeria in	918	25	75.8	295	2	Q7WCY9_BORBR	Q7WCY9	bordeitella
846	25	75.8	255	2	Q722L8_LISMP	Q722l8	listeria mo	919	25	75.8	295	2	Q9Z2Y0_RAT	Q9Z2Y0	rattus norv
847	25	75.8	257	2	Q6KZIO_PICTO	Q6kzi0	microphilus	920	25	75.8	295	2	Q9DCY0_MOUSE	Q9DCY0	mus musculu
848	25	75.8	257	2	Q7R1X9_GIALA	Q7r1x9	giardia lam	921	25	75.8	295	2	Q68G42_RAT	Q68G42	rattus norv
849	25	75.8	257	2	Q6D5Y1_ERMCT	Q6d5y1	erwinia car	922	25	75.8	297	1	PDXS_CORDI	PDXS	corynebacte
850	25	75.8	258	2	Q8NLA5_CORGL	Q8nla5	corynebacte	923	25	75.8	297	1	PDXS_CORF	PDXS	corynebacte
851	25	75.8	259	2	Q4QAC7_LEIMA	Q4qac7	leishmania	924	25	75.8	297	2	Q6MIF6_BDEBA	Q6MIF6	bdellovibri
852	25	75.8	259	2	Q74OX5_MYCPA	Q74ox5	mycobacteri	925	25	75.8	298	2	Q6CYT7_ERMCT	Q6CYT7	erwinia car
853	25	75.8	259	2	Q9BEG0_RHILO	Q9beg0	rhizobium l	926	25	75.8	299	1	PDXS_LEIXX	PDXS	leifsonia x
854	25	75.8	259	2	Q5LXE7_SILPO	Q5lxe7	silicibacte	927	25	75.8	299	1	PDXS_MYCBO	PDXS	mycobacteri
855	25	75.8	260	2	Q580F0_9TRYP	Q580f0	trypanosoma	928	25	75.8	299	2	PDXS_MYCTU	PDXS	acinetobact
856	25	75.8	260	2	Q89IG0_BRAJA	Q89ig0	bradyrhizob	929	25	75.8	299	1	Q7WSA9_9GAMM	Q7WSA9	acinetobact
857	25	75.8	264	2	Q5UG11_AEDAE	Q5ug11	aedes aegypt	930	25	75.8	300	1	RANT_BP22	RANT	bacterioph
858	25	75.8	264	2	Q4NB90_9MICC	Q4nb90	arthrobacte	931	25	75.8	300	2	Q55ZQ3_CRYNE	Q55ZQ3	cryptococc
859	25	75.8	265	1	Y737_HABIN	O05031	haemophilus	932	25	75.8	300	2	Q5KP15_CRYNE	Q5KP15	cryptococc
860	25	75.8	265	2	Q7FAN5_THEVO	Q7fan5	thermoplas	933	25	75.8	300	2	Q77D83_BP22	Q77D83	bacterioph
861	25	75.8	265	2	Q7V3H9_PROMP	Q7v3h9	prochloroco	934	25	75.8	300	2	Q4JVD3_CORJK	Q4JVD3	corynebacte
862	25	75.8	267	2	Q4XW8_ASPFU	Q4xw8	aspergillus	935	25	75.8	301	1	PORI_RHOCA	PORI	rhodobacter
863	25	75.8	270	2	Q41HA0_GIBZE	Q41ha0	gibberella	936	25	75.8	302	1	THYX_SILPO	THYX	silicibacte
864	25	75.8	270	2	Q7V8V8_PROMM	Q7v8v8	prochloroco	937	25	75.8	302	2	Q4ZOV5_PLABE	Q4ZOV5	plasmodium
865	25	75.8	270	2	Q7VE98_PROMA	Q7ve98	prochloroco	938	25	75.8	302	2	Q50J47_FUGRU	Q50J47	fugu rubrip
866	25	75.8	271	2	Q9ACK2_9SPIO	Q9ack2	treponema s	939	25	75.8	303	1	HEMH_CAMJE	HEMH	campylobact
867	25	75.8	271	2	Q4UYL2_XANCP	Q4uyl2	xanthomonas	940	25	75.8	303	1	PDXS_MYCPA	PDXS	mycobacteri
868	25	75.8	271	2	Q8P5G0_XANCP	Q8p5g0	xanthomonas	941	25	75.8	303	1	PDXS_STRCO	PDXS	streptomyce
869	25	75.8	273	2	Q81F04_BACCR	Q81fd4	bacillus ce	942	25	75.8	303	2	Q4NA51_9MICC	Q4NA51	arthrobacte
870	25	75.8	274	2	Q9ACL7_TREMA	Q9acl7	treponema m	943	25	75.8	303	2	Q4HE19_CAMJO	Q4HE19	campylobact
871	25	75.8	274	2	Q9ACL6_TREMA	Q9acl6	treponema m	944	25	75.8	303	2	Q5HVR0_CAMJO	Q5HVR0	campylobact
872	25	75.8	274	2	Q9ACL9_TRELE	Q9acl9	treponema l	945	25	75.8	304	1	PDXS_PROAC	PDXS	propionibac
873	25	75.8	274	2	Q8XV21_RALSO	Q8xv21	raistonia l	946	25	75.8	304	1	PDXS_STRAW	PDXS	streptomyce
874	25	75.8	275	2	Q29045_ARCFU	Q29045	archaeoglob	947	25	75.8	304	2	Q729C7_DBSVH	Q729C7	desulfovibr
875	25	75.8	276	2	Q45761_BACTL	Q45761	bacillus th	948	25	75.8	305	2	Q41V08_AZOV1	Q41V08	azotobacter
876	25	75.8	276	2	Q89WM1_BRAJA	Q89wm1	bradyrhizob	949	25	75.8	305	2	Q5Z2B2_NOCFA	Q5Z2B2	nocardia fa
877	25	75.8	277	2	Q79AJ1_BACTL	Q79aj1	bacillus th	950	25	75.8	306	1	PDXS_NOCFA	PDXS	nocardia fa
878	25	75.8	279	2	Q9HSF9_HALSA	Q9hsf9	halobacteri	951	25	75.8	306	2	Q5LN71_SILPO	Q5LN71	silicibacte
879	25	75.8	279	2	Q4NTL6_9DELT	Q4ntl6	anaeromyxob	952	25	75.8	307	1	PDXS_MYCLE	PDXS	mycobacteri
880	25	75.8	279	2	Q9Z5A8_STRCO	Q9z5a8	streptomyce	953	25	75.8	308	2	Q6CTH9_KULUA	Q6CTH9	kluveromyce
881	25	75.8	279	2	Q3K878_BACHD	Q3k878	bacillus ha	954	25	75.8	309	2	Q4V285_BACCT	Q4V285	bacillus ce
882	25	75.8	280	2	Q79AJ2_BACTL	Q79aj2	bacillus th	955	25	75.8	309	2	Q8A4K4_BACTN	Q8A4K4	bacteroides
883	25	75.8	283	2	Q8SRQ3_ENCCU	Q8srq3	encephalito	956	25	75.8	310	2	Q89D23_BRAJA	Q89D23	bradyrhizob
884	25	75.8	283	2	Q411B6_GIBZE	Q411b6	gibberella	957	25	75.8	310	2	Q5TWM0_ANOGA	Q5TWM0	anopheles g
885	25	75.8	285	1	COQ5_CABEL	P34666	caenorhabdi	958	25	75.8	310	2	O01460_CABEL	O01460	caenorhabdi
886	25	75.8	285	2	Q53936_STRCO	Q53936	streptomyce	959	25	75.8	310	2	Q6ZXY1_FUGRU	Q6ZXY1	fugu rubrip
887	25	75.8	286	1	FLAB2_TREMA	Q9kwx0	treponema m	960	25	75.8	311	1	ISPE_SYNEL	ISPE	synechococc
888	25	75.8	287	1	PDXS_TROW8	Q83hms	tropheryma	961	25	75.8	311	2	Q4TSB8_9SPHN	Q4TSB8	erythroba
889	25	75.8	287	1	PDXS_TROWT	Q83mz9	tropheryma	962	25	75.8	312	2	Q5AF82_CANAL	Q5AF82	candida alb
890	25	75.8	287	1	Q5WRX1_LEGPL	Q5wxr1	legionella	963	25	75.8	312	2	Q7NCM8_GLOVI	Q7NCM8	gloeobacter
891	25	75.8	287	2	Q9F7D9_9GAMM	Q9f7d9	acinetobact	964	25	75.8	313	2	Q5FRQ3_GLUOX	Q5FRQ3	gluconobact
892	25	75.8	287	2	Q6RSW7_KLEPN	Q6rsw7	klebsiella	965	25	75.8	314	1	RLA0_EIMTE	RLA0	emerla ten
893	25	75.8	287	2	Q6RSW8_ECOLI	Q6rsw8	escherichia	966	25	75.8	314	2	Q5FKI8_LACAC	Q5FKI8	lactobacill
894	25	75.8	287	2	Q764B7_KLEPN	Q764b7	klebsiella	967	25	75.8	314	2	Q7UVB1_RHOBA	Q7UVB1	rhodopirell
895	25	75.8	287	2	Q767E8_KLEPN	Q767e8	klebsiella	968	25	75.8	315	2	Q87V43_PSEGM	Q87V43	pseudomonas
896	25	75.8	287	2	Q9AGN8_PSEAE	Q9agn8	pseudomonas	969	25	75.8	315	2	Q8PK97_XANAC	Q8PK97	xanthomonas
897	25	75.8	287	2	Q9L8E3_ENTCL	Q9l8e3	enterobacte	970	25	75.8	316	2	Q66JB4_XENTR	Q66JB4	xenopus tro
898	25	75.8	287	2	Q83Z98_ECOLI	Q83z98	escherichia	971	25	75.8	317	1	ISPE_ANASP	ISPE	anabaena ep
899	25	75.8	287	2	Q7BEB3_PSEAE	Q7beb3	pseudomonas	972	25	75.8	317	2	PDXS_CORGL	PDXS	corynebacte
900	25	75.8	287	2	Q93F76_PSEAE	Q93f76	pseudomonas	973	25	75.8	317	2	Q07086_YEAST	Q07086	saccharomyc
901	25	75.8	288	2	Q9KJ77_KLEPN	Q9kij77	klebsiella	974	25	75.8	319	2	Q69MK1_ORYSA	Q69MK1	oryza sativ
902	25	75.8	288	1	ISPE_CLOPE	Q8xia9	clostridium	975	25	75.8	319	2	Q92PG1_RHIME	Q92PG1	rhizobium m
903	25	75.8	288	2	Q41Y16_AZOV1	Q4iy16	azotobacter	976	25	75.8	320	2	Q6H738_ORYSA	Q6H738	oryza sativ
904	25	75.8	288	2	Q4J260_AZOV1	Q4j260	azotobacter	977	25	75.8	320	2	Q4L237_9BURK	Q4L237	burkholderi
905	25	75.8	292	1	DGOK_ECOLI	Q4j260	azotobacter	978	25	75.8	320	2	Q9KXT3_STRCO	Q9KXT3	streptomyce
906	25	75.8	292	2	Q8ZX54_PYRAE	Q8zxe4	pyrobaculum	979	25	75.8	320	2	Q5Z093_NOCFA	Q5Z093	nocardia fa
907	25	75.8	292	2	Q57I09_SALCH	Q57i09	salmonella	980	25	75.8	321	2	Q63UI5_BURPS	Q63UI5	burkholderi

RT "Complete genome sequence of the plant commensal Pseudomonas
fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY95137.1; -; Genomic DNA.
SQ SEQUENCE 535 AA; 57327 MW; 3E5F347365AAC14 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 535;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||:
Db 291 GATNWAA 297

RESULT 5

Q9P3R4 NEUCR
ID Q9P3R4 NEUCR PRELIMINARY; PRT; 321 AA.
AC Q9P3R4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein B24P7.210.
GN Name=B24P7.210;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL398890; CAB97286.1; -; Genomic DNA.
DR PIR; T50966; T50966.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 33921 MW; 4FF62126A23C0930 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 321;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||:
Db 78 GATNLAS 84

RESULT 6

Q7NCF3 GLOVI
ID Q7NCF3 GLOVI PRELIMINARY; PRT; 606 AA.
AC Q7NCF3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gll3026 protein.
GN OrderedLocustNames=gll3026;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a cyanobacterium that lacks thylakoids.";

RL DNA Res. 10:137-145(2003).
DR EMBL; BA000045; BAC30967.1; -; Genomic DNA.
KW Complete proteome.
SQ SEQUENCE 606 AA; 65119 MW; B9044983DBA17F74 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 606;
Best Local Similarity 85.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||:
Db 87 GATNVAA 93

RESULT 7

Q4MIJ6 BACCE
ID Q4MIJ6 BACCE PRELIMINARY; PRT; 666 AA.
AC Q4MIJ6
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein, putative.
GN ORFNames=BCE_G9241_5357, BCE_G9241_5379, BCE_G9241_CNI_0020;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hofmeister A.R., Ravel J., Raeko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rilestone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AAOK01000055; EAL12001.1; -; Genomic DNA.
DR EMBL; AAOK01000067; EAL11710.1; -; Genomic DNA.
DR EMBL; AAOK01000029; EAL13246.1; -; Genomic DNA.
SQ SEQUENCE 666 AA; 71897 MW; 476F4EED422AB2E0 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 666;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||:
Db 379 GATNLAS 385

RESULT 8

Q72XPI BACCI
ID Q72XPI BACCI PRELIMINARY; PRT; 666 AA.
AC Q72XPI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BCE5334;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,

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RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AB017281; AA944234.1; -; Genomic_DNA.
DR TIGR; BC55334; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 666 AA; 71796 MW; 0505A9B563FD0BC9 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 666;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 379 GATNLAS 385

RESULT 9
Q88X96_LACPL PRELIMINARY; PRT; 983 AA.
AC Q88X96;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Integral membrane protein.
GN OrderedLocustNames=lp_1332;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nisroep Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935255; CAD63818.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 983 AA; 103421 MW; 0ADP5C2604B4CD66 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 983;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 564 GATNLAS 570

RESULT 10
Q80UR2_MESAU PRELIMINARY; PRT; 136 AA.
ID Q80UR2;
AC Q80UR2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Perilipin (Fragment).
GN Name=perilipin;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Sebaceous glands;
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RX PubMed=15955086; DOI=10.1111/j.0022-202x.2005.23718.x;
RA Akimoto N., Sato T., Iwata C., Koshizuka M., Shibata F., Nagai A.,
RA Sumida M., Ito A.;
RT "Expression of Perilipin A on the Surface of Lipid Droplets Increases
RT along with the Differentiation of Hamster Sebocytes In Vivo and In
RT Vitro.";
RL J. Invest. Dermatol. 124:1127-1133(2005).
DR EMBL; AB091681; BAC76043.1; -; mRNA.
DR InterPro; IPR004279; Perilipin.
DR Pfam; PF03036; Perilipin; 1.
FT NON_TER 1
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 14896 MW; 3D1C214BFBF5A9A3 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 57 GASNLAA 63

RESULT 11
Q51T81_MAGGR PRELIMINARY; PRT; 166 AA.
ID Q51T81;
AC Q51T81;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Predicted protein.
GN ORFNames=MG08717.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Girke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvesselis M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menes L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Nicks C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotohso B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,
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RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea.";
 RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACU01001197; EAA51195.1; -; Genomic DNA.
 SQ SEQUENCE 166 AA; 17624 MW; 3A637AEBB7A5FF14 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 GATNLA 6
 DB 86 GATNLA 91
 |||||
 |||||
 RESULT 12
 Q69MC6_ORYSA PRELIMINARY; PRT; 166 AA.
 ID Q69MC6_ORYSA PRELIMINARY;
 AC Q69MC6;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Hypothetical protein OSJNB0019B14.27.
 GN Name=OSJNB0019B14.27;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
 RT clone:OSJNB0019B14.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005755; BAD33956.1; -; Genomic DNA.
 DR Gramene; Q69MC6; -;
 KW Hypothetical protein.
 SQ SEQUENCE 166 AA; 17462 MW; 40B44F36B6A96AE CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 GATNLA 6
 DB 74 GATNLA 79
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 |||||
 RESULT 13
 Q827C0_SALTI PRELIMINARY; PRT; 166 AA.
 ID Q827C0_SALTI PRELIMINARY;
 AC Q827C0; Q7C914;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Hypothetical protein STY1360.

GN Ordered locus names=STY1360, t1605;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TY2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 DR EMBL; AL627270; CAD01629.1; -; Genomic DNA.
 DR EMBL; AB016839; AAO69233.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 166 AA; 18143 MW; A88804EE1456E3E4 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 GATNLA 6
 DB 27 GATNLA 32
 |||||
 |||||
 RESULT 14
 THIG_MYCBO STANDARD; PRT; 252 AA.
 ID THIG_MYCBO STANDARD; PRT; 252 AA.
 AC P59948;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thiazole biosynthesis protein thig.
 GN Name=thig; Ordered locus names=Mb0425;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1765;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of Mycobacterium bovis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 CC -!- FUNCTION: Required for the synthesis of the thiazole moiety of
 CC thiamine (By similarity).
 CC -!- COFACTOR: FMN (Potential).
 CC -!- PATHWAY: Thiamine biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

```
CC -|- SIMILARITY: Belongs to the thiG family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX248335; CA093288.1; -; Genomic_DNA.
DR HAMAP; MF_00443; -; 1.
DR InterPro; IPR003009; Related_FMN_bd.
DR InterPro; IPR008867; ThiG.
DR Pfam; PF05690; ThiG; 1.
DR Complete proteome; Flavoprotein; FMN; Thiamine biosynthesis.
SQ SEQUENCE 252 AA; 25894 MW; 91B8B1AE28115512 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 23 GATNLA 28

RESULT 15
THIS_MYCTU STANDARD; PRT; 252 AA.
AC P96263;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thiazole biosynthesis protein thiG.
GN Name=thiG; OrderedLocNames=KV0417, MT0430; ORFNames=MTCY22G10.14;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / Oshkosh;
RC MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
CC -|- FUNCTION: Required for the synthesis of the thiazole moiety of
CC thiamine (By similarity).
CC -|- COFACTOR: FMN (Potential).
CC -|- PATHWAY: Thiamine biosynthesis.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

```
CC -|- SIMILARITY: Belongs to the thiG family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX842573; CAB06587.1; -; Genomic_DNA.
DR EMBL; AE000516; AAK44654.1; -; Genomic_DNA.
DR FJR; G70629; G70629.
DR TIGR; MT0430; -.
DR TubercuList; RV0417; -.
DR HAMAP; MF_00443; -; 1.
DR InterPro; IPR003009; Related_FMN_bd.
DR InterPro; IPR008867; ThiG.
DR Pfam; PF05690; ThiG; 1.
DR Complete proteome; Flavoprotein; FMN; Thiamine biosynthesis.
FT CONFLICT 75 75 S -> C (in Ref. 2).
SQ SEQUENCE 252 AA; 25878 MW; C1B4DC1492B7920E CRC64;

Query Match 87.9%; Score 29; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 23 GATNLA 28

RESULT 16
O32397_ERYLO PRELIMINARY; PRT; 258 AA.
ID O32397_ERYLO
AC O32397;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center M subunit (Fragment).
GN Name=pufM;
OS Erythrobacter longus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=1044;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97383243; PubMed=9236272;
RA Nagashima K.V., Hiraishi A., Shimada K., Matsuura K.;
RT "Horizontal transfer of genes coding for the photosynthetic reaction
RT centers of purple bacteria.";
RL J. Mol. Evol. 45:131-136(1997).
DR EMBL; D50648; BAA22640.1; -; Genomic_DNA.
DR HSP; P02953; lU9B.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. .; IEA.
DR GO; GO:0030090; C:reaction center (sensu Proteobacteria); IEA.
DR GO; GO:0042314; F:bacteriochlorophyll binding; IEA.
DR GO; GO:0045156; F:electron transporter, transferring electron. .; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR GO; GO:0019684; F:photosynthesis, light reaction; IEA.
DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005781; Photo M.
DR InterPro; IPR004484; Photo_RC.
DR Pfam; PF00124; Photo RC; 1.
DR TIGRfams; TIGR0115; pufM; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
FT NON TER 258 258
SQ SEQUENCE 258 AA; 29248 MW; 303F2B1C274F51FE CRC64;

Query Match 87.9%; Score 29; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
|||||
Db 221 GATNLA 226

RESULT 17

Q7Q7D3 ANOGA
ID Q7Q7D3 ANOGA PRELIMINARY; PRT; 268 AA.
AC Q7Q7D3;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENSANGP0000021073 (Fragment).
GN ORFNames=ENSANG0000018584;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
(1)
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG "Anopheles gambiae re-annotation."
RT Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAAB01008960; EAA11330.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 268 AA; 28133 MW; F48C32CC7E22B1A2 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
|||||
Db 23 GATNLA 28

RESULT 18

Q6S9M2 LEPBO
ID Q6S9M2 LEPBO PRELIMINARY; PRT; 281 AA.
AC Q6S9M2;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE OmpL1 (Fragment).
GN Name=ompL1;
OS Leptospira borgpetersenii.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=174;
(1)
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Sari;
RC STRAIN=Sari;
RX PubMed=15090524; DOI=10.1128/JB.186.9.2818-2828.2004;
RA Haake D.A., Suchard M.A., Kelley M.M., Dundoo M., Alt D.P.,
RA Zuerner R.B.;
RT "Molecular evolution and mosaicism of leptospiral outer membrane
proteins involves horizontal DNA transfer."
RL J. Bacteriol. 186:2818-2828(2004).
DR EMBL; AY461973; AAS21843.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 281 AA; 29199 MW; 8AAB2B58A5572B75 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
|||||
Db 272 GATNLA 277

RESULT 19

Q87GM7 VIBPA
ID Q87GM7 VIBPA PRELIMINARY; PRT; 282 AA.
AC Q87GM7;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein VPA1288.
GN OrderedLocusNames=VPA1288;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
(1)
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=RIMD 2210633 / Serotype O3:K6;
RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nejima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; BA000032; BAC62631.1; -; Genomic DNA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; I.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 282 AA; 31480 MW; EEC3C400A79E557B CRC64;

Query Match 87.9%; Score 29; DB 2; Length 282;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 7
|||||
Db 45 GASNLAA 51

RESULT 20

QSP193 SALPA
ID QSP193 SALPA PRELIMINARY; PRT; 294 AA.
AC QSP193;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SPAL186;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
(1)
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du P., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Florea L.,
RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;


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RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
PL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; AAV77144.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 294 AA; 32077 MW; 6F8E276CC09FA686 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
Db 24 GATNLAA 29

RESULT 21
Q5V2S2 HALMA
ID Q5V2S2 HALMA PRELIMINARY; PRT; 303 AA.
AC Q5V2S2
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Cysteine synthase (EC 2.5.1.47).
GN Name=cysK1; OrderedLocusNames=rnAC1236;
OS Haloarcula marismortui (Haloacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STPAIN=NCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
DR EMBL; AY596297; AAV46180.1; -; Genomic_DNA.
DR GO; GO:0004124; F:cysteine synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR001216; Cys_synthase_BS.
DR Pfam; PF00291; PALP; 1.
DR PROSITE; PS00901; CYS_SYNTHASE; UNKNOWN 1.
KW Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 303 AA; 32332 MW; 161705E9BE8A006D CRC64;

Query Match 87.9%; Score 29; DB 2; Length 303;
Best Local Similarity 85.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 262 GASNLAA 269

RESULT 22
Q965J1 CABEL
ID Q965J1 CABEL PRELIMINARY; PRT; 309 AA.
AC Q965J1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORENAMES-T24A6.20;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF068713; AAK73896.2; -; Genomic_DNA.
DR Ensembl; T24A6.20; Caenorhabditis elegans.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 309 AA; 35340 MW; 82C6B57A6B9781E5 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 309;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 54 GTTNLAA 60

RESULT 23
Q8UDP2 AGRTS
ID Q8UDP2 AGRT5 PRELIMINARY; PRT; 309 AA.
AC Q8UDP2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ABC transporter, membrane spanning protein.
GN OrderedLocusNames=Atu2079;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yeo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009158; AAL43070.1; -; Genomic_DNA.
DR PIR; AH2831; AH2831.
DR PIR; D97609; D97609.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6_TM.
DR Pfam; PF00892; DUF6; 2.
KW Complete proteome.
SQ SEQUENCE 309 AA; 32531 MW; 554D18DC75A88F65 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
Db 247 GATNLAA 252

RESULT 24
Q7CXX5 AGRT5
ID Q7CXX5 AGRT5 PRELIMINARY; PRT; 329 AA.
AC Q7CXX5;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR C 3767p.
GN OrderedLocusNames=AGR C 3767;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cereon;
EX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
DR EMBL: AE008124; AAK87829.1; -: Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR000820; DUF6_TW.
DR Pfam: PF00892; DUF6; 2.
SQ SEQUENCE 329 AA; 34794 MW; 5C38B645E01C3122 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 267 GATNLA 272

RESULT 25
Q89J14 BRAJA
ID Q89J14 BRAJA PRELIMINARY; PRT; 341 AA.
AC Q89J14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Blx5470 protein.
GN OrderedLocusNames=blx5470;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
EX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideawa K., Iriiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197 (2002).
DR EMBL: BA000040; BAC50735.1; -: Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 341 AA; 36376 MW; C06380842D3821D8 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 278 GATNLA 283

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR C 3767p.
GN OrderedLocusNames=AGR C 3767;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cereon;
EX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
DR EMBL: AE008124; AAK87829.1; -: Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR000820; DUF6_TW.
DR Pfam: PF00892; DUF6; 2.
SQ SEQUENCE 329 AA; 34794 MW; 5C38B645E01C3122 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 267 GATNLA 272

RESULT 26
Q54SD6 DICDI
ID Q54SD6 DICDI PRELIMINARY; PRT; 416 AA.
AC Q54SD6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DOB0204814;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wadrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lushneg H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Uruishihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Shugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauleky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0 (2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 48587 MW; F59404E8929376BA CRC64;

Query Match 87.9%; Score 29; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 185 GATNLA 190

RESULT 27
Q53TX6 HUMAN
ID Q53TX6 HUMAN PRELIMINARY; PRT; 419 AA.
AC Q53TX6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein MGC39518 (Fragment).
GN Name=MGC39518;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Abbott A., Le T.;
RT "The sequence of Homo sapiens BAC clone RP11-469M7."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RA Waterston R.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005037; AAY14726.1; -, Genomic_DNA.
KW Hypothetical protein.
FT NPT
SQ SEQUENCE 419 AA; 45672 MW; 903F77CA4E200E2E CRC64;

Query Match 87.9%; Score 29; DB 2; Length 419;
Best Local Similarity 85.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 364 GGTNLAA 370

RESULT 28
Q8SVJ6_DROME
ID Q8SVJ6_DROME PRELIMINARY; PRT; 460 AA.
AC Q8SVJ6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Putative Na+/H+ antiporter.
DE RE56061p
GN Name=CG6328; ORFNames=CG31176;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.G., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071506; AAL49128.1; -, mRNA.
DR Ensembl; CG31176; Drosophila melanogaster.
DR FlyBase; FBgn0051176; CG31176.
SQ SEQUENCE 460 AA; 47918 MW; 286E147E39FB73DA CRC64;

Query Match 87.9%; Score 29; DB 2; Length 460;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 364 GGTNLAA 370

RESULT 29
Q58A59_TETHA
ID Q58A59_TETHA PRELIMINARY; PRT; 462 AA.
AC Q58A59;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Putative Na+/H+ antiporter.
DE Name=nharth;
GN Tetragenococcus halophilus (Pediococcus halophilus).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;

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OC Tetragenococcus.
OX NCBI_TaxID=51669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Takahashi K.;
RT "Cloning and Nucleotide Sequence of Tyrosine Decarboxylase gene from
RT Tetragenococcus halophilus.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB059363; BAD93618.1; -, Genomic_DNA.
SQ SEQUENCE 462 AA; 49939 MW; D940131E5E041D87 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 462;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 175 GTTNLAA 181

RESULT 30
Q529X3_ORYZA
ID Q529X3_ORYZA PRELIMINARY; PRT; 477 AA.
AC Q529X3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative UDP-glycosyltransferase 88B1.
GN Name=P0459H02.26;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0459H02.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY; Belongs to the UDP-glycosyltransferase family.
DR EMBL; AP003572; BAD61637.1; -, Genomic_DNA.
DR Gramene; Q529X3; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP-glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
DR Glycosyltransferase; Transferase.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 477 AA; 50410 MW; C0C9BA04947EE8D6 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
Db 141 GATNLAA 146

RESULT 31
Q6Y9B4_BORHE
ID Q6Y9B4_BORHE PRELIMINARY; PRT; 481 AA.
AC Q6Y9B4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Borrelia hermsii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=140;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RA Putteet-Driver A.D., Zhong J., Barbour A.G.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY169385; AAC3712.1; -; Genomic DNA.
 DR GO; GO:0004516; P:nicotinate phosphoribosyltransferase activity; IEA.
 DR GO; GO:0019363; P:pyridine nucleotide biosynthesis; IEA.
 DR InterPro; IPR007229; NARPTase.
 DR InterPro; IPR006405; Nic_PRRans_like.
 DR Pfam; PF04095; NARPTase; 1.
 DR TIGRPFAMs; TIGR01513; NARPTase_put; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 55481 MW; 2E5CALP54B1CD98 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 481;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
 |||||
 DB 146 GATNLA 151

RESULT 32
 PLIN MOUSE
 ID PLIN MOUSE STANDARD; PRT; 517 AA.
 AC Q8CGN5;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Perilipin (PERI) (Lipid droplet-associated protein).
 GN Name=Plin; Synonyms=Peri;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Tansey J.T., Lu X., Londres C., Kimmel A.R.;
 RT "Mouse perilipin."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP INTERACTION WITH ABHD5.
 RX PubMed15292255; DOI=10.1074/jbc.M407462200;
 RA Subramanian V., Rothenberg A., Gomez C., Cohen A.W., Garcia A.,
 RA Bhattacharya S., Shapiro L., Dolios G., Wang R., Lisanti M.P.,
 RA Braaele D.L.;
 RT "Perilipin A mediates the reversible binding of CGI-58 to lipid droplets in 3T3-L1 adipocytes."
 RL J. Biol. Chem. 279:42062-42071(2004).
 CC -!- FUNCTION: Modulator of adipocyte lipid metabolism, it coats lipid storage droplets to protect them to be broken down by hormone-sensitive lipase (HSL). Its absence may result in leanness (By similarity).
 CC -!- SUBUNIT: Interacts with ABHD5.
 CC -!- SUBCELLULAR LOCATION: Lipid droplet surface-associated (By similarity).
 CC -!- PTM: Major camp-dependent protein kinase-substrate in adipocytes, also dephosphorylated by pp1. When phosphorylated, may be maximally sensitive to HSL and when unphosphorylated, may play a role in the inhibition of lipolysis, by acting as a barrier in lipid droplet (By similarity).
 CC -!- SIMILARITY: Belongs to the perilipin family.
 CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 10 of May 2001; WWW="http://www.expasy.org/spotlight/back_issues/spt10.0.shtml".
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC
 CC EMBL; AY161165; AAN77870.1; -; mRNA.
 DR Ensembl; ENSMUSG00000030546; Mus musculus.

DR Reactome; Q8CGN5; -;
 DR MGI; MGI:1890505; Plin.
 DR GO; GO:0005811; C:Lipid particle; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0016042; P:lipid catabolism; IMP.
 DR InterPro; IPR004279; Perilipin.
 DR Pfam; PF03036; Perilipin; 1.
 KW Lipid metabolism; Phosphorylation.
 FT COMPIAS 308 319 Poly-Glu.
 SQ SEQUENCE 517 AA; 55578 MW; 906AE0F4743D65AE CRC64;

Query Match 87.9%; Score 29; DB 1; Length 517;
 Best Local Similarity 85.7%; Pred. No. 7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 7
 |||||
 DB 64 GATNLA 70

RESULT 33
 PLIN RAT
 ID PLIN RAT STANDARD; PRT; 517 AA.
 AC P43884;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Perilipin (PERI) (Lipid droplet-associated protein).
 GN Name=Plin;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS A AND B), AND PARTIAL PROTEIN SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
 RX MEDLINE=94089764; PubMed=7505452;
 RA Greenberg A.S., Egan J.J., Wek S.A., Moos M.C. Jr., Londres C., Kimmel A.R.;
 RT "Isolation of cDNAs for perilipins A and B: sequence and expression of lipid droplet-associated proteins of adipocytes."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:12035-12039(1993).
 RN [2]
 RP PHOSPHORYLATION.
 RX MEDLINE=98427303; PubMed=9755872; DOI=10.1016/S0014-5793(98)01052-7;
 RA Clifford G.M., McCormick D.K., Londres C., Vernon R.G., Yeaman S.J.;
 RT "Dephosphorylation of perilipin by protein phosphatases present in rat adipocytes."
 RL FEBS Lett. 435:125-129(1998).
 CC -!- FUNCTION: Modulator of adipocyte lipid metabolism, it coats lipid storage droplets to protect them to be broken down by hormone-sensitive lipase (HSL). Its absence may result in leanness.
 CC -!- SUBUNIT: Interacts with ABHD5.
 CC -!- SUBCELLULAR LOCATION: Lipid droplet surface-associated.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A; Synonyms=PERIA;
 CC IsoId=P43884-1; Sequence=Displayed;
 CC Name=B; Synonyms=PERIB;
 CC IsoId=P43884-2; Sequence=VSP_004662, VSP_004663;
 CC -!- TISSUE SPECIFICITY: Adipocytes.
 CC -!- PTM: Major camp-dependent protein kinase substrate in adipocytes, also dephosphorylated by pp1. When phosphorylated, may be maximally sensitive to HSL. When unphosphorylated, may play a role in the inhibition of lipolysis, by acting as a barrier in lipid droplet.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the perilipin family.
 CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 10 of May 2001; WWW="http://www.expasy.org/spotlight/back_issues/spt10.0.shtml".
 CC

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CC -----
 CC ENBL; L26043; AAA41830.1; -; mRNA.
 CC DR ENBL; L26044; AAA41831.1; -; mRNA.
 CC DR PTR; A49413; A49413.
 CC DR Ensembl; ENSRNOG00000015086; Rattus norvegicus.
 CC DR Reactome; P43884; -.
 CC DR RGD; 3351; Plin.
 CC DR InterPro; IPR004279; Perilipin.
 CC DR Pfam; PF03036; Perilipin; 1
 CC DR Alternative splicing; Direct protein sequencing; Lipid metabolism;
 KW Phosphorylation.
 FT COMPBIAS 308 Poly-Glu.
 FT VARSPLIC 407 LPRLSLMEPSEFQDI -> VSPAPGPPSDSQGRFD (in
 FT isoform B).
 FT VARSPLIC 423 /FTid=VSP_004662.
 FT Missing (in isoform B).
 FT /FTid=VSP_004663.
 SQ SEQUENCE 517 AA; 55614 MW; 1041F76DC2F55A25 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 517;
 Best Local Similarity 85.7%; Pred. No. 7e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0;

Qy 1 GATNLAA 7
 ||:||||
 Db 64 GASNLAA 70

RESULT 34

Q8OCF5 MOUSE
 ID Q8OCF5 MOUSE PRELIMINARY; PRT; 517 AA.
 AC Q8OCF5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
 DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
 DE enriched library, clone:6030432J05 product:PERILIPIN (PERI) (LIPID
 DE DROPLT-ASSOCIATED PROTEIN) homolog.
 GN Name=Plin;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:11617-1630(2000).
 RN [5]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
 RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Kagawa I., Kasukawa T.,
 RA Hori F., Imotani K., Iehii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AK031445; BAC27409.1; -; mRNA.
 DR Ensembl; ENSMUSG00000030546; Mus musculus.
 DR MGI; MGI-1890505; Plin.
 DR GO; GO:0005811; C:lipid particle; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0016042; F:lipid catabolism; IMP.
 DR InterPro; IPR004279; Perilipin.
 DR Pfam; PF03036; Perilipin; 1.
 SQ SEQUENCE 517 AA; 55581 MW; FB85D453F11250AF CRC64;

Query Match 87.9%; Score 29; DB 2; Length 517;

Best Local Similarity 85.7%; Pred. No. 7e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0;

Qy 1 GATNLAA 7
 ||:||||
 Db 64 GASNLAA 70

RESULT 35

Q4V9U2_MOUSE
 ID Q4V9U2_MOUSE PRELIMINARY; PRT; 517 AA.
 AC Q4V9U2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Perilipin.
 GN Name=Plin;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC096685; AAH96685.1; -; mRNA.
 SQ SEQUENCE 517 AA; 55536 MW; 906AE1CCSAF65AE CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 517;
 Best Local Similarity 85.7%; Pred. No. 7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLAA 7
 ||:||||
 DB 64 GASNLAA 70

RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACW01000321; EAA77277.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 525 AA; 59957 MW; 814CA016D5783F26 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 525;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GATNLAA 6
 ||:||||
 DB 135 GATNLAA 140

RESULT 37
 Q4HWP9_GIBZE PRELIMINARY; PRT; 529 AA.
 ID Q4HWP9;
 AC Q4HWP9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG10609.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepl Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

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RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACW01000444; EAA68618.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 529 AA; 5638 MW; E6A6190C71BF2316 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 493 GATNLA 498

RESULT 38
Q8IXS8_HUMAN
ID Q8IXS8_HUMAN PRELIMINARY; PRT; 530 AA.
AC Q8IXS8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein MGC39518.
GN Name=MGC39518;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 1 GATNLA 6
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Carninci P.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 1 GATNLA 6
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Testis;
RG NIH MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC039295; AAH39295.1; -; mRNA.
DR EMBL; ENSG00000155744; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 530 AA; 58647 MW; FD48E6AAB39D5AC CRC64;

Query Match 87.9%; Score 29; DB 2; Length 530;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 475 GATNLAA 481

RESULT 39
Q5R977_PONPY
ID Q5R977_PONPY PRELIMINARY; PRT; 530 AA.
AC Q5R977;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459C1125.
GN Name=DKFZp459C1125;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN 1 GATNLAA 7
RP NUCLEOTIDE SEQUENCE.
RS TISSUE=Cortex;
RG The German cDNA Consortium;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR859515; CAH91683.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 530 AA; 58634 MW; 43B492A7B7B818B0 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 530;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 475 GATNLAA 481

RESULT 40
Q8C729_MOUSE
ID Q8C729_MOUSE PRELIMINARY; PRT; 530 AA.
AC Q8C729;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
DE library, clone:D630010C10 product:weakly similar to DRCTNNB1A.
GN Name=BC049806;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1 GATNLAA 7
RP NUCLEOTIDE SEQUENCE.
RS STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN 1 GATNLAA 7
RP NUCLEOTIDE SEQUENCE.
RS STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Kashiwagi K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052638; RAC35073.1; -; mRNA.
DR Ensembl; ENSMUSG00000038174; Mus musculus.
DR MGI; MGI:2674086; BC049806.
SQ SEQUENCE 530 AA; 58586 MW; 7C57D7C10D047FD7 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 530;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
Db 475 GVTNLAA 481

RESULT 41
Q6NV64_MOUSE

ID Q6NV64_MOUSE PRELIMINARY; PRT; 530 AA.
AC Q6NV64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA sequence BC049806.
GN Name=BC049806;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068302; AAH68302.1; -; mRNA.
SQ SEQUENCE 530 AA; 58614 MW; 74F55C51BB461B46 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 530;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
Db 475 GVTNLAA 481

RESULT 42
Q4JUN7_CORJK
ID Q4JUN7_CORJK PRELIMINARY; PRT; 563 AA.
AC Q4JUN7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Formate hydrogenlyase subunit precursor (EC 1.6.5.3).
GN Name=mhD; ORFNames=jki1988;
OS Corynebacterium jeikeium (strain K411).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=306537;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K411;
RX PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
RA Tauch A., Kaiser O., Hain T., Goessmann A., Weisshaar B.,
RA Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty T.,
RA Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoveer P.,


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RA Publer A.;
RT "Complete Genome Sequence and Analysis of the Multiresistant
RT Nosocomial Pathogen Corynebacterium jeikeium K411, a Lipid-Requiring
RT Bacterium of the Human Skin Flora.";
RL J. Bacteriol. 187:4671-4682 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K411;
RA Linke B., Tauch A.;
RL Submitted (DSC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR931997; CA138170.1; -; Genomic_DNA.
KW Lyase; Oxidoreductase; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 563 AA; 59886 MW; 96BA3826FE7A1214 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 563;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 185 GTTNLAA 191

RESULT 43
Q7VEM4 MYCBO PRELIMINARY; PRT; 592 AA.
AC Q7VEM4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical proline rich protein.
GN OrderedLocusNames=Mb2287c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
CX NCBI_TaxID=1765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12789972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
DR EMBL; BX248342; CAD97148.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR PRINTS; PR00301; HEATSHOCK70.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 592 AA; 59848 MW; E6D36B8B95786F9B CRC64;

Query Match 87.9%; Score 29; DB 2; Length 592;
Best Local Similarity 85.7%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 14 GVTNLAA 20

RESULT 44
O53538 MYCTU PRELIMINARY; PRT; 592 AA.
AC O53538; Q7D7C7;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved hypothetical proline rich protein (Hypothetical
DE protein).

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GN OrderedLocusNames=MT2324, RV2264c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
CX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekait F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
DR EMBL; BX842579; CAA17301.1; -; Genomic_DNA.
DR EMBL; AE000516; AAK46606.1; -; Genomic_DNA.
DR PIR; D70863; D70863.
DR TIGR; MT2324; -;
DR TubercuList; RV2264c; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR PRINTS; PR00301; HEATSHOCK70.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 592 AA; 59848 MW; E6D36B8B95786F9B CRC64;

Query Match 87.9%; Score 29; DB 2; Length 592;
Best Local Similarity 85.7%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 14 GVTNLAA 20

RESULT 45
O57CH5 BRUAB PRELIMINARY; PRT; 619 AA.
AC O57CH5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Potassium efflux system family protein.
GN OrderedLocusNames=BrUAb1_1325;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
CX NCBI_TaxID=235;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RX Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,

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RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT "Completion of the genome sequence of Brucella abortus and comparison
RT to the highly similar genomes of Brucella melitensis and Brucella
RT suis.";
RL J. Bacteriol. 187:2715-2726(2005).
DR EMBL; AF017223; AAX74659.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR003148; TrKA_N.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF02254; TrKA_N; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome.
SQ SEQUENCE 619 AA; 64800 MW; EAE2868E340797C8 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      408 GATNLTA 414
      |||||
      |||||

RESULT 46
QBPZ25 BRUSU
ID QBPZ25 BRUSU PRELIMINARY; PRT; 619 AA.
AC QBPZ25
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Potassium efflux system family protein.
GN OrderedLocusNames=BR1325;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kaul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.B., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AF014291; AAN30239.1; -; Genomic_DNA.
DR TIGR; BR1325; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR003148; TrKA_N.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF02254; TrKA_N; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.

QY      1 GATNLAA 7
DB      408 GATNLTA 414
      |||||
      |||||

RESULT 47
QBYHW7 BRUME
ID QBYHW7 BRUME PRELIMINARY; PRT; 619 AA.
AC QBYHW7
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE POTASSIUM/PROTON ANTIPORTER ROSB.
GN OrderedLocusNames=BMEI0679;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyripides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009509; AAL51860.1; -; Genomic_DNA.
DR PIR; A13336; A13336.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR003148; TrKA_N.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF02254; TrKA_N; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome.
SQ SEQUENCE 619 AA; 64822 MW; 8A3164B4A546DB1 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      408 GATNLTA 414
      |||||
      |||||

RESULT 48
QGV25 WHEAT
ID Q6GV25 WHEAT PRELIMINARY; PRT; 745 AA.
AC Q6GV25
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SET domain protein.
OS Triticum aestivum (Wheat).
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KW Complete proteome.
SQ SEQUENCE 619 AA; 64818 MW; CCF0BBD9372BD1DA CRC64;

Query Match      87.9%; Score 29; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      408 GATNLTA 414
      |||||
      |||||

RESULT 47
QBYHW7 BRUME
ID QBYHW7 BRUME PRELIMINARY; PRT; 619 AA.
AC QBYHW7
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE POTASSIUM/PROTON ANTIPORTER ROSB.
GN OrderedLocusNames=BMEI0679;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyripides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009509; AAL51860.1; -; Genomic_DNA.
DR PIR; A13336; A13336.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR003148; TrKA_N.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF02254; TrKA_N; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome.
SQ SEQUENCE 619 AA; 64822 MW; 8A3164B4A546DB1 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 619;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      408 GATNLTA 414
      |||||
      |||||

RESULT 48
QGV25 WHEAT
ID Q6GV25 WHEAT PRELIMINARY; PRT; 745 AA.
AC Q6GV25
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SET domain protein.
OS Triticum aestivum (Wheat).
```

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang Z.J., Li G.R., Ren Z.L.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY634575; AAT47546.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0018024; F:histone-lysine N-methyltransferase activity; IEA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016568; P:chromatin modification; IEA.
DR InterPro; IPR003616; PostSET.
DR InterPro; IPR007728; Pre-SET.
DR InterPro; IPR001214; SET.
DR InterPro; IPR003105; SRA_YDG.
DR InterPro; IPR003606; Zn2-binding.
DR Pfam; PF05033; Pre-SET; 1.
DR Pfam; PF00856; SET; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR SMART; SM00468; PreSET; 1.
DR SMART; SM00317; SET; 1.
DR SMART; SM00466; SRA; 1.
DR PROSITE; PS0868; POST_SET; 1.
DR PROSITE; PS0867; PRE_SET; 1.
DR PROSITE; PS0280; SET; 1.
DR PROSITE; PS1015; YDG; 1.
SQ SEQUENCE 745 AA; 81225 MW; DC18F6C6AEEC9039 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 745;
Best Local Similarity 85.7%; Pred. No. 1.e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GATNLAA 7
Db 128 GATNLGA 134

RESULT 49
O6CAY1 YARLI PRELIMINARY; PRT; 828 AA.
AC O6CAY1.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similarity.
GN OrderedLocusNames=YALI10C23430g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Catroli L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).

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DR EMBL; CR382129; CAG82501.1; -; Genomic_DNA.
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 828 AA; 92393 MW; 7FAD42F88AB99E3 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 828;
Best Local Similarity 85.7%; Pred. No. 1.e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GATNLAA 7
Db 23 GATNLFAA 29

RESULT 50
Q7QS38 GIALA PRELIMINARY; PRT; 845 AA.
AC Q7QS38;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP_661_336_2873.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000125; EAA37816.1; -; Genomic DNA.
SQ SEQUENCE 845 AA; 96240 MW; D59B70BF6A5A2E2D CRC64;

Query Match 87.9%; Score 29; DB 2; Length 845;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GATNLA 6
Db 204 GATNLA 209

Search completed: May 11, 2006, 16:36:16
Job time : 101.721 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:37 ; Search time 16.1803 Seconds
(without alignments)
35.767 Million cell updates/sec

Title: US-10-808-538-5

Perfect score: 33

Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA.*

1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgm2_6/ptodata/1/iaa/PCRUS COMB.pep.*

5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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264	25	75.8	1104	2	US-09-268-347-28	Sequence 28, Appl	337	24	72.7	284	2	US-10-193-002-157	Sequence 157, App
265	25	75.8	1104	2	US-09-268-347-34	Sequence 34, Appl	338	24	72.7	284	2	US-10-084-843-162	Sequence 162, App
266	25	75.8	1105	2	US-09-540-236-3299	Sequence 3299, Ap	339	24	72.7	285	1	US-08-964-631-4	Sequence 4, Appli
267	25	75.8	1849	2	US-08-851-567B-49	Sequence 49, Appl	340	24	72.7	285	2	US-09-210-000-4	Sequence 4, Appli
268	25	75.8	2283	2	US-10-172-502-4	Sequence 4, Appli	341	24	72.7	286	2	US-09-252-991A-27451	Sequence 27451, A
269	25	75.8	2353	2	US-09-377-155-33	Sequence 33, Appl	342	24	72.7	286	2	US-09-724-797-80	Sequence 80, Appl
270	25	75.8	2353	2	US-08-913-942-4	Sequence 4, Appli	343	24	72.7	289	2	US-09-252-991A-31795	Sequence 31795, A
271	25	75.8	2353	2	US-09-669-974-33	Sequence 33, Appl	344	24	72.7	303	2	US-09-982-616-10	Sequence 10, Appl
272	25	75.8	2353	2	US-09-797-862-33	Sequence 33, Appl	345	24	72.7	307	2	US-09-248-796A-17597	Sequence 17597, A
273	25	75.8	2353	2	US-09-684-707-4	Sequence 4, Appli	346	24	72.7	308	2	US-09-489-039A-7674	Sequence 7674, Ap
274	25	75.8	2354	2	US-09-268-347-36	Sequence 36, Appl	347	24	72.7	313	2	US-09-413-814-9	Sequence 9, Appli
275	25	75.8	2411	2	US-09-268-347-36	Sequence 36, Appl	348	24	72.7	315	2	US-09-362-318-2	Sequence 2, Appli
276	25	75.8	2516	2	US-08-851-567B-47	Sequence 47, Appl	349	24	72.7	324	2	US-09-902-540-12246	Sequence 12246, A
277	25	75.8	2516	2	US-09-817-514A-2	Sequence 2, Appli	350	24	72.7	326	2	US-09-252-991A-17002	Sequence 17002, A
278	25	75.8	2522	2	US-09-251-645-13	Sequence 13, Appl	351	24	72.7	328	2	US-09-489-039A-9462	Sequence 9462, Ap
279	25	75.8	6396	2	US-09-940-316B-72	Sequence 72, Appl	352	24	72.7	333	2	US-10-101-464A-561	Sequence 561, App
280	25	75.8	6396	2	US-09-940-316B-72	Sequence 72, Appl	353	24	72.7	338	2	US-09-489-039A-12908	Sequence 12908, A
281	24	72.7	63	2	US-09-328-352-5112	Sequence 5112, Ap	354	24	72.7	340	2	US-10-155-947-2	Sequence 2, Appli
282	24	72.7	65	2	US-09-248-796A-23985	Sequence 23985, A	355	24	72.7	341	2	US-09-248-796A-20398	Sequence 20398, A
283	24	72.7	89	2	US-09-489-039A-10643	Sequence 10643, A	356	24	72.7	345	2	US-09-252-991A-22818	Sequence 22818, A
284	24	72.7	100	2	US-09-534-717-607	Sequence 607, App	357	24	72.7	348	2	US-09-931-401B-2	Sequence 2, Appli
285	24	72.7	105	2	US-09-917-254-71	Sequence 71, Appl	358	24	72.7	353	2	US-09-982-616-2	Sequence 2, Appli
286	24	72.7	106	2	US-09-489-039A-10178	Sequence 10178, A	359	24	72.7	356	2	US-09-543-681A-6562	Sequence 6562, Ap
287	24	72.7	123	2	US-09-270-767-58097	Sequence 58097, A	360	24	72.7	359	2	US-09-270-767-42195	Sequence 42195, A
288	24	72.7	123	2	US-10-104-047-2234	Sequence 2234, Ap	361	24	72.7	362	2	US-09-252-991A-31349	Sequence 31349, A
289	24	72.7	128	2	US-09-134-000C-6453	Sequence 6453, Ap	362	24	72.7	363	2	US-09-489-039A-11134	Sequence 11134, A
290	24	72.7	129	2	US-09-302-626B-66	Sequence 66, Appl	363	24	72.7	370	2	US-08-857-076-104	Sequence 104, App
291	24	72.7	154	2	US-09-583-110-5042	Sequence 5042, Ap	364	24	72.7	370	2	US-09-205-658-104	Sequence 342, App
292	24	72.7	156	2	US-09-270-767-61803	Sequence 61803, A	365	24	72.7	375	2	US-09-602-777A-342	Sequence 342, App
293	24	72.7	158	2	US-09-107-433-4659	Sequence 4659, Ap	366	24	72.7	376	2	US-09-252-991A-30994	Sequence 30994, A
294	24	72.7	159	2	US-09-010-809-1	Sequence 1, Appli	367	24	72.7	376	2	US-09-489-039A-8789	Sequence 8789, Ap
295	24	72.7	161	2	US-09-489-039A-7732	Sequence 7732, Ap	368	24	72.7	385	2	US-09-902-540-10208	Sequence 10208, A
296	24	72.7	176	2	US-09-205-658-212	Sequence 212, App	369	24	72.7	385	2	US-09-540-236-3550	Sequence 3550, Ap
297	24	72.7	179	2	US-09-248-796A-27985	Sequence 27985, A	370	24	72.7	387	2	US-09-205-448-2	Sequence 2, Appli
298	24	72.7	196	2	US-09-328-352-4939	Sequence 4939, Ap	371	24	72.7	394	2	US-09-489-039A-7331	Sequence 7331, Ap
299	24	72.7	201	1	US-08-773-423-5	Sequence 5, Appli	372	24	72.7	397	2	US-08-964-631-2	Sequence 4210, A
300	24	72.7	201	1	US-08-773-423-9	Sequence 9, Appli	373	24	72.7	418	1	US-08-964-631-2	Sequence 2, Appli
301	24	72.7	201	2	US-09-902-540-12838	Sequence 12838, A	374	24	72.7	418	2	US-09-210-000-2	Sequence 2, Appli
302	24	72.7	203	2	US-09-252-991A-17732	Sequence 17732, A	375	24	72.7	421	2	US-09-328-352-5035	Sequence 5035, Ap
303	24	72.7	205	2	US-08-818-112-80	Sequence 80, Appl	376	24	72.7	422	1	US-08-758-621-12	Sequence 12, Appl
304	24	72.7	205	2	US-08-818-111-81	Sequence 81, Appl	377	24	72.7	422	2	US-09-107-858-12	Sequence 12, Appl
305	24	72.7	205	2	US-09-056-556-80	Sequence 80, Appl	378	24	72.7	422	2	US-09-579-174-12	Sequence 12, Appl
306	24	72.7	205	2	US-09-072-967-81	Sequence 81, Appl	379	24	72.7	423	2	US-09-134-001C-4717	Sequence 4717, Ap
307	24	72.7	205	2	US-09-072-967-80	Sequence 80, Appl	380	24	72.7	429	2	US-09-270-767-42323	Sequence 42323, A
308	24	72.7	205	2	US-10-193-002-81	Sequence 81, Appl	381	24	72.7	432	1	US-08-700-152A-4	Sequence 4, Appli
309	24	72.7	205	2	US-10-084-843-80	Sequence 80, Appl	382	24	72.7	438	2	US-09-252-991A-16758	Sequence 16758, A
310	24	72.7	208	2	US-09-134-000C-3736	Sequence 3736, Ap	383	24	72.7	470	2	US-09-252-991A-32300	Sequence 32300, A
311	24	72.7	213	2	US-09-583-110-4973	Sequence 4973, Ap	384	24	72.7	471	2	US-09-270-767-42784	Sequence 42784, A
312	24	72.7	223	2	US-09-710-219-2884	Sequence 2884, Ap	385	24	72.7	472	2	US-09-252-991A-17011	Sequence 17011, A
313	24	72.7	223	2	US-09-205-658-211	Sequence 211, App	386	24	72.7	477	2	US-09-107-532A-5448	Sequence 5448, Ap
314	24	72.7	223	2	US-09-205-658-213	Sequence 213, App	387	24	72.7	483	2	US-09-107-532A-4123	Sequence 4123, Ap
315	24	72.7	228	2	US-09-107-433-3620	Sequence 3620, Ap	388	24	72.7	488	2	US-08-311-731A-29	Sequence 29, Appl
316	24	72.7	233	2	US-08-818-112-77	Sequence 76, Appl	389	24	72.7	493	2	US-09-252-991A-32463	Sequence 32463, A
317	24	72.7	233	2	US-08-818-111-77	Sequence 77, Appl	390	24	72.7	496	2	US-09-538-092-705	Sequence 705, App
318	24	72.7	233	2	US-09-056-556-76	Sequence 76, Appl	391	24	72.7	499	2	US-09-487-558B-194	Sequence 194, App
319	24	72.7	233	2	US-09-072-967-77	Sequence 77, Appl	392	24	72.7	504	2	US-09-902-540-14106	Sequence 14106, A

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394	24	72.7	506	2	US-08-606-505B-65	Sequence 65, Appl	467	23	69.7	68	2	US-09-540-236-2709	Sequence 2709, Ap
395	24	72.7	506	2	US-09-616-990-65	Sequence 65, Appl	468	23	69.7	73	2	US-09-621-976-6032	Sequence 6032, Ap
396	24	72.7	508	2	US-09-118-420A-19	Sequence 19, Appl	469	23	69.7	74	2	US-09-252-991A-26625	Sequence 26625, A
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402	24	72.7	526	2	US-09-630-983A-5	Sequence 5, Appli	475	23	69.7	88	2	US-09-398-193-64	Sequence 64, Appl
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404	24	72.7	534	2	US-09-605-703B-1142	Sequence 1142, Ap	477	23	69.7	92	1	US-08-750-007-6	Sequence 6, Appli
405	24	72.7	542	2	US-09-489-039A-13022	Sequence 13022, A	478	23	69.7	95	2	US-09-270-767-58548	Sequence 58548, A
406	24	72.7	545	2	US-09-489-039A-13742	Sequence 13742, A	479	23	69.7	103	2	US-09-270-767-32928	Sequence 32928, A
407	24	72.7	556	2	US-09-252-991A-17793	Sequence 17793, A	480	23	69.7	103	2	US-09-270-767-48145	Sequence 48145, A
408	24	72.7	579	2	US-09-138-452A-918	Sequence 918, App	481	23	69.7	107	1	US-08-814-806-2	Sequence 2, Appli
409	24	72.7	583	2	US-08-481-190-19	Sequence 19, Appl	482	23	69.7	107	2	US-09-293-854-2	Sequence 2, Appli
410	24	72.7	583	4	PCT-US93-00869-19	Sequence 19, Appl	483	23	69.7	108	2	US-09-270-767-46391	Sequence 46391, A
411	24	72.7	584	2	US-09-693-746-22	Sequence 22, Appl	484	23	69.7	108	2	US-09-232-290-3	Sequence 3, Appli
412	24	72.7	587	2	US-08-481-190-4	Sequence 4, Appli	485	23	69.7	110	2	US-10-092-246-14	Sequence 14, Appl
413	24	72.7	587	4	PCT-US93-00869-4	Sequence 4, Appli	486	23	69.7	110	2	US-10-096-246A-14	Sequence 14, Appl
414	24	72.7	588	2	US-08-481-190-16	Sequence 16, Appl	487	23	69.7	112	2	US-09-071-035-214	Sequence 214, App
415	24	72.7	588	4	PCT-US93-00869-16	Sequence 16, Appl	488	23	69.7	112	2	US-10-206-576-214	Sequence 214, App
416	24	72.7	590	2	US-09-248-796A-18826	Sequence 18826, A	489	23	69.7	114	2	US-09-270-767-58835	Sequence 58835, A
417	24	72.7	606	2	US-09-438-185A-853	Sequence 853, App	490	23	69.7	120	2	US-09-107-532A-5392	Sequence 5392, Ap
418	24	72.7	610	2	US-09-455-777-2	Sequence 2, Appli	491	23	69.7	123	2	US-09-270-767-40697	Sequence 40697, A
419	24	72.7	610	2	US-10-138-713-2	Sequence 2, Appli	492	23	69.7	123	2	US-09-270-767-55913	Sequence 55913, A
420	24	72.7	610	2	US-09-605-703B-2812	Sequence 2812, Ap	493	23	69.7	127	2	US-09-136-315-4	Sequence 4, Appli
421	24	72.7	619	2	US-09-902-540-14582	Sequence 14582, A	494	23	69.7	127	2	US-09-136-315-8	Sequence 8, Appli
422	24	72.7	643	2	US-09-328-352-5146	Sequence 5146, Ap	495	23	69.7	127	2	US-09-767-888-4	Sequence 4, Appli
423	24	72.7	671	2	US-10-187-253B-25	Sequence 25, Appl	496	23	69.7	127	2	US-09-767-888-8	Sequence 8, Appli
424	24	72.7	671	2	US-10-187-253B-31	Sequence 31, Appl	497	23	69.7	127	2	US-09-134-000C-4832	Sequence 4832, Ap
425	24	72.7	706	2	US-09-902-540-12578	Sequence 12578, A	498	23	69.7	130	2	US-09-328-352-4578	Sequence 4578, Ap
426	24	72.7	709	2	US-09-949-016-6809	Sequence 6809, Ap	499	23	69.7	133	2	US-09-708-200-17	Sequence 17, Appl
427	24	72.7	711	2	US-09-489-039A-12188	Sequence 12188, A	500	23	69.7	133	2	US-09-707-468C-15	Sequence 15, Appl
428	24	72.7	712	2	US-09-270-767-46235	Sequence 46235, A	501	23	69.7	133	2	US-09-902-540-11940	Sequence 11940, A
429	24	72.7	717	2	US-09-902-540-11844	Sequence 11844, A	502	23	69.7	133	2	US-09-749-601A-13	Sequence 13, Appl
430	24	72.7	728	2	US-09-949-016-7213	Sequence 7213, Ap	503	23	69.7	135	6	5219996-19	Patent No. 5219996
431	24	72.7	730	2	US-09-902-540-16253	Sequence 16253, A	504	23	69.7	140	2	US-09-902-540-15133	Sequence 15133, A
432	24	72.7	730	2	US-09-248-796A-15523	Sequence 15523, A	505	23	69.7	142	2	US-09-270-767-33269	Sequence 33269, A
433	24	72.7	756	2	US-09-248-796A-14736	Sequence 14736, Ap	506	23	69.7	146	2	US-09-107-532A-5046	Sequence 5046, Ap
434	24	72.7	758	2	US-09-949-016-9816	Sequence 9816, Ap	507	23	69.7	149	2	US-09-543-681A-8072	Sequence 8072, Ap
435	24	72.7	768	2	US-09-902-540-15931	Sequence 15931, A	508	23	69.7	152	2	US-09-902-540-16741	Sequence 16741, A
436	24	72.7	779	2	US-09-934-899-8	Sequence 8, Appli	509	23	69.7	153	2	US-09-949-016-7661	Sequence 7661, Ap
437	24	72.7	779	2	US-09-934-868-28	Sequence 28, Appl	510	23	69.7	155	2	US-09-252-991A-24526	Sequence 24526, A
438	24	72.7	779	2	US-10-701-200-28	Sequence 28, Appl	511	23	69.7	164	2	US-09-605-703B-976	Sequence 976, App
439	24	72.7	792	2	US-09-902-540-12692	Sequence 12692, A	512	23	69.7	164	2	US-09-605-703B-978	Sequence 978, App
440	24	72.7	795	2	US-09-107-532A-5429	Sequence 5429, Ap	513	23	69.7	167	2	US-09-252-991A-22963	Sequence 22963, A
441	24	72.7	809	2	US-09-252-991A-31759	Sequence 31759, A	514	23	69.7	170	2	US-09-270-767-43206	Sequence 43206, A
442	24	72.7	923	2	US-09-252-991A-22409	Sequence 22409, A	515	23	69.7	170	2	US-09-270-767-60691	Sequence 60691, A
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445	24	72.7	969	1	US-08-145-138A-3	Sequence 3, Appli	518	23	69.7	180	2	US-09-270-767-43466	Sequence 43466, A
446	24	72.7	969	4	PCT-US92-06888-3	Sequence 3, Appli	519	23	69.7	181	2	US-09-710-279-560	Sequence 560, App
447	24	72.7	969	5	PCT-US93-03027-4	Sequence 4, Appli	520	23	69.7	189	2	US-09-134-000C-3438	Sequence 3438, Ap
448	24	72.7	974	2	US-08-365-689-3	Sequence 3, Appli	521	23	69.7	189	2	US-09-270-767-42627	Sequence 42627, A
449	24	72.7	1056	1	US-10-101-464A-921	Sequence 921, App	522	23	69.7	197	2	US-09-902-540-14467	Sequence 14467, A
450	24	72.7	1066	1	US-08-627-873-7	Sequence 7, Appli	523	23	69.7	199	2	US-09-270-767-43423	Sequence 43423, A
451	24	72.7	1274	2	US-08-308-818-1	Sequence 1, Appli	524	23	69.7	200	2	US-09-809-665A-63	Sequence 63, Appl
452	24	72.7	1382	1	US-09-602-777A-360	Sequence 360, App	525	23	69.7	202	2	US-09-270-767-45195	Sequence 45195, A
453	24	72.7	1382	1	US-08-737-715-2	Sequence 2, Appli	526	23	69.7	207	1	US-07-732-242C-5	Sequence 5, Appli
454	24	72.7	1382	2	US-09-457-040B-7	Sequence 7, Appli	527	23	69.7	208	2	US-09-134-001C-5012	Sequence 5012, Ap
455	23	69.7	7	1	US-08-814-806-6	Sequence 6, Appli	528	23	69.7	209	2	US-09-270-767-57343	Sequence 57343, A
456	23	69.7	7	2	US-09-293-854-6	Sequence 6, Appli	529	23	69.7	210	2	US-09-270-767-57356	Sequence 57356, A
457	23	69.7	8	2	US-09-559-021-81	Sequence 81, Appl	530	23	69.7	210	2	US-09-248-796A-17236	Sequence 17236, A
458	23	69.7	27	1	US-08-967-999-3	Sequence 3, Appli	531	23	69.7	210	2	US-09-513-999C-4297	Sequence 4297, Ap
459	23	69.7	38	2	US-09-270-767-60889	Sequence 60889, A	532	23	69.7	214	2	US-09-252-991A-27795	Sequence 27795, A
460	23	69.7	45	1	US-08-824-379-2	Sequence 2, Appli	533	23	69.7	216	2	US-09-270-767-34814	Sequence 34814, A
461	23	69.7	45	2	US-08-071-035-216	Sequence 216, App	534	23	69.7	216	2	US-09-270-767-50031	Sequence 50031, A
462	23	69.7	49	2	US-10-206-576-216	Sequence 216, App	535	23	69.7	221	2	US-09-252-991A-17454	Sequence 17454, A
463	23	69.7	51	2	US-09-270-767-45387	Sequence 45387, A	536	23	69.7	222	2	US-09-634-238-301	Sequence 301, App
464	23	69.7	57	4	PCT-US94-05150-22	Sequence 22, Appl	537	23	69.7	227	2	US-09-410-464-4	Sequence 4, Appli
465	23	69.7	63	2	US-09-621-976-5640	Sequence 5640, Ap	538	23	69.7	227	2	US-09-902-540-12846	Sequence 12846, A

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540	23	69.7	230	2	US-10-090-185-27	Sequence 20, Appl	613	23	69.7	377	2	US-09-489-039A-9429	Sequence 9429, Ap
541	23	69.7	232	2	US-09-252-991A-20217	Sequence 20217, A	614	23	69.7	377	2	US-09-270-767-59051	Sequence 59051, A
542	23	69.7	234	2	US-08-311-731A-60	Sequence 60, Appl	615	23	69.7	383	2	US-09-902-540-16490	Sequence 16490, A
543	23	69.7	235	2	US-09-328-352-5715	Sequence 5715, Ap	616	23	69.7	384	2	US-09-252-991A-33095	Sequence 33095, A
544	23	69.7	236	2	US-09-489-039A-9735	Sequence 9735, Ap	617	23	69.7	386	1	US-08-758-213-1	Sequence 1, Appl
545	23	69.7	245	2	US-09-286-690-2	Sequence 2, Appl	618	23	69.7	386	1	US-08-692-787-48	Sequence 48, Appl
546	23	69.7	245	2	US-09-949-016-11327	Sequence 11327, A	619	23	69.7	386	2	US-09-097-199-48	Sequence 48, Appl
547	23	69.7	245	2	US-09-902-540-12541	Sequence 12541, A	620	23	69.7	386	2	US-09-949-016-6022	Sequence 6022, Ap
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550	23	69.7	251	2	US-09-198-452A-309	Sequence 309, App	623	23	69.7	389	2	US-09-543-681A-6397	Sequence 6397, Ap
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552	23	69.7	255	2	US-09-328-352-7865	Sequence 7865, Ap	625	23	69.7	403	2	US-08-887-534A-83	Sequence 83, Appl
553	23	69.7	256	2	US-09-270-767-46611	Sequence 46611, A	626	23	69.7	403	2	US-09-527-431-83	Sequence 83, Appl
554	23	69.7	257	2	US-09-252-991A-21740	Sequence 21740, A	627	23	69.7	403	2	US-09-446-861-83	Sequence 83, Appl
555	23	69.7	257	2	US-09-438-185A-298	Sequence 298, App	628	23	69.7	406	1	US-08-487-823B-5	Sequence 5, Appl
556	23	69.7	259	2	US-09-328-352-6237	Sequence 6237, Ap	629	23	69.7	406	1	US-08-997-040-5	Sequence 5, Appl
557	23	69.7	259	2	US-09-248-796A-22778	Sequence 22778, A	630	23	69.7	406	1	US-09-203-237-5	Sequence 5, Appl
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559	23	69.7	262	2	US-09-252-991A-29803	Sequence 29803, A	632	23	69.7	407	2	US-09-248-796A-20092	Sequence 20092, A
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561	23	69.7	264	2	US-09-788-657-25	Sequence 25, Appl	634	23	69.7	408	2	US-09-492-709A-255	Sequence 255, App
562	23	69.7	264	2	US-10-641-068-24	Sequence 24, Appl	635	23	69.7	420	1	US-08-487-823B-4	Sequence 4, Appl
563	23	69.7	264	2	US-10-641-068-25	Sequence 25, Appl	636	23	69.7	420	1	US-08-997-040-4	Sequence 4, Appl
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565	23	69.7	271	1	US-08-400-115-4	Sequence 4, Appl	638	23	69.7	420	2	US-09-239-303-9	Sequence 9, Appl
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567	23	69.7	276	2	US-10-104-047-3850	Sequence 3850, Ap	640	23	69.7	421	2	US-09-902-540-10971	Sequence 10971, A
568	23	69.7	277	2	US-09-489-039A-3545	Sequence 3545, Ap	641	23	69.7	422	2	US-09-949-016-7927	Sequence 7927, Ap
569	23	69.7	279	2	US-09-809-665A-77	Sequence 77, Appl	642	23	69.7	423	2	US-09-976-594-19	Sequence 19, Appl
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571	23	69.7	285	2	US-09-489-039A-10832	Sequence 10832, A	644	23	69.7	424	1	US-08-614-155B-1	Sequence 1, Appl
572	23	69.7	286	2	US-09-902-540-14525	Sequence 14525, A	645	23	69.7	424	1	US-08-614-155B-3	Sequence 3, Appl
573	23	69.7	289	2	US-09-949-016-6295	Sequence 6295, Ap	646	23	69.7	424	2	US-09-166-963-1	Sequence 1, Appl
574	23	69.7	290	2	US-09-252-991A-32501	Sequence 32501, A	647	23	69.7	424	2	US-09-166-963-3	Sequence 3, Appl
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576	23	69.7	291	2	US-09-107-532A-5152	Sequence 5152, Ap	649	23	69.7	425	2	US-09-860-768-4	Sequence 4, Appl
577	23	69.7	294	2	US-09-949-016-11136	Sequence 11136, A	650	23	69.7	427	2	US-09-489-039A-11442	Sequence 11442, A
578	23	69.7	296	2	US-09-270-767-37980	Sequence 37980, A	651	23	69.7	428	2	US-09-134-001C-3801	Sequence 3801, Ap
579	23	69.7	296	2	US-09-270-767-53197	Sequence 53197, A	652	23	69.7	431	4	PCT-US91-00909-6	Sequence 6, Appl
580	23	69.7	300	2	US-09-252-991A-27203	Sequence 27203, A	653	23	69.7	436	2	US-09-712-363-258	Sequence 258, App
581	23	69.7	301	2	US-09-543-681A-5408	Sequence 5408, Ap	654	23	69.7	437	2	US-09-538-092-816	Sequence 816, App
582	23	69.7	304	2	US-09-248-796A-20160	Sequence 20160, A	655	23	69.7	441	2	US-09-134-000C-6563	Sequence 6563, Ap
583	23	69.7	305	2	US-09-252-991A-26224	Sequence 26224, A	656	23	69.7	444	2	US-09-489-039A-10106	Sequence 10106, A
584	23	69.7	307	2	US-09-949-016-7702	Sequence 7702, Ap	657	23	69.7	444	2	US-09-248-796A-23448	Sequence 23448, A
585	23	69.7	309	2	US-09-949-016-10025	Sequence 10025, A	658	23	69.7	446	2	US-09-252-991A-22844	Sequence 22844, A
586	23	69.7	312	2	US-09-634-238-254	Sequence 238-254, App	659	23	69.7	447	2	US-09-248-796A-20541	Sequence 20541, A
587	23	69.7	313	2	US-09-583-110-4236	Sequence 4236, Ap	660	23	69.7	448	2	US-09-288-326A-7	Sequence 7, Appl
588	23	69.7	315	2	US-09-434-774-16	Sequence 16, Appl	661	23	69.7	448	2	US-09-548-409B-7	Sequence 7, Appl
589	23	69.7	315	2	US-09-107-433-3706	Sequence 3706, Ap	662	23	69.7	448	2	US-10-104-047-3380	Sequence 3380, Ap
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591	23	69.7	321	2	US-09-489-039A-13361	Sequence 13361, A	664	23	69.7	456	2	US-09-328-352-4415	Sequence 4415, Ap
592	23	69.7	323	2	US-09-679-279-18	Sequence 18, Appl	665	23	69.7	457	2	US-09-142-759-1	Sequence 1, Appl
593	23	69.7	326	2	US-09-248-796A-17792	Sequence 17792, A	666	23	69.7	457	2	US-09-270-767-42082	Sequence 42082, A
594	23	69.7	326	2	US-09-710-279-2952	Sequence 2952, Ap	667	23	69.7	457	2	US-09-902-540-11961	Sequence 11961, A
595	23	69.7	331	2	US-09-134-001C-5254	Sequence 5254, A	668	23	69.7	458	2	US-09-252-991A-27645	Sequence 27645, Ap
596	23	69.7	331	2	US-09-252-991A-33051	Sequence 33051, A	669	23	69.7	460	2	US-09-107-532A-3760	Sequence 3760, Ap
597	23	69.7	332	2	US-09-602-787A-598	Sequence 598, App	670	23	69.7	463	2	US-09-902-540-15406	Sequence 15406, A
598	23	69.7	335	2	US-09-134-000C-4305	Sequence 4305, Ap	671	23	69.7	465	2	US-09-710-279-1676	Sequence 1676, Ap
599	23	69.7	335	2	US-09-902-540-12406	Sequence 12406, A	672	23	69.7	467	2	US-09-328-352-7510	Sequence 7510, Ap
600	23	69.7	337	2	US-09-489-039A-13095	Sequence 13095, A	673	23	69.7	467	2	US-09-543-681A-7427	Sequence 7427, Ap
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602	23	69.7	340	2	US-10-155-947-6	Sequence 6, Appl	675	23	69.7	469	2	US-09-487-558B-182	Sequence 182, App
603	23	69.7	344	2	US-09-902-540-14026	Sequence 14026, A	676	23	69.7	474	2	US-09-902-540-10946	Sequence 10946, A
604	23	69.7	349	2	US-09-270-767-44336	Sequence 44336, A	677	23	69.7	475	2	US-10-130-798A-2	Sequence 2, Appl
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689	23	69.7	492	2	US-09-134-000C-4808	Sequence 4808, Ap	762	23	69.7	700	2	US-08-272-247-2	Sequence 2, Appli
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691	23	69.7	494	2	US-08-198-452A-13	Sequence 13, Appli	764	23	69.7	704	2	US-09-902-540-10479	Sequence 10479, A
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695	23	69.7	495	1	US-08-455-559-10	Sequence 10, Appli	768	23	69.7	727	2	US-09-445-023A-1	Sequence 1, Appli
696	23	69.7	495	2	US-09-145-060-10	Sequence 10, Appli	769	23	69.7	727	2	US-09-445-023A-12	Sequence 12, Appli
697	23	69.7	495	4	PCT-US94-00657-10	Sequence 10, Appli	770	23	69.7	734	2	US-09-809-665A-117	Sequence 117, App
698	23	69.7	501	2	US-09-270-767-42092	Sequence 42092, A	771	23	69.7	745	2	US-09-919-835-2	Sequence 2, Appli
699	23	69.7	503	2	US-09-215-694-8	Sequence 8, Appli	772	23	69.7	747	2	US-09-949-016-6552	Sequence 6552, Ap
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702	23	69.7	506	2	US-09-134-000C-6170	Sequence 6170, Ap	775	23	69.7	761	2	US-09-518-550-26	Sequence 26, Appl
703	23	69.7	506	2	US-09-540-236-2360	Sequence 2360, Ap	776	23	69.7	782	2	US-09-861-451A-12	Sequence 12, Appl
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705	23	69.7	512	2	US-09-107-532A-6559	Sequence 6559, Ap	778	23	69.7	812	1	US-08-446-794A-2	Sequence 2, Appli
706	23	69.7	515	1	US-08-146-283-2	Sequence 2, Appli	779	23	69.7	812	1	US-08-750-007-3	Sequence 3, Appli
707	23	69.7	515	2	US-08-579-823A-2	Sequence 2, Appli	780	23	69.7	812	1	US-08-945-024-2	Sequence 2, Appli
708	23	69.7	515	2	US-09-344-195-2	Sequence 2, Appli	781	23	69.7	832	2	US-10-464-839-2	Sequence 2, Appli
709	23	69.7	521	2	US-09-252-991A-30835	Sequence 30835, A	782	23	69.7	833	2	US-09-252-991A-32338	Sequence 32338, A
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712	23	69.7	524	1	US-08-624-125-21	Sequence 21, Appli	785	23	69.7	846	2	US-10-697-263-4	Sequence 4, Appli
713	23	69.7	524	2	US-08-937-155-2	Sequence 2, Appli	786	23	69.7	856	2	US-09-902-540-15925	Sequence 15925, A
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715	23	69.7	524	2	US-09-323-998E-21	Sequence 21, Appli	788	23	69.7	862	1	US-08-209-521-30	Sequence 23, Appl
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717	23	69.7	524	2	US-09-323-998E-49	Sequence 49, Appli	790	23	69.7	862	2	US-09-059-461-2	Sequence 2, Appli
718	23	69.7	526	2	US-09-252-991A-32984	Sequence 32984, A	791	23	69.7	862	2	US-08-961-810-133	Sequence 133, App
719	23	69.7	532	2	US-09-252-991A-19913	Sequence 19913, A	792	23	69.7	862	2	US-08-352-902D-133	Sequence 133, App
720	23	69.7	532	2	US-08-948-564-10	Sequence 10, Appl	793	23	69.7	862	2	US-08-294-312B-6	Sequence 6, Appli
721	23	69.7	541	2	US-09-252-991A-24521	Sequence 24521, A	794	23	69.7	862	2	US-08-468-024B-6	Sequence 6, Appli
722	23	69.7	544	2	US-09-902-540-16154	Sequence 16154, A	795	23	69.7	862	2	US-09-265-503B-133	Sequence 133, App
723	23	69.7	547	2	US-08-538-092-984	Sequence 984, App	796	23	69.7	862	2	US-09-708-200-9	Sequence 9, Appli
724	23	69.7	551	1	US-09-033-537A-1	Sequence 1, Appli	797	23	69.7	862	2	US-08-465-679-6	Sequence 6, Appli
725	23	69.7	551	2	US-09-130-491-16	Sequence 16, Appl	798	23	69.7	862	2	US-09-712-691-7	Sequence 7, Appli
726	23	69.7	551	2	US-09-602-787A-510	Sequence 510, App	799	23	69.7	862	2	US-09-707-468C-7	Sequence 7, Appli
727	23	69.7	554	2	US-08-943-714-2	Sequence 2, Appli	800	23	69.7	871	2	US-09-749-601A-11	Sequence 11, Appl
728	23	69.7	555	2	US-09-712-338-2	Sequence 2, Appli	801	23	69.7	871	2	US-09-255-829-2	Sequence 2, Appli
729	23	69.7	556	2	US-09-489-039A-12263	Sequence 12263, A	802	23	69.7	871	2	US-09-255-829-8	Sequence 8, Appli
730	23	69.7	558	2	US-09-770-517C-2	Sequence 2, Appli	803	23	69.7	871	2	US-09-255-829-26	Sequence 26, Appl
731	23	69.7	558	2	US-10-750-026-2	Sequence 2, Appli	804	23	69.7	871	2	US-09-252-991A-33057	Sequence 33057, A
732	23	69.7	567	2	US-08-252-991A-23004	Sequence 23004, A	805	23	69.7	871	2	US-09-792-024-81	Sequence 81, Appl
733	23	69.7	572	2	US-08-311-731A-32	Sequence 32, Appl	806	23	69.7	873	2	US-09-255-829-6	Sequence 6, Appli
734	23	69.7	578	2	US-09-489-039A-7288	Sequence 7288, Ap	807	23	69.7	875	2	US-09-255-829-10	Sequence 10, Appl
735	23	69.7	582	2	US-09-477-962-94	Sequence 94, Appli	808	23	69.7	878	2	US-09-255-829-12	Sequence 12, Appl
736	23	69.7	592	2	US-09-477-135A-132	Sequence 132, App	809	23	69.7	887	2	US-09-949-002-534	Sequence 534, App
737	23	69.7	599	2	US-09-489-039A-13050	Sequence 13050, A	810	23	69.7	890	2	US-09-949-002-394	Sequence 394, App
738	23	69.7	608	2	US-09-130-491-13	Sequence 13, Appl	811	23	69.7	894	2	US-09-255-829-4	Sequence 4, Appli
739	23	69.7	613	2	US-09-758-759-151	Sequence 151, App	812	23	69.7	904	2	US-09-252-991A-25286	Sequence 25286, A
740	23	69.7	618	2	US-09-252-991A-23373	Sequence 23373, A	813	23	69.7	905	2	US-09-369-364A-9	Sequence 9, Appli
741	23	69.7	618	2	US-08-252-991A-27666	Sequence 27666, A	814	23	69.7	907	2	US-09-255-829-16	Sequence 16, Appl
742	23	69.7	620	2	US-09-489-039A-13601	Sequence 13601, A	815	23	69.7	933	1	US-08-370-193A-8	Sequence 8, Appli
743	23	69.7	627	2	US-09-252-991A-31696	Sequence 31696, A	816	23	69.7	933	2	US-09-271-438A-9	Sequence 9, Appli
744	23	69.7	634	2	US-09-902-540-10050	Sequence 10050, A	817	23	69.7	933	2	US-10-078-107-5	Sequence 5, Appli
745	23	69.7	639	1	US-08-637-899-1	Sequence 1, Appli	818	23	69.7	935	2	US-10-077-751-5	Sequence 3, Appli
746	23	69.7	642	1	US-08-706-936-2	Sequence 2, Appli	819	23	69.7	935	2	US-09-271-438A-3	Sequence 3, Appli
747	23	69.7	642	1	US-08-706-936-3	Sequence 3, Appli	820	23	69.7	935	2	US-10-078-107-1	Sequence 1, Appli
748	23	69.7	643	1	US-08-616-844-39	Sequence 39, Appli	821	23	69.7	935	2	US-10-077-751-1	Sequence 1, Appli
749	23	69.7	643	1	US-08-599-654-39	Sequence 39, Appl	822	23	69.7	938	2	US-09-489-039A-13504	Sequence 13504, A
750	23	69.7	643	2	US-08-944-668A-39	Sequence 39, Appl	823	23	69.7	948	2	US-09-328-352-6123	Sequence 6123, Ap
751	23	69.7	643	2	US-08-944-423A-39	Sequence 39, Appl	824	23	69.7	949	2	US-09-568-559-2	Sequence 2, Appli
752	23	69.7	643	2	US-08-944-436-39	Sequence 39, Appl	825	23	69.7	950	2	US-09-321-987B-4	Sequence 4, Appli
753	23	69.7	643	2	US-08-575-081B-28	Sequence 28, Appl	826	23	69.7	951	2	US-09-328-352-4456	Sequence 4456, Ap
754	23	69.7	643	2	US-09-949-016-6645	Sequence 6645, Ap	827	23	69.7	951	2	US-09-924-097A-15	Sequence 15, Appl
755	23	69.7	648	2	US-10-104-047-2032	Sequence 2032, Ap	828	23	69.7	951	2	US-09-255-829-14	Sequence 14, Appl
756	23	69.7	660	2	US-09-489-039A-8557	Sequence 8557, Ap	829	23	69.7	953	2	US-09-255-829-14	Sequence 2, Appli
757	23	69.7	662	1	US-07-841-651-4	Sequence 4, Appli	830	23	69.7	967	2	US-09-130-491-2	Sequence 2, Appli

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832	23	69.7	977	2	US-10-193-764-49	Sequence 49, Appl	905	23	69.7	7257	2	US-09-567-899-5	Sequence 5, Appl
833	23	69.7	983	2	US-09-206-942-51	Sequence 51, Appl	906	23	69.7	7257	2	US-10-014-717-5	Sequence 5, Appl
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835	23	69.7	992	2	US-09-252-991A-27095	Sequence 27095, A	908	23	66.7	12	2	US-09-339-596A-38	Sequence 38, Appl
836	23	69.7	1013	2	US-09-255-829-18	Sequence 18, Appl	909	22	66.7	12	2	US-10-394-980-108	Sequence 108, App
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847	23	69.7	1179	2	US-09-949-016-7088	Sequence 7088, Ap	920	22	66.7	15	2	US-09-768-080-91	Sequence 91, Appl
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872	23	69.7	1562	2	US-09-320-878-3	Sequence 3, Appl	945	22	66.7	96	2	US-09-328-352-5574	Sequence 5574, Ap
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876	23	69.7	1562	2	US-09-793-708-3	Sequence 3, Appl	949	22	66.7	103	2	US-09-270-767-39672	Sequence 39672, A
877	23	69.7	1574	2	US-09-302-626B-179	Sequence 179, App	950	22	66.7	103	2	US-09-270-767-54889	Sequence 54889, A
878	23	69.7	1769	2	US-09-949-016-8280	Sequence 8280, Ap	951	22	66.7	103	2	US-09-248-796A-16658	Sequence 16658, A
879	23	69.7	1769	2	US-09-949-016-8281	Sequence 8281, Ap	952	22	66.7	103	2	US-09-902-540-16691	Sequence 16691, A
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886	23	69.7	1882	2	US-09-369-364A-13	Sequence 13, Appl	959	22	66.7	110	1	US-08-207-996-29	Sequence 29, Appl
887	23	69.7	1933	2	US-10-152-866-83	Sequence 83, Appl	960	22	66.7	110	1	US-08-760-840A-23	Sequence 23, Appl
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889	23	69.7	2475	2	US-09-413-814-48	Sequence 48, Appl	962	22	66.7	110	1	US-08-760-840A-25	Sequence 25, Appl
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984      22      66.7      130      2      US-09-339-596A-24      Sequence 24, Appl
985      22      66.7      130      2      US-09-339-596A-28      Sequence 28, Appl
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990      22      66.7      145      2      US-09-937-296-2      Sequence 2, Appli
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996      22      66.7      149      2      US-09-270-767-48760      Sequence 48760, A
997      22      66.7      150      2      US-09-438-185A-621      Sequence 621, App
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999      22      66.7      151      2      US-09-022-765-20      Sequence 20, Appl
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ALIGNMENTS

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RESULT 1
US-09-155-106-5
; Sequence 5, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-5

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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GATNLAA 7

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RESULT 2
US-09-155-106-22
; Sequence 22, Application US/09155106

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; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22

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Best Local Similarity 100.0%; Pred. No. 3;
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Db      50 GATNLAA 56

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; Patent No. 6730300
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; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23

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Query Match      100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3;
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[illegible]

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/132,649
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-145-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-132-649-4

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Best Local Similarity 85.7%; Pred. No. 1.2e+02;
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Qy 1 GATNLAA 7
Db 64 GASNLAA 70

RESULT 8
US-08-767-579-4
Sequence 4, Application US/08/767579
Patent No. 6074842
GENERAL INFORMATION:
APPLICANT: Londres, Constantine
APPLICANT: Greenberg, Andrew S.
APPLICANT: Kimmel, Alan R.
APPLICANT: Egan, John J.
TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/767,579
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-145-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-579-4

Query Match 87.9%; Score 29; DB 2; Length 422;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 64 GASNLAA 70

RESULT 9
US-08-132-649-2
Sequence 2, Application US/08132649
Patent No. 5585462
GENERAL INFORMATION:
APPLICANT: Londres, Constantine
APPLICANT: Greenberg, Andrew S.
APPLICANT: Kimmel, Alan R.
APPLICANT: Egan, John J.
TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/132,649
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-145-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-132-649-2

Query Match 87.9%; Score 29; DB 1; Length 517;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 64 GASNLAA 70

RESULT 10
US-08-764-343-4
Sequence 4, Application US/08764343
Patent No. 5739009
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL ADIPOCYTE-SPECIFIC
DIFFERENTIATION-RELATED PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,343
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0167 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1172433
US-08-764-343-4

Query Match 87.9%; Score 29; DB 1; Length 517;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||:||||
Db 64 GASNLAA 70

RESULT 11
US-08-767-579-2
Sequence 2, Application US/08767579
Patent No. 6074842
GENERAL INFORMATION:
APPLICANT: Londres, Constantine
APPLICANT: Greenberg, Andrew S.
APPLICANT: Kimmel, Alan R.
APPLICANT: Egan, John J.
TITLE OF INVENTION: CLONING OF PERILIPIN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,579
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia

REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-145-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-579-2

Query Match 87.9%; Score 29; DB 2; Length 517;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||:||||
Db 64 GASNLAA 70

RESULT 12
US-08-653-648A-15
Sequence 15, Application US/08653648A
Patent No. 6379945
GENERAL INFORMATION:
APPLICANT: Jepsen, Ian
APPLICANT: Greenland, Andrew
APPLICANT: Martinez, Alberto
TITLE OF INVENTION: A Gene Switch
FILE REFERENCE: PPD50047/US
CURRENT APPLICATION NUMBER: US/08/653,648A
CURRENT FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: GB 9510759.5
PRIOR FILING DATE: 1995-05-26
PRIOR APPLICATION NUMBER: GB 9605656.9
PRIOR FILING DATE: 1996-03-18
PRIOR APPLICATION NUMBER: GB 9513882.2
PRIOR FILING DATE: 1995-07-07
PRIOR APPLICATION NUMBER: GB 9517316.7
PRIOR FILING DATE: 1995-08-24
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 878
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-08-653-648A-15

Query Match 87.9%; Score 29; DB 2; Length 878;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||:||||
Db 116 GATNLGA 122

RESULT 13
US-09-564-418-8
Sequence 8, Application US/09564418
Patent No. 6610828
GENERAL INFORMATION:
APPLICANT: Syngenta
APPLICANT: Jepsen, Ian
APPLICANT: Martinez, Alberto
APPLICANT: Greenland, Andrew James
TITLE OF INVENTION: A GENE SWITCH
FILE REFERENCE: 1392/4/3
CURRENT APPLICATION NUMBER: US/09/564,418
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/564,418

;; PRIOR FILING DATE: 2000-05-03
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 8
;; LENGTH: 878
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
US-09-564-418-8

Query Match 87.9%; Score 29; DB 2; Length 878;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 116 GATNLGA 122

RESULT 14
US-09-248-796A-21762
; Sequence 21762, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21762
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (297)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-21762

Query Match 84.8%; Score 28; DB 2; Length 304;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 69 GAANLAA 75

RESULT 15
US-09-328-352-6108
; Sequence 6108, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03FA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6108
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6108

Query Match 84.8%; Score 28; DB 2; Length 323;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 318 GATNTAA 324

RESULT 16
US-09-107-532A-5282
; Sequence 5282, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...361
; SEQUENCE DESCRIPTION: SEQ ID NO: 5282:
US-09-107-532A-5282

Query Match 84.8%; Score 28; DB 2; Length 361;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 318 GATNTAA 324

RESULT 17
US-09-949-016-6037
; Sequence 6037, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 6037
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6037

Query Match 84.8%; Score 28; DB 2; Length 665;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:||||

DB 37 GATSLAA 43

RESULT 18
US-09-949-016-10305
; Sequence 10305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 10305
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10305

Query Match 84.8%; Score 28; DB 2; Length 665;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:||||

DB 37 GATSLAA 43

RESULT 19
US-09-328-352-4744
; Sequence 4744, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4744
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4744

Query Match 84.8%; Score 28; DB 2; Length 1151;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:||||

DB 948 GAVNLAA 954

RESULT 20
US-09-540-236-3011
; Sequence 3011, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3011
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3011

Query Match 84.8%; Score 28; DB 2; Length 1220;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:||||

DB 1010 GAVNLAA 1016

RESULT 21
US-08-286-819A-28
; Sequence 28, Application US/08286819A
; Patent No. 5871910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-MALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/286,819A
; APPLICATION NUMBER: US/08/286,819A
; FILING DATE: 05-AUG-1994

CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 08/174,682
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5871910man P.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 660-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2254 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-286-819A-28

Query Match 84.8%; Score 28; DB 1; Length 2254;
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 ||||:|
 Db 642 GATNISA 648

RESULT 22
 US-08-980-357-28
 ; Sequence 28, Application US/08980357
 ; Patent No. 6013508
 ; GENERAL INFORMATION:
 ; APPLICANT: ARTHUR, MICHEL
 ; APPLICANT: DUKTA-MALEN, SYLVIE
 ; APPLICANT: MOLINAS, CATHERINE
 ; APPLICANT: COURVALIN, PATRICE
 ; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
 ; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
 ; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/980,357
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,819
 FILING DATE: 05-AUG-1994
 APPLICATION NUMBER: US 08/174,682
 FILING DATE: 28-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 6013508man P.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 660-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2254 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-980-357-28

Query Match 84.8%; Score 28; DB 2; Length 2254;
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
 ||||:|
 Db 642 GATNISA 648

RESULT 23
 US-09-357-375-28
 ; Sequence 28, Application US/09357375
 ; Patent No. 6916906
 ; GENERAL INFORMATION:
 ; APPLICANT: ARTHUR, MICHEL
 ; APPLICANT: DUKTA-MALEN, SYLVIE
 ; APPLICANT: MOLINAS, CATHERINE
 ; APPLICANT: COURVALIN, PATRICE
 ; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
 ; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
 ; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/357,375
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,819
 ; FILING DATE: 05-AUG-1994
 ; APPLICATION NUMBER: US 08/174,682

;
; FILING DATE: 28-DEC-1993
; PRIOR APPLICATION DATA: US 07/917,146
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA: PCT/FR/91/00855
; APPLICATION NUMBER: 29-OCT-1991
; PRIOR APPLICATION DATA: FR 9013579
; FILING DATE: 31-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Obion, No. 6916906man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-357-375-28

Query Match 84.8%; Score 28; DB 2; Length 2254;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
Db 642 GATNISA 648

RESULT 24
US-09-068-804-8
; Sequence 8, Application US/09068804
; Patent No. 6861247
; GENERAL INFORMATION:
; APPLICANT: Miller, Samuel I.
; TITLE OF INVENTION: SALMONELLA SECRETED PROTEINS
; NUMBER OF INVENTIONS: AND USES THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,804
; FILING DATE: 14-MAY-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/18504
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/006,733
; FILING DATE: 14-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/292002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 64 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-068-804-8

Query Match 81.8%; Score 27; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATNLAA 7
Db 24 ATNLAA 29

RESULT 25
US-09-068-804-46
; Sequence 46, Application US/09068804
; Patent No. 6861247
; GENERAL INFORMATION:
; APPLICANT: Miller, Samuel I.
; TITLE OF INVENTION: SALMONELLA SECRETED PROTEINS
; NUMBER OF INVENTIONS: AND USES THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,804
; FILING DATE: 14-MAY-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/18504
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/006,733
; FILING DATE: 14-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/292002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-068-804-46

Query Match 81.8%; Score 27; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATNLAA 7
Db 24 ATNLAA 29

RESULT 26
US-09-248-796A-20396
; Sequence 20396, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:

```
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20396
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-20396

Query Match      81.8%; Score 27; DB 2; Length 357;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 217 GATELAA 223

RESULT 27
US-09-489-039A-12299
; Sequence 3, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12299
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-12299

Query Match      81.8%; Score 27; DB 2; Length 432;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 32 GATGLAA 38

RESULT 28
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-09-044-718-3

Query Match      81.8%; Score 27; DB 2; Length 439;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 159 GATNRAA 165

RESULT 29
US-10-062-848-3
; Sequence 3, Application US/10062848
; Patent No. 6734004
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-062-848-3

Query Match      81.8%; Score 27; DB 2; Length 439;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 159 GATNRAA 165

RESULT 30
US-09-684-855-106
; Sequence 106, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 13073
; US-09-684-855-106
```

```
Query Match      81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      160 GATNRAA 166

RESULT 31
US-09-684-855-107
; Sequence 107, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 32722
US-09-684-855-107

Query Match      81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      160 GATNRAA 166

RESULT 32
US-09-684-855-108
; Sequence 108, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 58128
US-09-684-855-108

Query Match      81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      160 GATNRAA 166

RESULT 33
US-09-684-855-109
; Sequence 109, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 26906
US-09-684-855-109

Query Match      81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      160 GATNRAA 166

RESULT 34
US-09-684-855-110
; Sequence 110, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 32239
US-09-684-855-110

Query Match      81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      160 GATNRAA 166

RESULT 35
US-09-684-855-128
; Sequence 128, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
```

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; PRIOR APPLICATION NUMBER: EP 99120289.8
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 128
; LENGTH: 440
; TYPE: PR1
; ORGANISM: A. fumigatus 13073
US-09-684-855-128

```

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6: Conservative 0; Mismatches 1; Indels

Qy 1 GATNLAA 7
|||
Db 160 GATNRAA 166

```

RESULT 36
US-09-684-855-129
; Sequence 129, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 32722
US-09-684-855-129

```

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6: Conservative 0; Mismatches 1: Indels

Qy 1 GATNLAA 7
|||
pb 160 GATNRAA 166

```

RESULT 37
US-09-684-855-130
; Sequence 130, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 130
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 58128
US-09-684-855-130

```

Query Match 81.8%; Score 27; DB 2; Length 440;

Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GATNLAA 7
Db 160 GATNRAA 166
|||||

```

RESULT 38
US-09-684-855-131
; Sequence 131, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 26906
US-09-684-855-131

```

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6: Conservative 0: Mismatches 1: Indels

Qy 1 GATNLAA 7
Dy 160 GATNRAA 166

```

RESULT 39
US-09-684-855-132
; Sequence 132, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 32239
; US-09-684-855-132

```

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6: Conservative 0; Mismatches 1; Indels

QY 1 GATNLAA 7
|||
Db 160 GATNRAA 166

RESULT 40
US-09-684-855-151
: Sequence 151. Application US/09684855

; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus 32722
US-09-684-855-151

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| |||
Db 160 GATNRAA 166

RESULT 41
US-09-684-855-152
; Sequence 152, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:A. fumigatus ATCC32722
US-09-684-855-152

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| |||
Db 160 GATNRAA 166

RESULT 42
US-09-684-855-153
; Sequence 153, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus ATCC58128
US-09-684-855-153

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| |||
Db 160 GATNRAA 166

RESULT 43
US-09-684-855-154
; Sequence 154, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus ATCC26906
US-09-684-855-154

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| |||
Db 160 GATNRAA 166

RESULT 44
US-09-684-855-155
; Sequence 155, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 440
; TYPE: PRT
; ORGANISM: A. fumigatus ATCC32239
US-09-684-855-155

Query Match 81.8%; Score 27; DB 2; Length 440;

Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

RESULT 45

US-09-488-265B-6
; Sequence 6, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus 13073
US-09-488-265B-6

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

RESULT 46

US-09-488-265B-7
; Sequence 7, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus 32722
US-09-488-265B-7

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

RESULT 47

US-09-488-265B-8
; Sequence 8, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US

; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus 58128
US-09-488-265B-8

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

RESULT 48

US-09-488-265B-9
; Sequence 9, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; APPLICANT: Lassen, Soren F
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus 26906
US-09-488-265B-9

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

RESULT 49

US-09-488-265B-10
; Sequence 10, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; APPLICANT: Lassen, Soren F
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488,265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus 32239
US-09-488-265B-10

Query Match 81.8%; Score 27; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 160 GATNRAA 166

```

RESULT 50
US-09-044-718-12
; Sequence 12, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match      81.8%; Score 27; DB 2; Length 449;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
Db      169 GATNRAA 175

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Search completed: May 11, 2006, 16:41:22
Job time : 26.347 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:41 ; Search time 52.7869 Seconds
(without alignments)
55.408 Million cell updates/sec

Title: US-10-808-538-5
Perfect score: 33
Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	33	100.0	108	3	US-09-155-106-24
6	33	100.0	108	3	US-09-155-106-28
7	33	100.0	108	3	US-09-155-106-30
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11	33	100.0	108	5	US-10-808-538-28
12	33	100.0	108	5	US-10-808-538-30
13	30	90.9	130	4	US-10-767-701-55746
14	30	90.9	411	4	US-10-437-963-127994
15	29	87.9	13	4	US-10-468-496-1768
16	29	87.9	13	4	US-10-468-496-1769
17	29	87.9	13	4	US-10-468-496-1770
18	29	87.9	13	4	US-10-468-496-1771
19	29	87.9	88	4	US-10-425-115-246833
20	29	87.9	131	4	US-10-424-599-270261
21	29	87.9	235	5	US-10-516-429-11
22	29	87.9	236	4	US-10-006-593-69
23	29	87.9	236	4	US-10-307-724-69
24	29	87.9	236	5	US-10-737-290-69
25	29	87.9	336	4	US-10-108-260A-4140
26	29	87.9	477	4	US-10-437-963-144974
27	29	87.9	702	6	US-11-035-599-52
28	29	87.9	702	6	US-11-035-599-53
29	29	87.9	731	6	US-11-035-599-51
30	29	87.9	734	6	US-11-035-599-50
31	29	87.9	878	4	US-10-606-060A-8
32	29	87.9	881	6	US-11-097-143-2256
33	29	87.9	945	5	US-10-450-763-32765
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35	28	84.8	78	4	US-10-424-599-182384
36	28	84.8	84	4	US-10-437-963-146270
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76	27	81.8	113	4	US-10-425-115-314752
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78	27	81.8	146	4	US-10-424-599-235870
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83	27	81.8	164	4	US-10-425-114-59469
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86	27	81.8	184	4	US-10-425-115-293302
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88	27	81.8	199	4	US-10-425-114-68692
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401	25	75.8	229	4	US-10-425-115-275602	Sequence 275602,	474	25	75.8	383	5	US-10-450-763-52154	Sequence 52154, A
402	25	75.8	231	4	US-10-781-014-234	Sequence 234, App	475	25	75.8	385	5	US-10-450-763-52155	Sequence 52155, A
403	25	75.8	233	4	US-10-425-115-320128	Sequence 320128,	476	25	75.8	391	4	US-10-438-969-6	Sequence 6, Appli
404	25	75.8	240	4	US-10-437-963-105605	Sequence 105605,	477	25	75.8	392	6	US-11-097-143-20391	Sequence 20391, A
405	25	75.8	241	4	US-10-425-114-70090	Sequence 70090, A	478	25	75.8	393	4	US-10-369-493-13700	Sequence 13700, A
406	25	75.8	243	4	US-10-425-115-256768	Sequence 256768,	479	25	75.8	394	4	US-10-369-493-5606	Sequence 5606, Ap
407	25	75.8	245	3	US-09-880-748-1900	Sequence 1900, Ap	480	25	75.8	400	4	US-10-282-122A-54368	Sequence 54368, A
408	25	75.8	245	4	US-10-293-418-1900	Sequence 1900, Ap	481	25	75.8	405	4	US-10-369-493-19245	Sequence 19245, A
409	25	75.8	246	4	US-10-437-963-171238	Sequence 171238,	482	25	75.8	409	6	US-11-097-143-18078	Sequence 18078, A
410	25	75.8	248	4	US-10-425-115-298108	Sequence 298108,	483	25	75.8	414	4	US-10-282-122A-48141	Sequence 48141, A
411	25	75.8	249	4	US-10-437-963-174199	Sequence 174199,	484	25	75.8	416	4	US-10-369-493-550	Sequence 550, App
412	25	75.8	258	3	US-09-738-626-6867	Sequence 6867, Ap	485	25	75.8	421	4	US-10-369-493-9736	Sequence 9736, Ap
413	25	75.8	259	4	US-10-369-493-12052	Sequence 12052, A	486	25	75.8	426	4	US-10-437-963-178467	Sequence 178467,
414	25	75.8	265	4	US-10-425-115-305732	Sequence 305732,	487	25	75.8	430	4	US-10-669-161-10	Sequence 10, Appl
415	25	75.8	266	4	US-10-369-493-4469	Sequence 4469, Ap	488	25	75.8	431	4	US-10-282-122A-45758	Sequence 45758, A
416	25	75.8	266	4	US-10-369-493-7229	Sequence 7229, Ap	489	25	75.8	431	4	US-10-282-122A-46646	Sequence 46646, A
417	25	75.8	266	4	US-10-425-115-305758	Sequence 305758,	490	25	75.8	433	4	US-10-369-493-4963	Sequence 4963, Ap
418	25	75.8	268	4	US-10-425-114-32554	Sequence 42554, A	491	25	75.8	433	4	US-10-369-493-7721	Sequence 7721, Ap
419	25	75.8	274	4	US-10-437-963-186558	Sequence 186558,	492	25	75.8	436	6	US-11-097-143-11781	Sequence 11781, Ap
420	25	75.8	276	4	US-10-425-114-37474	Sequence 37474, A	493	25	75.8	436	4	US-10-289-762-711	Sequence 711, App
421	25	75.8	276	4	US-10-425-114-66498	Sequence 66498, A	494	25	75.8	437	4	US-10-425-115-311741	Sequence 311741,
422	25	75.8	276	4	US-10-425-114-66538	Sequence 66538, A	495	25	75.8	439	3	US-09-984-130-145	Sequence 145, App
423	25	75.8	277	4	US-10-237-551-234	Sequence 234, App	496	25	75.8	439	3	US-09-836-353A-145	Sequence 145, App
424	25	75.8	277	5	US-10-945-050-234	Sequence 234, App	497	25	75.8	440	4	US-10-437-963-149244	Sequence 149244,
425	25	75.8	283	5	US-10-732-923-4082	Sequence 4082, Ap	498	25	75.8	441	4	US-10-425-114-64080	Sequence 64080, A
426	25	75.8	292	4	US-10-287-274-336	Sequence 336, App	499	25	75.8	443	5	US-10-408-765A-2345	Sequence 2345, Ap
427	25	75.8	295	4	US-10-437-963-171242	Sequence 171242,	500	25	75.8	443	5	US-10-684-422-332	Sequence 332, App
428	25	75.8	295	4	US-10-425-115-212068	Sequence 212068,	501	25	75.8	457	5	US-10-732-923-10439	Sequence 10439, A
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431	25	75.8	300	4	US-10-282-122A-62364	Sequence 62364, A	504	25	75.8	467	4	US-10-369-493-10855	Sequence 10855, A
432	25	75.8	301	3	US-09-905-176-23	Sequence 23, Appl	505	25	75.8	471	4	US-10-003-392-10	Sequence 10, Appl
433	25	75.8	302	4	US-10-369-493-13673	Sequence 13673, A	506	25	75.8	471	5	US-10-916-247-10	Sequence 10, Appl
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435	25	75.8	303	4	US-10-168-506-23	Sequence 23, Appl	508	25	75.8	476	4	US-10-369-493-6760	Sequence 6760, Ap
436	25	75.8	303	5	US-10-838-181-23	Sequence 23, Appl	509	25	75.8	478	4	US-10-389-566-1527	Sequence 1527, Ap
437	25	75.8	304	4	US-10-156-761-14358	Sequence 14358, A	510	25	75.8	482	4	US-10-369-493-23531	Sequence 23531, A
438	25	75.8	306	4	US-10-282-122A-62364	Sequence 62364, A	511	25	75.8	485	4	US-10-172-502-18	Sequence 18, Appl
439	25	75.8	307	4	US-10-282-122A-63702	Sequence 63702, A	512	25	75.8	485	4	US-10-389-566-960	Sequence 960, App
440	25	75.8	313	4	US-10-369-493-15673	Sequence 15673, A	513	25	75.8	485	6	US-10-732-923-9765	Sequence 9765, Ap
441	25	75.8	313	4	US-10-369-493-16063	Sequence 16063, A	514	25	75.8	485	6	US-11-020-509-18	Sequence 18, Appl
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443	25	75.8	317	3	US-09-738-626-4379	Sequence 4379, Ap	516	25	75.8	494	4	US-10-424-599-256057	Sequence 256057,
444	25	75.8	322	4	US-10-425-114-68173	Sequence 68173, A	517	25	75.8	495	4	US-10-003-392-8	Sequence 8, Appli
445	25	75.8	322	4	US-10-425-115-355450	Sequence 355450,	518	25	75.8	495	5	US-10-437-963-127101	Sequence 127101,
446	25	75.8	322	4	US-10-425-115-355453	Sequence 355453,	519	25	75.8	495	5	US-10-916-247-8	Sequence 8, Appli
447	25	75.8	327	3	US-09-815-242-10407	Sequence 10407, A	520	25	75.8	502	4	US-10-369-493-20608	Sequence 20608, A
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449	25	75.8	339	4	US-10-437-963-118410	Sequence 118410,	522	25	75.8	504	4	US-10-425-115-207356	Sequence 207356,
450	25	75.8	340	4	US-10-264-213-225	Sequence 225, App	523	25	75.8	505	5	US-10-389-566-887	Sequence 887, App
451	25	75.8	340	4	US-10-282-122A-46441	Sequence 46441, A	524	25	75.8	505	5	US-10-732-923-9766	Sequence 9766, Ap
452	25	75.8	341	4	US-10-425-114-46072	Sequence 46072, A	525	25	75.8	506	4	US-10-369-493-5064	Sequence 5064, Ap
453	25	75.8	341	4	US-10-425-114-48284	Sequence 48284, A	526	25	75.8	509	4	US-10-282-122A-76665	Sequence 76665, A
454	25	75.8	342	4	US-10-310-154-677	Sequence 677, App	527	25	75.8	513	4	US-10-437-963-154884	Sequence 154884,
455	25	75.8	342	4	US-10-437-963-185725	Sequence 185725,	528	25	75.8	516	4	US-10-168-853-17	Sequence 17, Appl
456	25	75.8	342	5	US-10-732-923-592	Sequence 592, App	529	25	75.8	520	5	US-10-450-763-46025	Sequence 46025, A
457	25	75.8	343	4	US-10-369-493-15307	Sequence 15307, A	530	25	75.8	520	6	US-11-097-143-32946	Sequence 32946, A
458	25	75.8	343	4	US-10-424-599-215379	Sequence 215379,	531	25	75.8	525	4	US-10-437-963-105709	Sequence 105709,
459	25	75.8	347	4	US-10-425-115-242139	Sequence 242139,	532	25	75.8	525	4	US-10-600-070-122	Sequence 122, App
460	25	75.8	347	5	US-10-739-930-6416	Sequence 6416, Ap	533	25	75.8	528	4	US-10-424-599-271614	Sequence 271614,
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462	25	75.8	352	4	US-10-437-963-105979	Sequence 105979,	535	25	75.8	532	4	US-10-425-115-357974	Sequence 357974,
463	25	75.8	358	4	US-10-425-114-59428	Sequence 59428, A	536	25	75.8	536	4	US-10-425-114-44244	Sequence 44244, A
464	25	75.8	358	4	US-10-425-114-64758	Sequence 64758, A	537	25	75.8	540	2	US-08-781-986A-5225	Sequence 5225, Ap
465	25	75.8	358	4	US-10-425-114-65925	Sequence 65925, A	538	25	75.8	540	2	US-08-781-986A-5242	Sequence 5242, Ap

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540	25	75.8	4	US-10-329-624-5242	Sequence 5242, Ap	613	25	75.8	4	US-10-156-761-12875	Sequence 12875, A	
541	25	75.8	540	US-10-984-449-87	Sequence 87, Appl	614	25	75.8	629	4	US-10-156-761-14676	Sequence 14676, A
542	25	75.8	540	US-10-732-923-23465	Sequence 23465, A	615	25	75.8	631	4	US-10-120-1988-2	Sequence 2, Appli
543	25	75.8	541	US-10-472-928-3908	Sequence 3908, Ap	616	25	75.8	633	4	US-10-437-963-143875	Sequence 143875,
544	25	75.8	546	US-10-282-122A-55999	Sequence 55999, A	617	25	75.8	633	4	US-10-782-020-8	Sequence 8, Appli
545	25	75.8	547	US-09-815-242-11982	Sequence 11982, A	618	25	75.8	633	4	US-10-782-141-9	Sequence 9, Appli
546	25	75.8	547	US-10-282-122A-66610	Sequence 66610, A	619	25	75.8	633	5	US-10-781-979-11	Sequence 11, Appl
547	25	75.8	547	US-10-282-122A-68106	Sequence 68106, A	620	25	75.8	634	4	US-10-198-478-12	Sequence 12, Appl
548	25	75.8	547	US-10-282-122A-68314	Sequence 68314, A	621	25	75.8	634	4	US-10-102-469-18	Sequence 18, Appl
549	25	75.8	548	US-09-815-242-14035	Sequence 14035, A	622	25	75.8	635	4	US-10-428-961-46	Sequence 46, Appl
550	25	75.8	548	US-10-096-571-12	Sequence 12, Appl	623	25	75.8	635	4	US-10-437-963-146769	Sequence 146769,
551	25	75.8	548	US-10-096-5958-12	Sequence 12, Appl	624	25	75.8	637	4	US-10-781-014-230	Sequence 230, App
552	25	75.8	548	US-10-282-122A-59635	Sequence 59635, A	625	25	75.8	637	5	US-10-494-836-30	Sequence 30, Appl
553	25	75.8	548	US-10-282-122A-73238	Sequence 73238, A	626	25	75.8	648	4	US-10-437-963-154885	Sequence 154885,
554	25	75.8	548	US-10-282-122A-74957	Sequence 74957, A	627	25	75.8	655	4	US-10-282-122A-53712	Sequence 53712, A
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557	25	75.8	550	US-09-815-242-10756	Sequence 10756, A	630	25	75.8	660	3	US-09-727-801-10	Sequence 10, Appl
558	25	75.8	550	US-10-282-122A-49653	Sequence 49653, A	631	25	75.8	667	6	US-11-097-143-20325	Sequence 20325, A
559	25	75.8	550	US-10-282-122A-56991	Sequence 56991, A	632	25	75.8	703	4	US-10-282-122A-47690	Sequence 47690, A
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561	25	75.8	554	US-10-282-122A-57978	Sequence 57978, A	634	25	75.8	712	4	US-10-369-493-22762	Sequence 22762, A
562	25	75.8	556	US-10-617-320-3006	Sequence 3006, Ap	635	25	75.8	725	5	US-10-450-763-58207	Sequence 58207, A
563	25	75.8	559	US-10-437-963-145139	Sequence 145139, A	636	25	75.8	722	3	US-09-894-998-15	Sequence 15, Appl
564	25	75.8	560	US-10-617-038-14	Sequence 14, Appl	637	25	75.8	722	4	US-10-121-988-15	Sequence 15, Appl
565	25	75.8	562	US-09-741-669-363	Sequence 363, App	638	25	75.8	722	4	US-10-121-988-159	Sequence 159, App
566	25	75.8	562	US-10-369-493-21657	Sequence 21657, A	639	25	75.8	722	4	US-10-200-562-15	Sequence 15, Appl
567	25	75.8	562	US-10-732-923-18366	Sequence 18366, A	640	25	75.8	722	4	US-10-200-562-159	Sequence 159, App
568	25	75.8	563	US-10-282-122A-31514	Sequence 31514, A	641	25	75.8	722	4	US-10-237-551-15	Sequence 15, Appl
569	25	75.8	564	US-10-732-923-18279	Sequence 18279, A	642	25	75.8	722	4	US-10-237-551-159	Sequence 159, App
570	25	75.8	565	US-10-282-122A-60953	Sequence 60953, A	643	25	75.8	722	4	US-10-237-551-235	Sequence 235, App
571	25	75.8	570	US-10-282-122A-50415	Sequence 50415, A	644	25	75.8	722	4	US-10-623-429-10	Sequence 10, Appl
572	25	75.8	572	US-10-732-923-18419	Sequence 18419, A	645	25	75.8	722	5	US-10-945-050-15	Sequence 15, Appl
573	25	75.8	574	US-10-984-449-32	Sequence 32, Appl	646	25	75.8	722	5	US-10-945-050-159	Sequence 159, App
574	25	75.8	575	US-11-097-143-17316	Sequence 17316, A	647	25	75.8	722	5	US-10-945-050-235	Sequence 235, App
575	25	75.8	576	US-09-738-626-3682	Sequence 3682, Ap	648	25	75.8	727	4	US-10-033-174-11	Sequence 11, Appl
576	25	75.8	576	US-10-282-122A-50825	Sequence 50825, A	649	25	75.8	760	4	US-10-600-070-125	Sequence 125, App
577	25	75.8	577	US-10-282-122A-49260	Sequence 49260, A	650	25	75.8	768	4	US-10-437-963-196918	Sequence 196918,
578	25	75.8	577	US-10-739-930-5910	Sequence 5910, Ap	651	25	75.8	786	4	US-10-282-122A-62995	Sequence 62995, A
579	25	75.8	577	US-10-732-923-18284	Sequence 18284, A	652	25	75.8	790	5	US-10-779-597-74	Sequence 74, Appl
580	25	75.8	578	US-10-282-122A-62667	Sequence 62667, A	653	25	75.8	798	4	US-10-282-122A-63988	Sequence 63988, A
581	25	75.8	582	US-10-282-122A-64783	Sequence 64783, A	654	25	75.8	798	4	US-10-425-115-292207	Sequence 292207,
582	25	75.8	591	US-10-437-963-143877	Sequence 143877, A	655	25	75.8	800	4	US-10-767-701-45770	Sequence 45770, A
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584	25	75.8	596	US-10-282-122A-47912	Sequence 47912, A	657	25	75.8	828	4	US-10-282-122A-62205	Sequence 62205, A
585	25	75.8	596	US-11-097-143-42057	Sequence 42057, A	658	25	75.8	829	4	US-10-128-714-8460	Sequence 8460, Ap
586	25	75.8	598	US-10-437-963-162631	Sequence 162631, A	659	25	75.8	831	4	US-10-282-122A-64588	Sequence 64588, A
587	25	75.8	600	US-10-003-392-20	Sequence 20, Appl	660	25	75.8	845	4	US-10-262-794A-37	Sequence 37, Appl
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589	25	75.8	603	US-10-425-114-68167	Sequence 68167, A	662	25	75.8	882	4	US-10-669-161-12	Sequence 12, Appl
590	25	75.8	605	US-10-369-493-18933	Sequence 18933, A	663	25	75.8	883	4	US-10-041-018-304	Sequence 304, App
591	25	75.8	605	US-10-369-493-20034	Sequence 20034, A	664	25	75.8	890	4	US-10-298-122-9	Sequence 9, Appli
592	25	75.8	616	US-10-156-761-10270	Sequence 10270, A	665	25	75.8	926	4	US-10-408-765A-1645	Sequence 1645, Ap
593	25	75.8	616	US-10-389-566-1435	Sequence 1435, Ap	666	25	75.8	937	4	US-10-126-927-66	Sequence 66, Appl
594	25	75.8	616	US-10-732-923-9761	Sequence 9761, Ap	667	25	75.8	937	6	US-11-009-635-66	Sequence 66, Appl
595	25	75.8	618	US-09-934-901-18	Sequence 18, Appl	668	25	75.8	940	4	US-10-425-115-265279	Sequence 265279,
596	25	75.8	618	US-09-934-868-8	Sequence 8, Appli	669	25	75.8	944	4	US-10-425-114-58539	Sequence 58539, A
597	25	75.8	618	US-10-320-924-18	Sequence 18, Appl	670	25	75.8	969	6	US-10-108-605-317	Sequence 317, App
598	25	75.8	618	US-10-320-874-18	Sequence 18, Appl	671	25	75.8	971	4	US-10-108-605-317	Sequence 317, App
599	25	75.8	618	US-10-282-122A-62448	Sequence 62448, A	672	25	75.8	997	4	US-10-437-963-187883	Sequence 187883,
600	25	75.8	618	US-10-282-122A-64823	Sequence 64823, A	673	25	75.8	1024	4	US-10-211-962-43	Sequence 43, Appl
601	25	75.8	618	US-10-321-210-18	Sequence 21, Appl	674	25	75.8	1081	4	US-10-437-963-196915	Sequence 196915,
602	25	75.8	618	US-10-701-200-8	Sequence 8, Appli	675	25	75.8	1094	4	US-10-437-963-196915	Sequence 196915,
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604	25	75.8	622	US-10-282-122A-60778	Sequence 60778, A	677	25	75.8	1098	3	US-09-797-862-32	Sequence 32, Appl
605	25	75.8	622	US-10-282-122A-61744	Sequence 61744, A	678	25	75.8	1098	5	US-10-637-659-32	Sequence 32, Appl
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607	25	75.8	625	US-10-389-566-1272	Sequence 1272, Ap	680	25	75.8	1194	4	US-10-437-963-175889	Sequence 175889,
608	25	75.8	625	US-10-282-122A-63917	Sequence 63917, A	681	25	75.8	1349	4	US-10-437-963-144453	Sequence 144453,
609	25	75.8	625	US-10-916-247-21	Sequence 21, Appl	682	25	75.8	1384	4	US-10-437-963-192417	Sequence 192417,
610	25	75.8	625	US-10-732-923-9752	Sequence 9752, Ap	683	25	75.8	1538	4	US-10-437-963-421-21	Sequence 21, Appl
611	25	75.8	626	US-09-738-626-6957	Sequence 6957, Ap	684	25	75.8	1571	5	US-10-864-138-2	Sequence 2, Appli

685	25	75.8	1579	5	US-10-482-929-2	Sequence 2, Appli	758	24	72.7	100	4	US-10-425-115-216534	Sequence 216534,
686	25	75.8	1623	4	US-10-437-963-202524	Sequence 202524,	759	24	72.7	100	5	US-10-884-830-607	Sequence 607, App
687	25	75.8	1624	6	US-11-097-143-8424	Sequence 8424, Ap	760	24	72.7	102	4	US-10-335-977-6335	Sequence 6335, Ap
688	25	75.8	1801	6	US-11-097-143-6627	Sequence 6627, Ap	761	24	72.7	103	5	US-10-450-763-35231	Sequence 35291, A
689	25	75.8	1849	4	US-10-282-794A-49	Sequence 49, Appl	762	24	72.7	104	4	US-10-425-115-244367	Sequence 244367, A
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691	25	75.8	1954	4	US-10-147-299A-4	Sequence 4, Appli	764	24	72.7	106	4	US-10-425-115-209828	Sequence 209828,
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695	25	75.8	2283	4	US-10-172-502-4	Sequence 4, Appli	768	24	72.7	109	4	US-10-425-115-240294	Sequence 240294, A
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707	25	75.8	2479	4	US-10-437-963-126085	Sequence 126085,	780	24	72.7	115	5	US-10-982-359-26	Sequence 26, Appl
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835	24	72.7	176	3	US-09-205-658-212	Sequence 212, App	908	24	72.7	245	4	US-10-293-418-1714	Sequence 1714, Ap
836	24	72.7	176	3	US-09-963-693-212	Sequence 212, App	909	24	72.7	245	4	US-10-424-599-249194	Sequence 249194, Ap
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839	24	72.7	177	5	US-10-732-923-4029	Sequence 4029, Ap	912	24	72.7	247	3	US-10-293-418-969	Sequence 969, App
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862	24	72.7	205	6	US-11-028-898-80	Sequence 80, Appl	935	24	72.7	251	5	US-10-724-264A-21	Sequence 21, Appl
863	24	72.7	205	6	US-11-083-005-81	Sequence 81, Appl	936	24	72.7	252	3	US-09-880-748-1772	Sequence 1772, Ap
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879	24	72.7	224	4	US-10-156-761-12608	Sequence 12608, A	952	24	72.7	264	4	US-10-282-122A-66163	Sequence 66163, A
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889	24	72.7	233	6	US-11-082-005-77	Sequence 77, Appl	962	24	72.7	273	4	US-10-767-701-38821	Sequence 38821, A
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892	24	72.7	238	4	US-10-112-944-923	Sequence 923, App	965	24	72.7	279	4	US-10-156-761-9570	Sequence 9570, Ap
893	24	72.7	238	4	US-10-437-963-180039	Sequence 180039,	966	24	72.7	279	4	US-10-424-599-153142	Sequence 153142, A
894	24	72.7	239	3	US-10-369-493-20844	Sequence 20844, A	967	24	72.7	281	4	US-10-430-011-133	Sequence 133, App
895	24	72.7	241	3	US-09-880-748-1303	Sequence 1303, Ap	968	24	72.7	281	4	US-10-369-493-18679	Sequence 18679, A
896	24	72.7	241	4	US-10-293-418-1303	Sequence 1303, Ap	969	24	72.7	284	4	US-10-193-002-157	Sequence 157, App
897	24	72.7	244	3	US-09-880-748-1210	Sequence 1210, Ap	970	24	72.7	284	4	US-10-084-843-162	Sequence 162, App
898	24	72.7	244	3	US-09-880-748-1214	Sequence 1214, Ap	971	24	72.7	284	6	US-11-028-898-162	Sequence 162, App
899	24	72.7	244	3	US-09-880-748-1371	Sequence 1371, Ap	972	24	72.7	284	6	US-11-082-005-157	Sequence 157, App
900	24	72.7	244	3	US-09-880-748-1372	Sequence 1372, Ap	973	24	72.7	286	4	US-10-282-122A-47557	Sequence 47557, A
901	24	72.7	244	3	US-09-880-748-1507	Sequence 1507, Ap	974	24	72.7	286	4	US-10-437-963-163258	Sequence 163258, A
902	24	72.7	244	3	US-10-293-418-1210	Sequence 1210, Ap	975	24	72.7	288	4	US-10-156-761-13451	Sequence 13451, A
903	24	72.7	244	4	US-10-293-418-1214	Sequence 1214, Ap	976	24	72.7	288	4	US-10-425-114-59540	Sequence 59540, A


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977 24 72.7 289 4 US-10-437-963-158435
978 24 72.7 289 4 US-10-425-115-284052
979 24 72.7 292 4 US-10-369-493-16821
980 24 72.7 292 4 US-10-425-114-55715
981 24 72.7 292 4 US-10-634-548-57
982 24 72.7 292 6 US-11-097-143-11061
983 24 72.7 294 6 US-11-097-143-27861
984 24 72.7 298 4 US-10-437-963-169792
985 24 72.7 299 4 US-10-156-761-11947
986 24 72.7 301 4 US-10-032-585-7194
987 24 72.7 301 5 US-10-739-930-8255
988 24 72.7 301 5 US-10-450-763-36226
989 24 72.7 303 3 US-09-982-616-10
990 24 72.7 303 4 US-10-402-842-23
991 24 72.7 303 4 US-10-282-122A-60839
992 24 72.7 303 4 US-10-746-795-23
993 24 72.7 304 4 US-10-424-599-179906
994 24 72.7 306 4 US-10-384-974-116
995 24 72.7 308 4 US-10-282-122A-49745
996 24 72.7 312 4 US-10-437-963-130654
997 24 72.7 313 5 US-10-500-530-14
998 24 72.7 316 4 US-10-437-963-167614
999 24 72.7 317 6 US-11-097-143-16758
1000 24 72.7 318 5 US-10-739-930-7595

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ALIGNMENTS

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RESULT 1
US-09-155-106-5
; Sequence 5, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-5

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```

Query Match 100.0%; Score 33; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 GATNLAA 7
    |||||
Db 1 GATNLAA 7

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RESULT 2
US-10-808-538-5
; Sequence 5, Application US/10808538

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; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-808-538-5

```

```

Query Match 100.0%; Score 33; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Oy 1 GATNLAA 7
    |||||
Db 1 GATNLAA 7

```

```

RESULT 3
US-09-155-106-22
; Sequence 22, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid

```

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22
  Query Match      100.0%; Score 33; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      |||||
Db      50 GATNLAA 56

RESULT 4
US-09-155-106-23
; Sequence 23, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23
  Query Match      100.0%; Score 33; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      |||||
Db      50 GATNLAA 56

RESULT 5
US-09-155-106-24
; Sequence 24, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23
  Query Match      100.0%; Score 33; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      |||||
Db      50 GATNLAA 56

RESULT 6
US-09-155-106-28
; Sequence 28, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-28
  Query Match      100.0%; Score 33; DB 3; Length 108;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      |||||
Db      50 GATNLAA 56

RESULT 7
US-09-155-106-30
; Sequence 30, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-30

Query Match 100.0%; Score 33; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 50 GATNLAA 56

RESULT 8

US-10-808-538-22
; Sequence 22, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-808-538-22

Query Match 100.0%; Score 33; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 50 GATNLAA 56

RESULT 9

US-10-808-538-23
; Sequence 23, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-808-538-23

Query Match 100.0%; Score 33; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
|||||
Db 50 GATNLAA 56

RESULT 10

US-10-808-538-24
; Sequence 24, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-808-538-24

Query Match 100.0%; Score 33; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||||
DB 50 GATNLAA 56

RESULT 11

US-10-808-538-28
Sequence 28, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:

APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-10-808-538-28

Query Match 100.0%; Score 33; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||||
DB 50 GATNLAA 56

RESULT 12

US-10-808-538-30
Sequence 30, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:

APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-808-538-30

Query Match 100.0%; Score 33; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||||
DB 50 GATNLAA 56

RESULT 13

US-10-767-701-55746
Sequence 55746, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 55746
LENGTH: 130

TYPE: PRT

ORGANISM: Sorghum bicolor

FEATURE:

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; OTHER INFORMATION: Clone ID: 30931920.pep
US-10-767-701-55746

Query Match      90.9%; Score 30; DB 4; Length 130;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      106 GATNVAA 112

RESULT 14
US-10-437-963-127994
; Sequence 127994, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127994
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30391C.1.pep
US-10-437-963-127994

Query Match      90.9%; Score 30; DB 4; Length 411;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      177 GATNVAA 183

RESULT 15
US-10-468-496-1768
; Sequence 1768, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1768
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1768

Query Match      87.9%; Score 29; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 6
Db      6 GATNLAA 11

RESULT 17
US-10-468-496-1770
; Sequence 1770, Application US/10468496
; Publication No. US20040180386A1
```

```
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1768
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1768

Query Match      87.9%; Score 29; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 6
Db      7 GATNLAA 12

RESULT 16
US-10-468-496-1769
; Sequence 1769, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1769
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1769

Query Match      87.9%; Score 29; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 6
Db      6 GATNLAA 11

RESULT 17
US-10-468-496-1770
; Sequence 1770, Application US/10468496
; Publication No. US20040180386A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1770
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1770

Query Match      87.9%; Score 29; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLA 6
Db      5 GATNLA 10
      |||||

RESULT 18
US-10-468-496-1771
; Sequence 1771, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 1771
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1771

Query Match      87.9%; Score 29; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLA 6
Db      4 GATNLA 9
      |||||

RESULT 19
US-10-425-115-246833
; Sequence 246833, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 246833
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_156695C.1.pep
US-10-425-115-246833

Query Match      87.9%; Score 29; DB 4; Length 88;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      45 GATNLGA 51
      |||||

RESULT 20
US-10-424-599-270261
; Sequence 270261, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 270261
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(131)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
```

; OTHER INFORMATION: Clone ID: PAT_MRT3847_86064C.1.pcp
US-10-424-599-270261

Query Match 87.9%; Score 29; DB 4; Length 131;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 24 GATNLVA 30

RESULT 21

US-10-516-429-11
; Sequence 11, Application US/10516429
; Publication No. US20050191617A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: HIRONAKA, Takashi
; TITLE OF INVENTION: Paranyxoviral Vectors Encoding
; TITLE OF INVENTION: Antibodies and Uses Thereof
; FILE REFERENCE: 50026/049001
; CURRENT APPLICATION NUMBER: US/10/516,429
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: PCT/JP03/07005
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 2002-161964
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: an immunoglobulin IN-1 light chain
US-10-516-429-11

Query Match 87.9%; Score 29; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
| | | | |
Db 71 GATNLAA 76

RESULT 22

US-10-006-593-69
; Sequence 69, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 236
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: an immunoglobulin IN-1 light chain

; OTHER INFORMATION: Humanized antibody light chain
US-10-006-593-69

Query Match 87.9%; Score 29; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
| | | | |
Db 72 GATNLAA 77

RESULT 23

US-10-307-724-69
; Sequence 69, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2cip
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 236
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody light chain
US-10-307-724-69

Query Match 87.9%; Score 29; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 6
| | | | |
Db 72 GATNLAA 77

RESULT 24

US-10-737-290-69
; Sequence 69, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orecchia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889

; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 236
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody light chain
US-10-737-290-69

Query Match 87.9%; Score 29; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
| | | | |
Db 72 GATNLA 77

RESULT 25
US-10-108-260A-4140
; Sequence 4140, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: H1-A0106
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4140
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4140

Query Match 87.9%; Score 29; DB 4; Length 336;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLA 7
| | | | |
Db 281 GGTNLA 287

RESULT 26
US-10-437-963-144974
; Sequence 144974, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144974
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_45738C.1.pep
US-10-437-963-144974

Query Match 87.9%; Score 29; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
| | | | |
Db 141 GATNLA 146

RESULT 27
US-11-035-599-52
; Sequence 52, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Pandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-52

Query Match 87.9%; Score 29; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLA 6
| | | | |
Db 190 GATNLA 195

RESULT 28
US-11-035-599-53
; Sequence 53, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Pandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-53

Query Match 87.9%; Score 29; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 190 GATNLA 195

RESULT 29
US-11-035-599-51
; Sequence 51, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Pandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-51

Query Match 87.9%; Score 29; DB 6; Length 731;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 670 GATNLA 675

RESULT 30
US-11-035-599-50
; Sequence 50, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Pandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-50

Query Match 87.9%; Score 29; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 190 GATNLA 195

RESULT 31
US-10-606-060A-8
; Sequence 8, Application US/10606060A
; Publication No. US20040058369A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3/2
; CURRENT APPLICATION NUMBER: US/10/606,060A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 08/653,648
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-606-060A-8

Query Match 87.9%; Score 29; DB 4; Length 878;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLA 7
Db 116 GATNLA 122

RESULT 32
US-11-097-143-2256
; Sequence 2256, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2256
; LENGTH: 881

; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-2256

Query Match 87.9%; Score 29; DB 6; Length 881;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:|
Db 116 GATNLGA 122

RESULT 33

US-10-450-763-32765
; Sequence 32765, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 32765
; LENGTH: 945
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-32765

Query Match 87.9%; Score 29; DB 5; Length 945;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:|
Db 284 GGTNLAA 290

RESULT 34

US-10-425-115-283669
; Sequence 283669, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283669
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21805C.1.pep
US-10-425-115-283669

Query Match 84.8%; Score 28; DB 4; Length 52;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:|
Db 24 GATSLAA 30

RESULT 35

US-10-424-599-182384
; Sequence 182384, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182384
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(78)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135705C.1.pep
US-10-424-599-182384

Query Match 84.8%; Score 28; DB 4; Length 78;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
|||:|
Db 9 GAANLAA 15

RESULT 36

US-10-437-963-146270
; Sequence 146270, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146270
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4690C.1.pep
US-10-437-963-146270

Query Match 84.8%; Score 28; DB 4; Length 84;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7

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Db      || |||||
      16 GAANLAA 22

RESULT 37
US-10-424-599-182386
; Sequence 182386, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182386
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135707C.1.pep
US-10-424-599-182386

Query Match      84.8%; Score 28; DB 4; Length 89;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
      || |||||
Db      17 GAANLAA 23

RESULT 38
US-10-424-599-182385
; Sequence 182385, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182385
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135706C.1.pep
US-10-424-599-182385

Query Match      84.8%; Score 28; DB 4; Length 90;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
      || |||||
Db      17 GAANLAA 23

RESULT 39
US-10-424-599-168348
; Sequence 168348, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 168348
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_123033C.1.pep
US-10-424-599-168348

Query Match      84.8%; Score 28; DB 4; Length 105;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
      || |||||
Db      17 GAANLAA 23

RESULT 40
US-10-424-599-182383
; Sequence 182383, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182383
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135704C.1.pep
US-10-424-599-182383

Query Match      84.8%; Score 28; DB 4; Length 158;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
      || |||||
Db      37 GAANLAA 43

RESULT 41
US-10-437-963-105903
; Sequence 105903, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105903
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10398C.1.pep
US-10-437-963-105903

Query Match 84.8%; Score 28; DB 4; Length 186;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 10 GATDLAA 16

RESULT 42

US-10-767-701-31863
; Sequence 31863, Application US/107677701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31863
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10791_1.pep
US-10-767-701-31863

Query Match 84.8%; Score 28; DB 4; Length 200;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 152 GETNLAA 158

RESULT 43

US-10-425-115-267428
; Sequence 267428, Application US/10425115
; Publication No. US20040214722A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267428
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_17549C.1.pep
US-10-425-115-267428

Query Match 84.8%; Score 28; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 155 GETNLAA 161

RESULT 44

US-10-425-114-37962
; Sequence 37962, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37962
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700457589_FLI.pep
US-10-425-114-37962

Query Match 84.8%; Score 28; DB 4; Length 226;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
| | | | |
Db 158 GETNLAA 164

RESULT 45

US-10-282-122A-63096
; Sequence 63096, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63096
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-282-122A-63096

Query Match      84.8%; Score 28; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 61 GATNLPA 67

RESULT 46
US-10-425-115-241036
; Sequence 241036, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 241036
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_151403C.1.pep
US-10-425-115-241036

Query Match      84.8%; Score 28; DB 4; Length 238;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 3 GATSLAA 9

RESULT 47
US-10-425-115-221431
; Sequence 221431, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
```

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221431
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(245)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133536C.1.pep
US-10-425-115-221431

Query Match      84.8%; Score 28; DB 4; Length 245;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 107 GAANLAA 113

RESULT 48
US-10-374-780A-1405
; Sequence 1405, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1405
; LENGTH: 289
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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1073
US-10-374-780A-1405

Query Match      84.8%; Score 28; DB 4; Length 289;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      171 GATSLAA 177

RESULT 49
US-10-437-963-120492
; Sequence 120492, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120492
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23606C.1.pep
US-10-437-963-120492

Query Match      84.8%; Score 28; DB 4; Length 289;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      171 GATSLAA 177

RESULT 50
US-10-669-824-12
; Sequence 12, Application US/10669824
; Publication No. US20040128712A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Guttersen, Neal
; APPLICANT: Hempel, Frederick
; APPLICANT: Kumimoto, Roderick W
; APPLICANT: Keddle, James S
; APPLICANT: Sherman, Bradley K
; TITLE OF INVENTION: METHODS FOR MODIFYING PLANT BIOMASS AND TOLERANCE TO ABIOTIC
; TITLE OF INVENTION: STRESS
; FILE REFERENCE: MBI-0034CIP
; CURRENT APPLICATION NUMBER: US/10/669,824
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/374,780
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/227,439
; PRIOR FILING DATE: 2000-08-22
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; PRIOR APPLICATION NUMBER: US 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/125,814
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: G3407 polypeptide
US-10-669-824-12

Query Match      84.8%; Score 28; DB 4; Length 289;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      171 GATSLAA 177
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Job time : 67.7869 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:42:11 ; Search time 8.72131 Seconds
(without alignments)
37.683 Million cell updates/sec

Title: US-10-808-538-5

Perfect score: 33

Sequence: 1 GATNLAA 7

Scoring table: BLOSUM62

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Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications_AA_New.*

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- 2: /SID85/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SID85/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SID85/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /SID85/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 9: /SID85/prodata/1/pubpaa/US10_NEW_PUB.pep1.*
- 10: /SID85/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 11: /SID85/prodata/1/pubpaa/US11_NEW_PUB.pep1.*
- 12: /SID85/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	87.9	309	11	US-11-188-298-14967
2	29	87.9	329	11	US-11-188-298-3030
3	28	84.8	152	11	US-11-096-568A-20137
4	28	84.8	181	11	US-11-087-099-10126
5	28	84.8	223	11	US-11-096-568A-20136
6	28	84.8	289	9	US-10-714-887-356
7	28	84.8	414	11	US-11-188-298-7053
8	28	84.8	462	11	US-11-096-568A-15981
9	28	84.8	480	11	US-11-096-568A-15980
10	28	84.8	573	11	US-11-188-298-14241
11	28	84.8	587	11	US-11-188-298-7430
12	28	84.8	1122	9	US-10-467-657-6112
13	27	81.8	156	11	US-11-096-568A-1394
14	27	81.8	190	11	US-11-096-568A-1393
15	27	81.8	354	9	US-10-467-657-7260
16	27	81.8	363	11	US-11-055-822-646
17	27	81.8	465	11	US-11-255-794-6
18	27	81.8	493	11	US-11-076-427A-4
19	27	81.8	494	9	US-10-971-560-7
20	27	81.8	553	11	US-11-188-298-7687
21	27	81.8	581	11	US-11-188-298-4736

22	81.8	581	11	US-11-188-298-10278	Sequence 10278, A
23	81.8	626	11	US-11-096-568A-32112	Sequence 32112, A
24	81.8	637	11	US-11-188-298-13299	Sequence 13299, A
25	81.8	637	11	US-11-188-298-14583	Sequence 14583, A
26	81.8	784	11	US-11-096-568A-32111	Sequence 32111, A
27	81.8	793	11	US-11-096-568A-32110	Sequence 32110, A
28	81.8	875	11	US-11-188-298-6082	Sequence 6082, Ap
29	78.8	98	11	US-11-188-298-12126	Sequence 12126, A
30	78.8	98	11	US-11-188-298-14158	Sequence 14158, A
31	78.8	103	11	US-11-188-298-5677	Sequence 5677, Ap
32	78.8	103	11	US-11-188-298-14076	Sequence 14076, A
33	78.8	104	11	US-11-188-298-1691	Sequence 1691, Ap
34	78.8	104	11	US-11-188-298-3955	Sequence 3955, Ap
35	78.8	106	11	US-11-188-298-18880	Sequence 18880, A
36	78.8	207	11	US-11-045-004-495	Sequence 495, App
37	78.8	212	11	US-11-188-298-17222	Sequence 17222, A
38	78.8	218	11	US-11-188-298-10321	Sequence 10321, A
39	78.8	240	11	US-11-188-298-5499	Sequence 5499, Ap
40	78.8	240	11	US-11-188-298-21300	Sequence 21300, A
41	78.8	241	11	US-11-188-298-22158	Sequence 22158, A
42	78.8	242	11	US-11-188-298-19893	Sequence 19893, A
43	78.8	252	11	US-11-188-298-20607	Sequence 20607, A
44	78.8	285	11	US-11-188-298-6948	Sequence 6948, Ap
45	78.8	427	11	US-11-045-004-1784	Sequence 1784, Ap
46	78.8	432	11	US-11-103-357-5	Sequence 5, Appli
47	78.8	432	11	US-11-018-868-34	Sequence 34, Appl
48	78.8	435	11	US-11-188-298-15735	Sequence 15735, A
49	78.8	467	11	US-11-188-298-1962	Sequence 1962, Ap
50	78.8	512	11	US-11-188-298-5948	Sequence 5948, Ap
51	78.8	521	11	US-11-188-298-6909	Sequence 6909, Ap
52	78.8	541	11	US-11-188-298-9888	Sequence 9888, Ap
53	78.8	567	11	US-11-188-298-10168	Sequence 10168, A
54	78.8	567	11	US-11-188-298-18477	Sequence 18477, A
55	78.8	583	11	US-11-188-298-795	Sequence 795, App
56	78.8	583	11	US-11-188-298-4277	Sequence 4277, Ap
57	78.8	585	11	US-11-188-298-3313	Sequence 3313, Ap
58	78.8	585	11	US-11-188-298-3744	Sequence 3744, Ap
59	78.8	585	11	US-11-188-298-5911	Sequence 5911, Ap
60	78.8	585	11	US-11-188-298-8243	Sequence 8243, Ap
61	78.8	585	11	US-11-188-298-9599	Sequence 9599, Ap
62	78.8	585	11	US-11-188-298-10486	Sequence 10486, A
63	78.8	585	11	US-11-188-298-15561	Sequence 15561, A
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65	78.8	585	11	US-11-188-298-19452	Sequence 19452, A
66	78.8	585	11	US-11-188-298-20104	Sequence 20104, A
67	78.8	585	11	US-11-188-298-22371	Sequence 22371, A
68	78.8	590	11	US-11-188-298-10579	Sequence 10579, A
69	78.8	596	11	US-11-152-903-2	Sequence 2, Appli
70	78.8	596	11	US-11-152-903-4	Sequence 4, Appli
71	78.8	596	11	US-11-152-903-6	Sequence 6, Appli
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73	78.8	596	11	US-11-152-903-10	Sequence 10, Appl
74	78.8	596	11	US-11-152-903-12	Sequence 12, Appl
75	78.8	596	11	US-11-188-298-5744	Sequence 5744, Ap
76	78.8	598	11	US-11-188-298-12810	Sequence 12810, A
77	78.8	598	11	US-11-188-298-13894	Sequence 13894, A
78	78.8	598	11	US-11-188-298-22254	Sequence 22254, A
79	78.8	599	11	US-11-188-298-15409	Sequence 15409, A
80	78.8	638	11	US-11-188-298-1569	Sequence 1569, Ap
81	78.8	638	11	US-11-188-298-2271	Sequence 2271, Ap
82	78.8	638	11	US-11-188-298-14582	Sequence 14582, A
83	78.8	638	11	US-11-188-298-17872	Sequence 17872, A
84	78.8	638	11	US-11-188-298-18598	Sequence 18598, A
85	78.8	640	11	US-11-188-298-11801	Sequence 11801, A
86	78.8	644	9	US-10-509-121-2	Sequence 2, Appli
87	78.8	644	9	US-10-509-121-4	Sequence 4, Appli
88	78.8	644	9	US-10-509-121-6	Sequence 6, Appli
89	78.8	644	9	US-10-509-121-8	Sequence 8, Appli
90	78.8	644	9	US-10-509-121-39	Sequence 39, Appl
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92	78.8	644	11	US-11-188-298-13073	Sequence 13073, A
93	78.8	644	11	US-11-188-298-16194	Sequence 16194, A
94	78.8	645	11	US-11-188-298-4201	Sequence 4201, Ap

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96	26	78.8	648	11	US-11-188-298-10623	Sequence 10623, A	169	25	75.8	472	11	US-11-079-463-5841	Sequence 5841, Ap
97	26	78.8	652	11	US-11-079-122-11	Sequence 11, Appl	170	25	75.8	478	11	US-11-096-568A-20204	Sequence 20204, A
98	26	78.8	652	11	US-11-188-298-13868	Sequence 13868, A	171	25	75.8	500	11	US-11-096-568A-32877	Sequence 32877, A
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103	26	78.8	656	11	US-11-076-733-25	Sequence 25, Appl	176	25	75.8	540	11	US-11-188-298-7275	Sequence 7275, Ap
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105	26	78.8	656	11	US-11-149-420-24	Sequence 24, Appl	178	25	75.8	547	11	US-11-113-270-6	Sequence 6, Appl
106	26	78.8	658	11	US-11-188-298-4461	Sequence 4461, Ap	179	25	75.8	548	11	US-11-113-270-4	Sequence 4, Appl
107	26	78.8	659	11	US-11-188-298-1456	Sequence 1456, Ap	180	25	75.8	548	11	US-11-188-298-2615	Sequence 2615, Ap
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109	26	78.8	662	11	US-11-188-298-16369	Sequence 16369, A	182	25	75.8	548	11	US-11-188-298-6464	Sequence 6464, Ap
110	26	78.8	663	11	US-11-188-298-5458	Sequence 5458, Ap	183	25	75.8	550	11	US-11-188-298-8167	Sequence 8167, Ap
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112	26	78.8	664	11	US-11-188-298-21482	Sequence 21482, A	185	25	75.8	552	11	US-11-188-298-13184	Sequence 13184, A
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114	26	78.8	665	11	US-11-188-298-19015	Sequence 19015, A	187	25	75.8	554	11	US-11-188-298-5302	Sequence 5302, Ap
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116	26	78.8	667	11	US-11-188-298-5413	Sequence 5413, Ap	189	25	75.8	555	11	US-11-188-298-20089	Sequence 20089, A
117	26	78.8	667	11	US-11-188-298-15770	Sequence 15770, A	190	25	75.8	556	11	US-11-188-298-13497	Sequence 13497, A
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122	26	78.8	670	11	US-11-188-298-9996	Sequence 9996, Ap	195	25	75.8	562	11	US-11-188-298-6782	Sequence 6782, Ap
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124	26	78.8	670	11	US-11-188-298-18745	Sequence 18745, A	197	25	75.8	564	11	US-11-188-298-22332	Sequence 22332, A
125	26	78.8	670	11	US-11-188-298-21602	Sequence 21602, A	198	25	75.8	565	9	US-10-506-454-531	Sequence 531, App
126	26	78.8	3343	11	US-11-122-396-7	Sequence 7, Appli	199	25	75.8	565	11	US-11-045-004-1227	Sequence 1227, Ap
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130	25	75.8	139	11	US-11-188-298-8190	Sequence 8190, Ap	203	25	75.8	573	11	US-11-188-298-2290	Sequence 2290, Ap
131	25	75.8	168	10	US-11-301-554-1907	Sequence 1907, Ap	204	25	75.8	575	11	US-11-188-298-9567	Sequence 9567, Ap
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133	25	75.8	180	11	US-11-047-224-3	Sequence 3, Appli	206	25	75.8	581	11	US-11-188-298-2006	Sequence 2006, Ap
134	25	75.8	202	11	US-11-188-298-14065	Sequence 14065, A	207	25	75.8	581	11	US-11-188-298-8803	Sequence 8803, Ap
135	25	75.8	210	11	US-11-045-004-57	Sequence 57, Appl	208	25	75.8	584	11	US-11-188-298-5097	Sequence 5097, Ap
136	25	75.8	237	11	US-11-188-298-12412	Sequence 12412, A	209	25	75.8	585	11	US-11-188-298-6388	Sequence 6388, Ap
137	25	75.8	237	11	US-11-188-298-16937	Sequence 16937, A	210	25	75.8	585	11	US-11-188-298-22021	Sequence 22021, A
138	25	75.8	245	11	US-11-054-515-1900	Sequence 1900, Ap	211	25	75.8	587	11	US-11-188-298-15082	Sequence 15082, A
139	25	75.8	245	11	US-11-266-444-1900	Sequence 1900, Ap	212	25	75.8	587	11	US-11-188-298-21116	Sequence 21116, A
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141	25	75.8	265	11	US-11-188-298-20995	Sequence 20995, A	214	25	75.8	594	11	US-11-188-298-2651	Sequence 2651, Ap
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143	25	75.8	287	11	US-11-188-298-9897	Sequence 9897, Ap	216	25	75.8	612	11	US-11-188-298-4121	Sequence 4121, Ap
144	25	75.8	297	11	US-11-188-298-20824	Sequence 20824, A	217	25	75.8	612	11	US-11-188-298-8878	Sequence 8878, Ap
145	25	75.8	299	11	US-11-055-822-408	Sequence 408, App	218	25	75.8	612	11	US-11-188-298-11696	Sequence 11696, A
146	25	75.8	299	11	US-11-188-298-15002	Sequence 15002, A	219	25	75.8	617	11	US-11-188-298-3213	Sequence 3213, Ap
147	25	75.8	299	11	US-11-188-298-19815	Sequence 19815, A	220	25	75.8	617	11	US-11-188-298-16623	Sequence 16623, A
148	25	75.8	300	11	US-11-096-568A-18358	Sequence 18358, A	221	25	75.8	618	11	US-11-188-298-10071	Sequence 10071, A
149	25	75.8	301	9	US-10-993-143-23	Sequence 23, Appl	222	25	75.8	620	11	US-11-188-298-20260	Sequence 20260, A
150	25	75.8	303	11	US-11-188-298-14137	Sequence 14137, A	223	25	75.8	621	11	US-11-188-298-22171	Sequence 22171, A
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152	25	75.8	306	11	US-11-188-298-5603	Sequence 5603, Ap	225	25	75.8	631	11	US-11-188-298-8083	Sequence 8083, Ap
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154	25	75.8	317	11	US-11-188-298-9502	Sequence 9502, Ap	227	25	75.8	681	11	US-11-188-298-15246	Sequence 15246, A
155	25	75.8	319	11	US-11-188-298-17620	Sequence 17620, A	228	25	75.8	681	11	US-11-188-298-19209	Sequence 19209, A
156	25	75.8	326	11	US-11-096-568A-26149	Sequence 26149, A	229	25	75.8	683	11	US-11-188-298-18155	Sequence 18155, A
157	25	75.8	333	11	US-11-113-270-2	Sequence 2, Appli	230	25	75.8	683	11	US-11-188-298-18529	Sequence 18529, A
158	25	75.8	337	11	US-11-096-568A-18356	Sequence 18356, A	231	25	75.8	760	11	US-11-052-554A-68	Sequence 68, Appl
159	25	75.8	342	11	US-11-188-298-4359	Sequence 4359, Ap	232	25	75.8	937	11	US-11-017-550-66	Sequence 66, Appl
160	25	75.8	342	11	US-11-087-099-435	Sequence 435, App	233	25	75.8	937	11	US-11-002-387-66	Sequence 66, Appl
161	25	75.8	355	11	US-11-096-568A-26148	Sequence 26148, A	234	25	75.8	1127	9	US-10-858-730-13	Sequence 13, Appl
162	25	75.8	362	11	US-11-188-298-19511	Sequence 19511, A	235	25	75.8	1216	9	US-10-647-956A-2	Sequence 2, Appli
163	25	75.8	366	11	US-11-096-568A-26147	Sequence 26147, A	236	25	75.8	7102	11	US-11-143-980-48	Sequence 48, Appl
164	25	75.8	379	11	US-11-096-568A-16450	Sequence 16450, A	237	24	72.7	53	9	US-10-467-657-3714	Sequence 3714, Ap
165	25	75.8	430	11	US-11-045-004-220	Sequence 220, App	238	24	72.7	73	11	US-11-051-481-27	Sequence 27, Appl
166	25	75.8	443	11	US-11-152-366-30	Sequence 30, Appl	239	24	72.7	73	11	US-11-051-481-31	Sequence 31, Appl
167	25	75.8	457	11	US-11-096-568A-20205	Sequence 20205, A	240	24	72.7	81	11	US-11-079-463-6085	Sequence 6085, Ap

241	24	72.7	87	11	US-11-051-481-26	Sequence 26, Appl	314	24	72.7	375	9	US-10-454-437-342	Sequence 342, App
242	24	72.7	87	11	US-11-051-481-30	Sequence 30, Appl	315	24	72.7	399	11	US-11-096-568A-22461	Sequence 22461, A
243	24	72.7	91	11	US-11-102-476-14	Sequence 14, Appl	316	24	72.7	399	11	US-11-188-298-6097	Sequence 6097, Ap
244	24	72.7	123	11	US-11-072-512-2234	Sequence 2234, Ap	317	24	72.7	418	11	US-11-079-463-6838	Sequence 6838, Ap
245	24	72.7	129	11	US-11-212-443-66	Sequence 66, Appl	318	24	72.7	422	11	US-11-087-099-4279	Sequence 4279, Ap
246	24	72.7	140	9	US-10-821-234-1347	Sequence 1347, Ap	319	24	72.7	422	11	US-11-087-099-5083	Sequence 5083, Ap
247	24	72.7	147	11	US-11-045-004-1280	Sequence 1280, Ap	320	24	72.7	422	11	US-11-188-298-15698	Sequence 15698, A
248	24	72.7	156	11	US-11-096-568A-11843	Sequence 11843, A	321	24	72.7	422	11	US-11-045-004-451	Sequence 451, App
249	24	72.7	156	11	US-11-045-004-2473	Sequence 2473, Ap	322	24	72.7	428	9	US-10-330-773-647	Sequence 647, App
250	24	72.7	182	11	US-11-096-568A-11842	Sequence 11842, A	323	24	72.7	432	11	US-11-096-568A-22460	Sequence 22460, A
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252	24	72.7	201	9	US-10-520-836-35	Sequence 35, Appl	325	24	72.7	472	11	US-11-087-099-12391	Sequence 12391, A
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257	24	72.7	223	9	US-10-793-626-2884	Sequence 2884, Ap	330	24	72.7	488	11	US-11-188-298-6414	Sequence 6414, Ap
258	24	72.7	226	9	US-10-467-657-8544	Sequence 8544, Ap	331	24	72.7	499	11	US-11-188-298-519	Sequence 519, App
259	24	72.7	229	11	US-11-096-568A-11517	Sequence 11517, A	332	24	72.7	502	11	US-11-087-099-7212	Sequence 7212, Ap
260	24	72.7	233	11	US-11-100-183-31	Sequence 31, Appl	333	24	72.7	502	11	US-11-188-298-17666	Sequence 17666, A
261	24	72.7	237	11	US-11-096-568A-11516	Sequence 11516, A	334	24	72.7	506	11	US-11-188-298-13419	Sequence 13419, A
262	24	72.7	241	11	US-11-054-515-1303	Sequence 1303, Ap	335	24	72.7	508	11	US-11-188-298-2771	Sequence 2771, Ap
263	24	72.7	241	11	US-11-266-444-1303	Sequence 1303, Ap	336	24	72.7	510	11	US-11-087-099-1197	Sequence 1197, Ap
264	24	72.7	244	11	US-11-054-515-1210	Sequence 1210, Ap	337	24	72.7	510	11	US-11-087-099-1859	Sequence 1859, Ap
265	24	72.7	244	11	US-11-054-515-1214	Sequence 1214, Ap	338	24	72.7	510	11	US-11-188-298-12151	Sequence 12151, A
266	24	72.7	244	11	US-11-054-515-1371	Sequence 1371, Ap	339	24	72.7	510	11	US-11-188-298-12808	Sequence 12808, A
267	24	72.7	244	11	US-11-054-515-1372	Sequence 1372, Ap	340	24	72.7	511	11	US-11-087-099-7567	Sequence 7567, Ap
268	24	72.7	244	11	US-11-054-515-1507	Sequence 1507, Ap	341	24	72.7	511	11	US-11-087-099-10617	Sequence 10617, A
269	24	72.7	244	11	US-11-266-444-1210	Sequence 1210, Ap	342	24	72.7	511	11	US-11-188-298-9818	Sequence 9818, A
270	24	72.7	244	11	US-11-266-444-1214	Sequence 1214, Ap	343	24	72.7	511	11	US-11-188-298-19503	Sequence 19503, A
271	24	72.7	244	11	US-11-266-444-1371	Sequence 1371, Ap	344	24	72.7	512	11	US-11-188-298-4771	Sequence 4771, Ap
272	24	72.7	244	11	US-11-266-444-1372	Sequence 1372, Ap	345	24	72.7	513	11	US-11-135-667-46	Sequence 46, Appl
273	24	72.7	244	11	US-11-266-444-1507	Sequence 1507, Ap	346	24	72.7	513	11	US-11-188-298-2716	Sequence 2716, Ap
274	24	72.7	245	11	US-11-054-515-1714	Sequence 1714, Ap	347	24	72.7	516	11	US-11-087-099-11062	Sequence 11062, A
275	24	72.7	245	11	US-11-266-444-1714	Sequence 1714, Ap	348	24	72.7	516	11	US-11-188-298-10215	Sequence 10215, A
276	24	72.7	245	11	US-11-188-298-11817	Sequence 11817, A	349	24	72.7	526	9	US-10-606-302-5	Sequence 5, Appl
277	24	72.7	247	11	US-11-054-515-969	Sequence 969, App	350	24	72.7	526	9	US-10-606-302-7	Sequence 7, Appl
278	24	72.7	247	11	US-11-266-444-969	Sequence 969, App	351	24	72.7	526	9	US-10-490-824-3	Sequence 3, Appl
279	24	72.7	250	11	US-11-054-515-2066	Sequence 2066, Ap	352	24	72.7	527	11	US-11-188-298-17484	Sequence 17484, A
280	24	72.7	250	11	US-11-266-444-2066	Sequence 2066, Ap	353	24	72.7	555	11	US-11-188-298-6221	Sequence 6221, Ap
281	24	72.7	251	11	US-11-054-515-1194	Sequence 1194, Ap	354	24	72.7	558	9	US-10-510-903-22	Sequence 22, Appl
282	24	72.7	251	11	US-11-266-444-1194	Sequence 1194, Ap	355	24	72.7	574	9	US-10-763-712A-6	Sequence 6, Appl
283	24	72.7	252	11	US-11-266-444-1772	Sequence 1772, Ap	356	24	72.7	583	11	US-11-052-554A-215	Sequence 215, App
284	24	72.7	252	11	US-11-266-444-1772	Sequence 1772, Ap	357	24	72.7	595	11	US-11-102-476-33	Sequence 33, Appl
285	24	72.7	254	11	US-11-054-515-2082	Sequence 2082, Ap	358	24	72.7	608	9	US-10-055-877-121	Sequence 121, Appl
286	24	72.7	254	11	US-11-266-444-2082	Sequence 2082, Ap	359	24	72.7	610	9	US-10-858-730-292	Sequence 292, App
287	24	72.7	260	11	US-11-188-298-8255	Sequence 8255, Ap	360	24	72.7	630	11	US-11-188-298-2043	Sequence 2043, Ap
288	24	72.7	260	11	US-11-188-298-9053	Sequence 9053, Ap	361	24	72.7	657	11	US-11-096-568A-32797	Sequence 32797, A
289	24	72.7	262	11	US-11-188-298-11748	Sequence 11748, A	362	24	72.7	667	11	US-11-096-568A-32796	Sequence 32796, A
290	24	72.7	263	11	US-11-188-298-1673	Sequence 1673, Ap	363	24	72.7	667	11	US-11-188-298-17195	Sequence 17195, A
291	24	72.7	272	11	US-11-188-298-9672	Sequence 9672, Ap	364	24	72.7	671	9	US-10-887-770-11	Sequence 11, Appl
292	24	72.7	294	11	US-11-188-298-13581	Sequence 13581, A	365	24	72.7	671	11	US-11-096-568A-32795	Sequence 32795, A
293	24	72.7	302	11	US-11-188-298-8762	Sequence 8762, Ap	366	24	72.7	706	11	US-11-096-568A-10524	Sequence 10524, A
294	24	72.7	303	11	US-11-058-924-5	Sequence 5, Appl	367	24	72.7	719	11	US-11-045-004-537	Sequence 537, App
295	24	72.7	303	11	US-11-045-004-2447	Sequence 2447, Ap	368	24	72.7	729	11	US-11-188-298-15540	Sequence 15540, A
296	24	72.7	305	11	US-11-188-298-10384	Sequence 10384, A	369	24	72.7	729	11	US-11-188-298-19918	Sequence 19918, A
297	24	72.7	315	11	US-11-096-568A-11515	Sequence 11515, A	370	24	72.7	749	9	US-10-453-372-800	Sequence 800, App
298	24	72.7	316	11	US-11-058-924-2	Sequence 2, Appl	371	24	72.7	755	11	US-11-087-099-2677	Sequence 2677, Ap
299	24	72.7	318	11	US-11-096-568A-5625	Sequence 5625, Ap	372	24	72.7	759	11	US-11-188-298-3579	Sequence 3579, Ap
300	24	72.7	323	11	US-11-096-568A-13748	Sequence 13748, A	373	24	72.7	759	11	US-11-188-298-13082	Sequence 13082, A
301	24	72.7	324	11	US-11-087-099-1340	Sequence 1340, Ap	374	24	72.7	759	11	US-11-188-298-22397	Sequence 22397, A
302	24	72.7	329	11	US-11-096-568A-21080	Sequence 21080, A	375	24	72.7	784	11	US-11-188-298-10249	Sequence 10249, A
303	24	72.7	327	11	US-11-096-568A-5624	Sequence 5624, Ap	376	24	72.7	786	11	US-11-087-099-1766	Sequence 1766, Ap
304	24	72.7	334	11	US-11-096-568A-5623	Sequence 5623, Ap	377	24	72.7	786	11	US-11-087-099-2023	Sequence 2023, Ap
305	24	72.7	336	11	US-11-096-568A-21079	Sequence 21079, A	378	24	72.7	786	11	US-11-188-298-1757	Sequence 1757, Ap
306	24	72.7	340	11	US-11-100-352-2	Sequence 2, Appl	379	24	72.7	786	11	US-11-188-298-2001	Sequence 2001, Ap
307	24	72.7	340	11	US-11-103-957-2	Sequence 2, Appl	380	24	72.7	787	11	US-11-087-099-11822	Sequence 11822, A
308	24	72.7	340	11	US-11-103-957-17	Sequence 17, Appl	381	24	72.7	787	11	US-11-188-298-19689	Sequence 19689, A
309	24	72.7	340	11	US-11-018-868-38	Sequence 38, Appl	382	24	72.7	787	11	US-11-188-298-21993	Sequence 21993, A
310	24	72.7	340	11	US-11-096-568A-13747	Sequence 13747, A	383	24	72.7	802	11	US-11-045-004-1971	Sequence 1971, Ap
311	24	72.7	346	11	US-11-087-099-8092	Sequence 8092, Ap	384	24	72.7	827	11	US-11-079-463-5812	Sequence 5812, Ap
312	24	72.7	357	11	US-11-188-298-15640	Sequence 15640, A	385	24	72.7	927	11	US-11-045-004-2425	Sequence 2425, Ap
313	24	72.7	363	11	US-11-188-298-5818	Sequence 5818, Ap	386	24	72.7	968	9	US-10-501-035-219	Sequence 219, App

387	24	72.7	1030	11	US-11-100-640-28	Sequence 28, Appl	460	23	69.7	225	9	US-10-506-454-657	Sequence 657, App
388	24	72.7	1033	11	US-11-037-243-75	Sequence 75, Appl	461	23	69.7	230	9	US-10-506-454-181	Sequence 181, App
389	24	72.7	1036	9	US-10-494-026A-2	Sequence 2, Appl	462	23	69.7	230	11	US-11-218-272-27	Sequence 27, Appl
390	24	72.7	1043	11	US-11-079-463-9451	Sequence 3451, Ap	463	23	69.7	238	11	US-11-087-099-7368	Sequence 7368, Ap
391	24	72.7	1052	8	US-10-497-088-21	Sequence 21, Appl	464	23	69.7	241	11	US-11-170-653-35	Sequence 35, Appl
392	24	72.7	1094	11	US-11-096-568A-27715	Sequence 27715, A	465	23	69.7	241	11	US-11-087-099-8214	Sequence 8214, Ap
393	24	72.7	1225	9	US-10-453-372-798	Sequence 798, App	466	23	69.7	244	11	US-11-087-099-3821	Sequence 3821, Ap
394	24	72.7	1225	9	US-10-453-372-808	Sequence 808, App	467	23	69.7	244	11	US-11-087-099-7369	Sequence 7369, Ap
395	24	72.7	1225	9	US-10-453-372-810	Sequence 810, App	468	23	69.7	245	11	US-11-087-099-3967	Sequence 3967, Ap
396	24	72.7	1225	9	US-10-453-372-812	Sequence 812, App	469	23	69.7	245	11	US-11-079-463-9676	Sequence 9676, Ap
397	24	72.7	1225	11	US-11-102-476-2	Sequence 2, Appli	470	23	69.7	245	11	US-11-188-298-16265	Sequence 16265, A
398	24	72.7	1274	9	US-10-454-437-360	Sequence 360, App	471	23	69.7	246	11	US-11-087-099-1274	Sequence 1274, Ap
399	24	72.7	1342	8	US-10-497-088-14	Sequence 14, Appl	472	23	69.7	246	11	US-11-087-099-8166	Sequence 8166, Ap
400	24	72.7	1372	9	US-10-453-372-794	Sequence 794, App	473	23	69.7	247	11	US-11-087-099-6204	Sequence 6204, Ap
401	24	72.7	1438	9	US-10-453-372-796	Sequence 796, App	474	23	69.7	247	11	US-11-087-099-9019	Sequence 9019, Ap
402	24	72.7	1493	9	US-10-330-773-502	Sequence 502, App	475	23	69.7	247	11	US-11-087-099-10446	Sequence 10446, A
403	24	72.7	1809	8	US-10-370-959-67	Sequence 67, Appl	476	23	69.7	248	11	US-11-087-099-580	Sequence 580, App
404	24	72.7	1826	9	US-10-330-773-499	Sequence 499, App	477	23	69.7	248	11	US-11-087-099-9914	Sequence 9914, Ap
405	24	72.7	3353	11	US-11-037-243-64	Sequence 64, Appl	478	23	69.7	254	11	US-11-054-515-1489	Sequence 1489, Ap
406	24	72.7	3716	11	US-11-052-554A-141	Sequence 141, App	479	23	69.7	254	11	US-11-266-444-1489	Sequence 1489, Ap
407	23	69.7	7	11	US-11-125-837-8	Sequence 8, Appli	480	23	69.7	255	11	US-11-188-298-6410	Sequence 6410, Ap
408	23	69.7	7	11	US-11-087-528-6	Sequence 6, Appli	481	23	69.7	258	9	US-10-714-887-414	Sequence 414, App
409	23	69.7	7	11	US-11-122-622-6	Sequence 6, Appli	482	23	69.7	260	11	US-11-055-822-514	Sequence 514, App
410	23	69.7	15	9	US-10-530-061-1981	Sequence 1981, Ap	483	23	69.7	261	9	US-10-821-234-1382	Sequence 1382, App
411	23	69.7	15	9	US-10-530-061-1982	Sequence 1982, Ap	484	23	69.7	261	11	US-11-124-368A-328	Sequence 328, App
412	23	69.7	15	9	US-10-530-061-1983	Sequence 1983, Ap	485	23	69.7	264	11	US-11-188-743-24	Sequence 24, Appl
413	23	69.7	17	11	US-11-007-428-4	Sequence 4, Appli	486	23	69.7	264	11	US-11-188-743-25	Sequence 25, Appl
414	23	69.7	39	11	US-11-036-532A-85	Sequence 85, Appl	487	23	69.7	264	11	US-11-216-267-24	Sequence 24, Appl
415	23	69.7	40	11	US-11-036-532A-87	Sequence 87, Appl	488	23	69.7	264	11	US-11-232-382-24	Sequence 24, Appl
416	23	69.7	42	11	US-11-036-532A-63	Sequence 63, Appl	489	23	69.7	273	9	US-10-537-897-17	Sequence 17, Appl
417	23	69.7	42	11	US-11-036-532A-89	Sequence 89, Appl	490	23	69.7	273	11	US-11-096-568A-20620	Sequence 20620, A
418	23	69.7	43	11	US-11-036-532A-57	Sequence 57, Appl	491	23	69.7	273	11	US-11-172-740-557	Sequence 557, App
419	23	69.7	44	11	US-11-036-532A-152	Sequence 152, App	492	23	69.7	273	11	US-11-188-298-5149	Sequence 5149, Ap
420	23	69.7	46	11	US-11-036-532A-59	Sequence 59, Appl	493	23	69.7	275	9	US-10-972-587-18	Sequence 18, Appl
421	23	69.7	48	11	US-11-036-532A-51	Sequence 51, Appl	494	23	69.7	276	9	US-10-972-587-12	Sequence 12, Appl
422	23	69.7	50	11	US-11-036-532A-15	Sequence 15, Appl	495	23	69.7	276	11	US-11-072-513-3850	Sequence 3850, Ap
423	23	69.7	50	11	US-11-036-532A-29	Sequence 29, Appl	496	23	69.7	277	11	US-11-108-173-693	Sequence 693, App
424	23	69.7	50	11	US-11-036-532A-31	Sequence 31, Appl	497	23	69.7	277	11	US-11-096-568A-20619	Sequence 20619, A
425	23	69.7	50	11	US-11-036-532A-33	Sequence 33, Appl	498	23	69.7	279	11	US-11-096-568A-20618	Sequence 20618, A
426	23	69.7	50	11	US-11-036-532A-35	Sequence 35, Appl	499	23	69.7	280	11	US-11-079-463-7570	Sequence 7570, Ap
427	23	69.7	52	9	US-10-467-657-1138	Sequence 1138, App	500	23	69.7	282	9	US-10-467-657-1342	Sequence 1342, App
428	23	69.7	75	9	US-10-506-454-547	Sequence 547, App	501	23	69.7	283	11	US-11-087-099-9363	Sequence 9363, Ap
429	23	69.7	90	9	US-10-467-657-4604	Sequence 4604, Ap	502	23	69.7	286	11	US-11-172-740-418	Sequence 418, App
430	23	69.7	101	9	US-10-821-234-1363	Sequence 1363, Ap	503	23	69.7	282	11	US-11-188-298-7123	Sequence 7123, Ap
431	23	69.7	106	11	US-11-172-571-25	Sequence 25, Appl	504	23	69.7	292	11	US-11-188-298-21802	Sequence 21802, A
432	23	69.7	106	11	US-11-096-568A-16768	Sequence 16768, A	505	23	69.7	294	11	US-11-055-822-674	Sequence 674, App
433	23	69.7	107	11	US-11-087-528-2	Sequence 2, Appli	506	23	69.7	297	9	US-10-453-372-766	Sequence 766, App
434	23	69.7	107	11	US-11-122-622-2	Sequence 2, Appli	507	23	69.7	297	11	US-11-096-568A-17559	Sequence 17559, A
435	23	69.7	109	11	US-11-049-536-400	Sequence 400, App	508	23	69.7	299	11	US-11-188-298-10005	Sequence 10005, A
436	23	69.7	109	11	US-11-199-739-400	Sequence 400, App	509	23	69.7	301	11	US-11-055-822-1062	Sequence 1062, Ap
437	23	69.7	109	11	US-11-045-004-2782	Sequence 2782, App	510	23	69.7	301	11	US-11-172-740-419	Sequence 419, App
438	23	69.7	130	11	US-11-125-837-21	Sequence 21, Appl	511	23	69.7	302	11	US-11-087-099-674	Sequence 674, App
439	23	69.7	133	11	US-11-128-420-13	Sequence 13, Appl	512	23	69.7	302	11	US-11-172-740-420	Sequence 420, App
440	23	69.7	133	11	US-11-007-428-1	Sequence 1, Appli	513	23	69.7	307	11	US-11-188-298-8100	Sequence 8100, Ap
441	23	69.7	133	11	US-11-235-037-17	Sequence 17, Appl	514	23	69.7	310	11	US-11-079-463-9722	Sequence 9722, Ap
442	23	69.7	133	11	US-11-079-463-9428	Sequence 9428, Ap	515	23	69.7	313	11	US-11-188-298-13663	Sequence 13663, A
443	23	69.7	138	11	US-11-087-099-11891	Sequence 11891, A	516	23	69.7	315	11	US-11-188-298-18131	Sequence 18131, A
444	23	69.7	144	11	US-11-096-568A-16767	Sequence 16767, A	517	23	69.7	316	9	US-10-467-657-4040	Sequence 4040, Ap
445	23	69.7	161	11	US-11-096-568A-16766	Sequence 16766, A	518	23	69.7	317	11	US-11-188-298-10252	Sequence 10252, A
446	23	69.7	175	11	US-11-087-099-7505	Sequence 7505, Ap	519	23	69.7	317	11	US-11-045-004-385	Sequence 385, App
447	23	69.7	175	11	US-11-096-568A-17560	Sequence 17560, A	520	23	69.7	323	11	US-11-140-625-9	Sequence 9, Appli
448	23	69.7	180	11	US-11-153-071-14	Sequence 14, Appl	521	23	69.7	323	11	US-11-087-099-7555	Sequence 7555, Ap
449	23	69.7	181	9	US-10-733-626-560	Sequence 560, App	522	23	69.7	323	11	US-11-079-463-7390	Sequence 7390, Ap
450	23	69.7	185	11	US-11-087-099-3423	Sequence 3423, Ap	523	23	69.7	326	9	US-10-793-626-2952	Sequence 2952, Ap
451	23	69.7	194	11	US-11-188-298-4727	Sequence 4727, Ap	524	23	69.7	326	11	US-11-188-298-12237	Sequence 12237, A
452	23	69.7	195	11	US-11-188-298-8682	Sequence 8682, Ap	525	23	69.7	327	11	US-11-129-143-89	Sequence 89, Appl
453	23	69.7	196	11	US-11-096-568A-24619	Sequence 24619, A	526	23	69.7	327	11	US-11-129-143-90	Sequence 90, Appl
454	23	69.7	198	11	US-11-098-686-10443	Sequence 10443, A	527	23	69.7	327	11	US-11-188-298-14919	Sequence 14919, A
455	23	69.7	198	11	US-11-087-099-11171	Sequence 11171, A	528	23	69.7	328	11	US-11-096-568A-18179	Sequence 18179, A
456	23	69.7	202	11	US-11-087-099-10245	Sequence 10245, A	529	23	69.7	329	11	US-11-082-389-226	Sequence 226, App
457	23	69.7	205	9	US-10-995-561-796	Sequence 796, App	530	23	69.7	329	11	US-11-087-099-3224	Sequence 3224, Ap
458	23	69.7	211	9	US-10-858-730-102	Sequence 102, App	531	23	69.7	331	11	US-11-172-740-1352	Sequence 1352, Ap
459	23	69.7	215	11	US-11-096-568A-24618	Sequence 24618, A	532	23	69.7	331	11	US-11-188-298-453	Sequence 453, App

533	23	69.7	332	11	US-11-082-389-224	Sequence 224, App	606	23	69.7	454	11	US-11-096-568A-18178	Sequence 18178, A
534	23	69.7	340	11	US-11-100-352-5	Sequence 5, Appl	607	23	69.7	456	11	US-11-036-532A-133	Sequence 133, App
535	23	69.7	340	11	US-11-100-352-6	Sequence 6, Appl	608	23	69.7	457	11	US-11-077-550-70	Sequence 70, Appl
536	23	69.7	342	11	US-11-188-298-18496	Sequence 18496, A	609	23	69.7	458	11	US-11-036-532A-130	Sequence 130, App
537	23	69.7	344	11	US-11-055-822-516	Sequence 516, App	610	23	69.7	460	11	US-11-096-568A-18177	Sequence 18177, A
538	23	69.7	345	9	US-10-453-372-758	Sequence 758, App	611	23	69.7	461	11	US-11-036-532A-132	Sequence 132, App
539	23	69.7	347	11	US-11-087-099-9989	Sequence 9989, App	612	23	69.7	461	11	US-11-087-099-1262	Sequence 1262, App
540	23	69.7	349	9	US-10-858-730-228	Sequence 228, App	613	23	69.7	461	11	US-11-188-298-1296	Sequence 1296, App
541	23	69.7	350	11	US-11-140-625-4	Sequence 4, Appl	614	23	69.7	462	11	US-11-096-568A-20936	Sequence 20936, A
542	23	69.7	351	11	US-11-188-298-1799	Sequence 1799, App	615	23	69.7	463	11	US-11-188-298-2207	Sequence 2207, App
543	23	69.7	352	11	US-11-188-298-7995	Sequence 7995, App	616	23	69.7	463	9	US-10-793-626-1676	Sequence 1676, App
544	23	69.7	353	11	US-11-087-099-8041	Sequence 8041, App	617	23	69.7	466	11	US-11-188-298-1731	Sequence 1731, App
545	23	69.7	354	9	US-10-467-657-4352	Sequence 4352, App	618	23	69.7	468	11	US-11-087-099-10159	Sequence 10159, A
546	23	69.7	356	9	US-10-506-454-16	Sequence 16, App	619	23	69.7	468	11	US-11-087-099-3606	Sequence 3606, App
547	23	69.7	357	9	US-10-453-372-760	Sequence 760, App	620	23	69.7	470	11	US-11-096-568A-17182	Sequence 17182, A
548	23	69.7	357	11	US-11-188-298-10911	Sequence 10911, A	621	23	69.7	471	11	US-11-079-463-9578	Sequence 9578, App
549	23	69.7	363	11	US-11-045-004-1179	Sequence 1179, App	622	23	69.7	471	11	US-11-188-298-3821	Sequence 3821, App
550	23	69.7	364	9	US-10-517-939-320	Sequence 320, App	623	23	69.7	471	11	US-11-188-298-19864	Sequence 19864, A
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552	23	69.7	368	11	US-11-096-568A-24617	Sequence 24617, A	625	23	69.7	474	11	US-11-079-463-5744	Sequence 5744, App
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554	23	69.7	369	11	US-11-087-099-2816	Sequence 2816, App	627	23	69.7	477	11	US-11-188-298-13373	Sequence 13373, A
555	23	69.7	369	11	US-11-188-298-4076	Sequence 4076, App	628	23	69.7	478	11	US-11-045-004-2663	Sequence 2663, App
556	23	69.7	370	11	US-11-045-004-127	Sequence 127, App	629	23	69.7	479	11	US-11-188-298-8059	Sequence 8059, App
557	23	69.7	371	11	US-11-087-099-11400	Sequence 11400, A	630	23	69.7	479	11	US-11-188-298-10322	Sequence 10322, A
558	23	69.7	378	11	US-11-087-099-2807	Sequence 2807, App	631	23	69.7	481	11	US-11-188-298-3813	Sequence 3813, App
559	23	69.7	378	11	US-11-045-004-517	Sequence 517, App	632	23	69.7	483	9	US-10-467-657-2894	Sequence 2894, App
560	23	69.7	381	9	US-10-784-004-398	Sequence 398, App	633	23	69.7	483	9	US-10-506-454-425	Sequence 425, App
561	23	69.7	381	9	US-10-784-004-938	Sequence 938, App	634	23	69.7	483	11	US-11-188-298-576	Sequence 576, App
562	23	69.7	382	11	US-11-096-568A-12912	Sequence 12912, A	635	23	69.7	483	11	US-11-188-298-8344	Sequence 8344, App
563	23	69.7	385	11	US-11-087-099-1570	Sequence 1570, App	636	23	69.7	484	11	US-11-188-298-12371	Sequence 12371, A
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565	23	69.7	386	9	US-10-784-004-1085	Sequence 1085, App	638	23	69.7	485	11	US-11-188-298-3696	Sequence 3696, App
566	23	69.7	386	11	US-11-188-298-7602	Sequence 7602, App	639	23	69.7	486	10	US-11-185-301-2	Sequence 2, Appl
567	23	69.7	388	11	US-11-188-298-11099	Sequence 11099, A	640	23	69.7	488	11	US-11-188-298-17856	Sequence 17856, A
568	23	69.7	390	11	US-11-052-554A-221	Sequence 221, App	641	23	69.7	489	9	US-10-858-730-198	Sequence 198, App
569	23	69.7	394	9	US-10-467-657-8414	Sequence 8414, App	642	23	69.7	489	11	US-11-055-822-1152	Sequence 1152, App
570	23	69.7	399	11	US-11-087-099-512	Sequence 512, App	643	23	69.7	493	11	US-11-188-298-12986	Sequence 12986, A
571	23	69.7	399	11	US-11-087-099-3783	Sequence 3783, App	644	23	69.7	496	11	US-11-188-298-12893	Sequence 12893, A
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573	23	69.7	405	11	US-11-089-551A-50	Sequence 50, Appl	646	23	69.7	505	11	US-11-096-568A-17181	Sequence 17181, A
574	23	69.7	406	11	US-11-087-099-6780	Sequence 6780, App	647	23	69.7	505	11	US-11-096-568A-20935	Sequence 20935, A
575	23	69.7	411	11	US-11-188-298-1602	Sequence 1602, App	648	23	69.7	507	11	US-11-188-298-10935	Sequence 10935, A
576	23	69.7	414	11	US-11-188-298-9083	Sequence 9083, App	649	23	69.7	510	11	US-11-188-298-9650	Sequence 9650, App
577	23	69.7	416	11	US-11-096-568A-3578	Sequence 3578, App	650	23	69.7	511	9	US-10-934-944-166	Sequence 166, App
578	23	69.7	418	9	US-10-506-454-1438	Sequence 1438, App	651	23	69.7	511	9	US-10-934-944-168	Sequence 168, App
579	23	69.7	419	11	US-11-045-004-1910	Sequence 1910, App	652	23	69.7	511	11	US-11-116-881A-175	Sequence 175, App
580	23	69.7	422	11	US-11-079-463-8185	Sequence 8185, App	653	23	69.7	511	11	US-11-116-881A-177	Sequence 177, App
581	23	69.7	422	11	US-11-188-298-8746	Sequence 8746, App	654	23	69.7	512	9	US-10-242-586-110	Sequence 110, App
582	23	69.7	422	11	US-11-188-298-17837	Sequence 17837, A	655	23	69.7	512	9	US-10-242-902-110	Sequence 110, App
583	23	69.7	422	11	US-11-188-298-22000	Sequence 22000, A	656	23	69.7	512	9	US-10-243-116-110	Sequence 110, App
584	23	69.7	423	9	US-10-995-561-794	Sequence 794, App	657	23	69.7	512	9	US-10-243-136-110	Sequence 110, App
585	23	69.7	423	9	US-10-995-561-795	Sequence 795, App	658	23	69.7	512	9	US-10-243-189-110	Sequence 110, App
586	23	69.7	424	11	US-11-096-568A-3577	Sequence 3577, App	659	23	69.7	512	9	US-10-243-215-110	Sequence 110, App
587	23	69.7	425	11	US-11-188-298-16598	Sequence 16598, A	660	23	69.7	512	9	US-10-243-236-110	Sequence 110, App
588	23	69.7	434	11	US-11-096-568A-20937	Sequence 20937, A	661	23	69.7	512	9	US-10-243-298-110	Sequence 110, App
589	23	69.7	436	11	US-11-087-099-11529	Sequence 11529, A	662	23	69.7	512	9	US-10-243-304-110	Sequence 110, App
590	23	69.7	437	11	US-10-753-537-19	Sequence 19, Appl	663	23	69.7	512	9	US-10-243-338-110	Sequence 110, App
591	23	69.7	437	11	US-11-087-099-6889	Sequence 6889, App	664	23	69.7	512	9	US-10-243-345-110	Sequence 110, App
592	23	69.7	438	9	US-10-909-769-17	Sequence 17, Appl	665	23	69.7	512	9	US-10-243-357-110	Sequence 110, App
593	23	69.7	442	11	US-11-087-099-11004	Sequence 11004, A	666	23	69.7	512	9	US-10-245-083-110	Sequence 110, App
594	23	69.7	443	9	US-10-036-532A-131	Sequence 131, App	667	23	69.7	512	9	US-10-247-015-110	Sequence 110, App
595	23	69.7	448	11	US-10-995-561-793	Sequence 793, App	668	23	69.7	512	11	US-11-108-172-1093	Sequence 1093, App
596	23	69.7	448	11	US-11-077-550-177	Sequence 177, App	669	23	69.7	514	11	US-11-188-298-5898	Sequence 5898, App
597	23	69.7	448	11	US-11-072-512-3380	Sequence 3380, App	670	23	69.7	516	11	US-11-188-298-17287	Sequence 17287, A
598	23	69.7	450	11	US-11-188-298-8913	Sequence 8913, App	671	23	69.7	520	11	US-11-055-822-862	Sequence 862, App
599	23	69.7	450	11	US-11-045-004-2619	Sequence 2619, App	672	23	69.7	522	11	US-11-188-298-12443	Sequence 12443, A
600	23	69.7	451	11	US-11-188-298-8764	Sequence 8764, App	673	23	69.7	525	11	US-11-096-568A-12402	Sequence 12402, A
601	23	69.7	453	11	US-11-188-298-17394	Sequence 17394, A	674	23	69.7	527	9	US-10-506-454-1269	Sequence 1269, App
602	23	69.7	454	11	US-11-077-550-72	Sequence 72, Appl	675	23	69.7	529	11	US-11-188-298-19628	Sequence 19628, A
603	23	69.7	454	11	US-11-077-550-74	Sequence 74, Appl	676	23	69.7	530	9	US-10-055-877-313	Sequence 313, App
604	23	69.7	454	11	US-11-077-550-76	Sequence 76, Appl	677	23	69.7	530	9	US-10-055-877-314	Sequence 314, App
605	23	69.7	454	11	US-11-077-550-78	Sequence 78, Appl	678	23	69.7	530	9	US-10-055-877-315	Sequence 315, App

679	23	69.7	530	9	US-10-055-877-316	Sequence 316, App	752	23	69.7	862	11	US-11-007-428-2	Sequence 2, Appli
680	23	69.7	534	11	US-11-096-568A-32022	Sequence 32022, A	753	23	69.7	862	11	US-11-183-294-16	Sequence 16, Appl
681	23	69.7	534	11	US-11-188-298-3124	Sequence 3124, Ap	754	23	69.7	862	11	US-11-235-037-9	Sequence 9, Appli
682	23	69.7	536	11	US-11-188-298-3635	Sequence 3635, Ap	755	23	69.7	863	11	US-11-077-550-34	Sequence 34, Appl
683	23	69.7	538	11	US-11-188-298-450	Sequence 450, App	756	23	69.7	863	11	US-11-077-550-36	Sequence 36, Appl
684	23	69.7	542	11	US-11-188-298-1227	Sequence 1227, Ap	757	23	69.7	863	11	US-11-077-550-38	Sequence 38, Appl
685	23	69.7	543	9	US-10-453-372-756	Sequence 756, App	758	23	69.7	866	11	US-11-077-550-32	Sequence 32, Appl
686	23	69.7	548	9	US-10-453-372-754	Sequence 754, App	759	23	69.7	867	11	US-11-077-550-179	Sequence 179, App
687	23	69.7	548	9	US-10-453-372-768	Sequence 768, App	760	23	69.7	871	11	US-11-077-550-2	Sequence 2, Appli
688	23	69.7	551	11	US-11-188-298-2614	Sequence 2614, Ap	761	23	69.7	871	11	US-11-077-550-8	Sequence 8, Appli
689	23	69.7	552	11	US-11-188-298-3792	Sequence 3792, Ap	762	23	69.7	871	11	US-11-077-550-26	Sequence 26, Appl
690	23	69.7	552	11	US-11-045-004-1947	Sequence 1947, Ap	763	23	69.7	871	11	US-11-077-550-153	Sequence 153, App
691	23	69.7	553	11	US-11-096-568A-32021	Sequence 32021, A	764	23	69.7	871	11	US-11-077-550-155	Sequence 155, App
692	23	69.7	555	9	US-10-453-372-764	Sequence 764, App	765	23	69.7	873	11	US-11-077-550-6	Sequence 6, Appli
693	23	69.7	555	11	US-11-188-298-16590	Sequence 16590, A	766	23	69.7	873	11	US-11-077-550-149	Sequence 149, App
694	23	69.7	560	11	US-11-096-568A-12401	Sequence 12401, A	767	23	69.7	873	11	US-11-077-550-151	Sequence 151, App
695	23	69.7	566	11	US-11-188-298-6416	Sequence 6416, Ap	768	23	69.7	873	11	US-11-077-550-163	Sequence 163, App
696	23	69.7	568	11	US-11-188-298-15917	Sequence 15917, A	769	23	69.7	873	11	US-11-077-550-165	Sequence 165, App
697	23	69.7	570	11	US-11-188-298-8318	Sequence 8318, Ap	770	23	69.7	873	11	US-11-077-550-167	Sequence 167, App
698	23	69.7	572	11	US-11-188-298-7169	Sequence 7169, Ap	771	23	69.7	873	11	US-11-077-550-169	Sequence 169, App
699	23	69.7	577	11	US-11-188-298-1376	Sequence 1376, Ap	772	23	69.7	875	11	US-11-077-550-10	Sequence 10, Appl
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701	23	69.7	589	11	US-11-045-004-11	Sequence 11, Appl	774	23	69.7	877	11	US-11-077-550-157	Sequence 157, App
702	23	69.7	592	11	US-11-079-463-5827	Sequence 5827, Ap	775	23	69.7	878	11	US-11-077-550-12	Sequence 12, Appl
703	23	69.7	595	11	US-11-188-298-15387	Sequence 15387, A	776	23	69.7	878	11	US-11-077-550-62	Sequence 62, Appl
704	23	69.7	600	8	US-10-196-749-586	Sequence 586, App	777	23	69.7	879	11	US-11-077-550-30	Sequence 30, Appl
705	23	69.7	600	9	US-10-194-487-586	Sequence 586, App	778	23	69.7	879	11	US-11-077-550-159	Sequence 159, App
706	23	69.7	600	9	US-10-195-883-586	Sequence 586, App	779	23	69.7	887	11	US-11-077-550-161	Sequence 161, App
707	23	69.7	600	9	US-10-195-888-586	Sequence 586, App	780	23	69.7	890	11	US-11-106-623-28	Sequence 28, Appl
708	23	69.7	600	9	US-10-195-889-586	Sequence 586, App	781	23	69.7	893	11	US-11-087-099-3696	Sequence 3696, Ap
709	23	69.7	600	11	US-11-055-822-228	Sequence 228, App	782	23	69.7	893	11	US-11-188-298-14462	Sequence 14462, A
710	23	69.7	600	11	US-11-055-822-716	Sequence 716, App	783	23	69.7	894	11	US-11-077-550-4	Sequence 4, Appli
711	23	69.7	600	11	US-11-055-822-716	Sequence 716, App	784	23	69.7	907	11	US-11-077-550-16	Sequence 16, Appl
712	23	69.7	600	11	US-11-239-674-106	Sequence 758, App	785	23	69.7	908	11	US-11-077-550-64	Sequence 64, Appl
713	23	69.7	605	11	US-11-188-298-18870	Sequence 106, App	786	23	69.7	914	11	US-11-077-550-60	Sequence 60, Appl
714	23	69.7	615	11	US-11-052-554A-152	Sequence 152, App	787	23	69.7	926	11	US-11-045-004-528	Sequence 528, App
715	23	69.7	621	11	US-11-188-298-1043	Sequence 1043, Ap	788	23	69.7	935	11	US-11-265-288-3	Sequence 3, Appli
716	23	69.7	637	11	US-11-188-298-2237	Sequence 2237, Ap	789	23	69.7	943	9	US-10-821-234-1012	Sequence 1012, Ap
717	23	69.7	638	9	US-10-506-454-536	Sequence 536, App	790	23	69.7	949	11	US-11-077-550-68	Sequence 68, Appl
718	23	69.7	644	11	US-11-188-298-3273	Sequence 3273, Ap	791	23	69.7	953	11	US-11-077-550-14	Sequence 14, Appl
719	23	69.7	645	11	US-11-188-298-19364	Sequence 19364, A	792	23	69.7	967	9	US-10-995-561-979	Sequence 979, App
720	23	69.7	648	11	US-11-072-512-2032	Sequence 2032, Ap	793	23	69.7	967	9	US-10-995-561-980	Sequence 980, App
721	23	69.7	650	9	US-10-878-556A-110	Sequence 110, App	794	23	69.7	967	11	US-11-169-041-191	Sequence 191, App
722	23	69.7	657	9	US-10-533-066-52	Sequence 52, Appl	795	23	69.7	999	9	US-10-821-234-1251	Sequence 1251, Ap
723	23	69.7	664	9	US-10-055-877-306	Sequence 306, App	796	23	69.7	1013	11	US-11-077-550-18	Sequence 18, Appl
724	23	69.7	664	9	US-10-055-877-307	Sequence 307, App	797	23	69.7	1076	11	US-11-109-157A-5	Sequence 5, Appli
725	23	69.7	670	9	US-10-821-234-879	Sequence 879, App	798	23	69.7	1127	11	US-11-077-550-40	Sequence 40, Appl
726	23	69.7	691	11	US-11-087-099-4595	Sequence 4595, Ap	799	23	69.7	1127	11	US-11-077-550-50	Sequence 50, Appl
727	23	69.7	691	11	US-11-188-298-4237	Sequence 4237, Ap	800	23	69.7	1127	11	US-11-077-550-54	Sequence 54, Appl
728	23	69.7	695	11	US-11-087-099-12250	Sequence 12250, A	801	23	69.7	1127	11	US-11-077-550-58	Sequence 58, Appl
729	23	69.7	711	9	US-10-517-939-4	Sequence 4, Appli	802	23	69.7	1129	11	US-11-077-550-42	Sequence 42, Appl
730	23	69.7	713	11	US-11-096-568A-32020	Sequence 32020, A	803	23	69.7	1129	11	US-11-077-550-48	Sequence 48, Appl
731	23	69.7	728	11	US-11-103-957-81	Sequence 81, Appl	804	23	69.7	1129	11	US-11-077-550-52	Sequence 52, Appl
732	23	69.7	745	9	US-10-858-730-224	Sequence 224, App	805	23	69.7	1129	11	US-11-077-550-56	Sequence 56, Appl
733	23	69.7	745	11	US-11-055-822-226	Sequence 226, App	806	23	69.7	1130	11	US-11-077-550-44	Sequence 44, Appl
734	23	69.7	745	11	US-11-055-822-714	Sequence 714, App	807	23	69.7	1130	11	US-11-077-550-44	Sequence 44, Appl
735	23	69.7	745	11	US-11-055-822-756	Sequence 756, App	808	23	69.7	1132	11	US-11-077-550-46	Sequence 46, Appl
736	23	69.7	745	11	US-11-168-476-2	Sequence 2, Appli	809	23	69.7	1290	9	US-10-485-517-141	Sequence 141, App
737	23	69.7	745	11	US-11-239-674-104	Sequence 104, App	810	23	69.7	1306	11	US-11-052-554A-139	Sequence 139, App
738	23	69.7	757	11	US-11-052-554A-378	Sequence 378, App	811	23	69.7	1329	11	US-11-052-554A-136	Sequence 136, App
739	23	69.7	758	9	US-10-485-517-144	Sequence 144, App	812	23	69.7	1329	11	US-11-087-099-882	Sequence 882, App
740	23	69.7	762	11	US-11-188-298-3588	Sequence 3588, Ap	813	23	69.7	1408	11	US-11-087-099-8482	Sequence 8482, Ap
741	23	69.7	766	9	US-10-453-372-752	Sequence 752, App	814	23	69.7	1496	11	US-11-079-463-8947	Sequence 8947, Ap
742	23	69.7	770	11	US-11-087-099-7757	Sequence 7757, Ap	815	23	69.7	1532	11	US-11-212-443-62	Sequence 62, Appl
743	23	69.7	770	11	US-11-188-298-18193	Sequence 18193, A	816	23	69.7	1574	11	US-11-212-443-179	Sequence 179, App
744	23	69.7	780	8	US-10-505-928-102	Sequence 102, App	817	23	69.7	1763	8	US-10-504-120-21	Sequence 21, Appl
745	23	69.7	785	11	US-11-109-1578-6	Sequence 6, Appli	818	23	69.7	1807	8	US-10-504-120-22	Sequence 22, Appl
746	23	69.7	798	8	US-10-511-937-2445	Sequence 2445, Ap	819	23	69.7	1907	11	US-11-039-398-25	Sequence 25, Appl
747	23	69.7	798	11	US-11-107-028-3	Sequence 3, Appli	820	23	69.7	1978	11	US-11-212-443-60	Sequence 60, Appl
748	23	69.7	809	11	US-11-087-099-12454	Sequence 12454, A	821	23	69.7	1981	11	US-11-045-208-38	Sequence 38, Appl
749	23	69.7	812	11	US-11-079-463-6485	Sequence 6485, Ap	822	23	69.7	2015	11	US-11-052-554A-374	Sequence 374, App
750	23	69.7	862	8	US-10-511-937-2974	Sequence 2974, Ap	823	23	69.7	3157	11	US-11-052-554A-142	Sequence 142, App
751	23	69.7	862	11	US-11-128-420-11	Sequence 11, Appl	824	23	69.7	3568	9	US-10-453-372-194	Sequence 194, App

825	23	69.7	3570	9	US-10-453-372-178	Sequence 178, App	898	22	66.7	188	11	US-11-087-099-627	Sequence 627, App
826	23	69.7	3570	9	US-10-453-372-196	Sequence 196, App	899	22	66.7	188	11	US-11-087-099-3298	Sequence 3298, App
827	23	69.7	3570	9	US-10-453-372-198	Sequence 198, App	900	22	66.7	188	11	US-11-087-099-6561	Sequence 6561, App
828	23	69.7	3570	9	US-10-453-372-200	Sequence 200, App	901	22	66.7	188	11	US-11-087-099-9413	Sequence 9413, App
829	23	69.7	3570	9	US-10-453-372-202	Sequence 202, App	902	22	66.7	190	11	US-11-055-822-958	Sequence 958, App
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833	23	69.7	4059	8	US-10-501-834-6	Sequence 6, Appl	906	22	66.7	193	11	US-11-188-298-1913	Sequence 1913, App
834	23	66.7	15	11	US-11-020-602-90	Sequence 90, Appl	907	22	66.7	193	11	US-11-188-298-11223	Sequence 11223, A
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860	22	66.7	144	11	US-11-087-099-5187	Sequence 5187, App	933	22	66.7	197	11	US-11-087-099-8658	Sequence 8658, App
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867	22	66.7	153	11	US-11-188-298-4544	Sequence 4544, App	940	22	66.7	198	11	US-11-087-099-2043	Sequence 2043, App
868	22	66.7	157	11	US-11-045-004-1870	Sequence 1870, App	941	22	66.7	198	11	US-11-087-099-2218	Sequence 2218, App
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974 22 66.7 210 11 US-11-087-099-10172 Sequence 10172, A
975 22 66.7 210 11 US-11-096-568A-18268 Sequence 18268, A
976 22 66.7 211 11 US-11-170-653-18 Sequence 18, Appl
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983 22 66.7 212 11 US-11-096-568A-3837 Sequence 3837, Ap
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990 22 66.7 214 11 US-11-087-099-1239 Sequence 1239, Ap
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995 22 66.7 214 11 US-11-087-099-2087 Sequence 2087, Ap
996 22 66.7 214 11 US-11-087-099-2539 Sequence 2539, Ap
997 22 66.7 214 11 US-11-087-099-2910 Sequence 2910, Ap
998 22 66.7 214 11 US-11-087-099-3069 Sequence 3069, Ap
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ALIGNMENTS

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RESULT 1
US-11-188-298-14967
; Sequence 14967, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14967
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens str. C58 (U. Washington)
US-11-188-298-14967

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Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 247 GATNLA 252
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US-11-188-298-3030
; Sequence 3030, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
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; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3030
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens str. C58 (Cereon)
US-11-188-298-3030
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 267 GATNLA 272
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RESULT 3
US-11-096-568A-20137
; Sequence 20137, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Tharby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20137
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(152)
; OTHER INFORMATION: Ceres Seq. ID no. 12377813
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119)..(119)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)..(138)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-20137
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Query Match 84.8%; Score 28; DB 11; Length 152;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 84 GATNLA 90
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RESULT 4
US-11-087-099-10126
; Sequence 10126, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10126
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Xanthomonas campestris pv. campestris str. ATCC 33913
US-11-087-099-10126
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Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      16 GATSLAA 22

RESULT 5
US-11-096-568A-20136
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; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20136
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(223)
; OTHER INFORMATION: Ceres Seq. ID no. 12377812
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (190)..(190)
; OTHER INFORMATION: Xaa is any aa, unknown or other
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; NAME/KEY: misc_feature
; LOCATION: (209)..(209)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-20136

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Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      155 GETNLAA 161

RESULT 6
US-10-714-887-356
; Sequence 356, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MBI0058-C1P
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
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; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 356
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
; FEATURE:
; OTHER INFORMATION: G3407 polypeptide Functionally related and homologous to G1073
US-10-714-887-356

Query Match      84.8%; Score 28; DB 9; Length 289;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GATNLAA 7
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Db      171 GATSLAA 177

RESULT 7
US-11-188-298-7053
; Sequence 7053, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7053
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Ostreococcus tauri
US-11-188-298-7053

Query Match      84.8%; Score 28; DB 11; Length 414;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
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Db      309 GPTNLAA 315

RESULT 8
US-11-096-568A-15981
; Sequence 15981, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15981
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(462)
; OTHER INFORMATION: Ceres Seq. ID no. 12350005
US-11-096-568A-15981

Query Match 84.8%; Score 28; DB 11; Length 462;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| ||
Db 13 GATNAAA 19

RESULT 9
US-11-096-568A-15980
; Sequence 15980, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15980
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(480)
; OTHER INFORMATION: Ceres Seq. ID no. 12350004
US-11-096-568A-15980

Query Match 84.8%; Score 28; DB 11; Length 480;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| ||
Db 31 GATNAAA 37

RESULT 10
US-11-188-298-14241
; Sequence 14241, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14241
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis MA-4680
US-11-188-298-14241

Query Match 84.8%; Score 28; DB 11; Length 573;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| ||
Db 284 GAVNLAA 290

RESULT 11
US-11-188-298-7430
; Sequence 7430, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2005-07-22
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7430
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis MA-4680
US-11-188-298-7430

Query Match 84.8%; Score 28; DB 11; Length 587;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| ||
Db 298 GAVNLAA 304

RESULT 12
US-10-467-657-6112
; Sequence 6112, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467.657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6112
; LENGTH: 1122
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6112

Query Match 84.8%; Score 28; DB 9; Length 1122;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
||| ||
Db 919 GAVNLAA 925

RESULT 13
US-11-096-568A-1394
; Sequence 1394, Application US/11096568A

```
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1394
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(156)
; OTHER INFORMATION: Ceres Seq. ID no. 14305792
US-11-096-568A-1394

Query Match      81.8%; Score 27; DB 11; Length 156;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      8 GATGLAA 14

RESULT 14
US-11-096-568A-1393
; Sequence 1393, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1393
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(190)
; OTHER INFORMATION: Ceres Seq. ID no. 14305791
US-11-096-568A-1393

Query Match      81.8%; Score 27; DB 11; Length 190;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      42 GATGLAA 48

RESULT 15
US-10-467-657-7260
; Sequence 7260, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
```

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; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7260
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7260

Query Match      81.8%; Score 27; DB 9; Length 354;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      330 GAQNLAA 336

RESULT 16
US-11-055-822-646
; Sequence 646, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 646
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-646

Query Match      81.8%; Score 27; DB 11; Length 363;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
DB      172 GATTLAA 178

RESULT 17
US-11-255-794-6
```

```
; Sequence 6, Application US/11255794
; Publication No. US2006004113A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/11/255,794
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-11-255-794-6

Query Match      81.8%; Score 27; DB 11; Length 465;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      185 GATNRAA 191

RESULT 18
US-11-076-427A-4
; Sequence 4, Application US/11076427A
; Publication No. US2006002538A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOUS
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/4008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-076-427A-4

Query Match      81.8%; Score 27; DB 11; Length 493;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      368 GATNLAA 374

RESULT 19
US-10-971-560-7
; Sequence 7, Application US/10971560
; Publication No. US20050244842A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/10/971,560
; CURRENT FILING DATE: 2004-10-22
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; PRIOR APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-971-560-7

Query Match      81.8%; Score 27; DB 9; Length 494;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      369 GATNLAA 375

RESULT 20
US-11-188-298-7687
; Sequence 7687, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7687
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa UCBPP-PA14
US-11-188-298-7687

Query Match      81.8%; Score 27; DB 11; Length 553;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GATNLAA 7
Db      15 GATNLAA 21

RESULT 21
US-11-188-298-4736
; Sequence 4736, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 4736
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-188-298-4736

Query Match      81.8%; Score 27; DB 11; Length 581;
```

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Best Local Similarity 85.7%; Pred. No. 2.1e+02; Mismatches 0; Gaps 0; Indels 0;
Matches 6; Conservative 0;

QY 1 GATNLAA 7
   ||| |||
Db 43 GATRLAA 49

RESULT 22
US-11-188-298-10278
; Sequence 10278, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10278
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-188-298-10278

Query Match 81.8%; Score 27; DB 11; Length 581;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 GATNLAA 7
   ||| |||
Db 43 GATRLAA 49

RESULT 23
US-11-096-568A-32112
; Sequence 32112, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32112
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(626)
; OTHER INFORMATION: Ceres Seq. ID no. 13592204
US-11-096-568A-32112

Query Match 81.8%; Score 27; DB 11; Length 626;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
   ||| |||
Db 330 GATKLAA 336

RESULT 24
US-11-188-298-13299
; Sequence 13299, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13299
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Rickettsia sibirica
US-11-188-298-13299

Query Match 81.8%; Score 27; DB 11; Length 637;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 6
   ||| |||
Db 498 GATNIA 503

RESULT 25
US-11-188-298-14583
; Sequence 14583, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14583
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Rickettsia rickettsii
US-11-188-298-14583

Query Match 81.8%; Score 27; DB 11; Length 637;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATNLAA 6
   ||| |||
Db 498 GATNIA 503

RESULT 26
US-11-096-568A-32111
; Sequence 32111, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32111
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(784)
; OTHER INFORMATION: Ceres Seq. ID no. 13592203
US-11-096-568A-32111

Query Match 81.8%; Score 27; DB 11; Length 784;
```

```
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
   ||| |||
Db 488 GATKLAA 494

RESULT 27
US-11-096-568A-32110
; Sequence 32110, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32110
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(793)
; OTHER INFORMATION: Ceres Seq. ID no. 13592202
US-11-096-568A-32110

Query Match 81.8%; Score 27; DB 11; Length 793;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
   ||| |||
Db 497 GATKLAA 503

RESULT 28
US-11-188-298-6082
; Sequence 6082, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6082
; LENGTH: 875
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-6082

Query Match 81.8%; Score 27; DB 11; Length 875;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
   ||| |||
Db 477 GAPNLAA 483

RESULT 29
US-11-188-298-12126
; Sequence 12126, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 12126
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papaver rhoeas
US-11-188-298-12126

Query Match 78.8%; Score 26; DB 11; Length 98;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
   ||| |||
Db 59 GATNLVS 65

RESULT 30
US-11-188-298-14158
; Sequence 14158, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14158
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papaver rhoeas
US-11-188-298-14158

Query Match 78.8%; Score 26; DB 11; Length 98;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
   ||| |||
Db 59 GATNLVS 65

RESULT 31
US-11-188-298-5677
; Sequence 5677, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188.298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 5677
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Amaranthus retroflexus
US-11-188-298-5677

Query Match 78.8%; Score 26; DB 11; Length 103;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GATNLAA 7
      ||||| :
Db      57 GATNLVS 63

RESULT 32
US-11-188-298-14076
; Sequence 14076, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 14076:
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Amaranthus retroflexus
US-11-188-298-14076

Query Match      78.8%; Score 26; DB 11; Length 103;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      ||||| :
Db      57 GATNLVS 63

RESULT 33
US-11-188-298-1691
; Sequence 1691, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1691
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Amaranthus blitoides
US-11-188-298-1691

Query Match      78.8%; Score 26; DB 11; Length 104;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      ||||| :
Db      58 GATNLVS 64

RESULT 34
US-11-188-298-3955
; Sequence 3955, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31

QY      1 GATNLAA 7
      ||||| :
Db      58 GATNLVS 64

RESULT 35
US-11-188-298-18880
; Sequence 18880, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18880
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Brassica tournefortii
US-11-188-298-18880

Query Match      78.8%; Score 26; DB 11; Length 106;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GATNLAA 7
      ||||| :
Db      61 GATNLVS 67

RESULT 36
US-11-045-004-495
; Sequence 495, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIEGER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GORBEI, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
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; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 21300
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Papaver rhoeas
US-11-188-298-21300

Query Match 78.8%; Score 26; DB 11; Length 240;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||||| :
Db 67 GATNLVS 73

RESULT 41

US-11-188-298-22158
; Sequence 22158, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 22158
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Bidens pilosa
US-11-188-298-22158

Query Match 78.8%; Score 26; DB 11; Length 241;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||||| :
Db 64 GATNLVS 70

RESULT 42

US-11-188-298-19893
; Sequence 19893, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19893
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Amaranthus quitensis
US-11-188-298-19893

Query Match 78.8%; Score 26; DB 11; Length 242;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||||| :
Db 64 GATNLVS 70

RESULT 43

US-11-188-298-20607
; Sequence 20607, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20607
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Amaranthus powellii
US-11-188-298-20607

Query Match 78.8%; Score 26; DB 11; Length 252;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||||| :
Db 69 GATNLVS 75

RESULT 44

US-11-188-298-6948
; Sequence 6948, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6948
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(285)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-6948

Query Match 78.8%; Score 26; DB 11; Length 285;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GATNLAA 7
||||| :
Db 140 GATNLVS 146

RESULT 45

US-11-045-004-1784
; Sequence 1784, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:

; APPLICANT: BUCHRIEGER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE


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; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHARGABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUP, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1784
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1784

Query Match 78.8%; Score 26; DB 11; Length 427;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 310 GRTNIAA 316

RESULT 46
US-11-103-957-5
; Sequence 5, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition

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; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-11-103-957-5

Query Match 78.8%; Score 26; DB 11; Length 432;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 18 GSTNLA 23

RESULT 47
US-11-018-868-34
; Sequence 34, Application US/11018868
; Publication No. US20060034871A1
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; APPLICANT: Grandi, Guido
; APPLICANT: Ratti, Giulio
; APPLICANT: Bonci, Alessandro
; APPLICANT: Finco, Oretta
; TITLE OF INVENTION: Immunogenic Compositions for Chlamydia trachomatis
; FILE REFERENCE: 002441.00099 (Pp23152.001)
; CURRENT APPLICATION NUMBER: US/11/018,868
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-11-018-868-34

Query Match 78.8%; Score 26; DB 11; Length 432;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATNLA 6
Db 18 GSTNLA 23

RESULT 48
US-11-188-298-15735
; Sequence 15735, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 15735
; LENGTH: 435
; TYPE: PRT

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; ORGANISM: Ferroplasma acidarmanus
US-11-188-298-15735

Query Match 78.8%; Score 26; DB 11; Length 435;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 202 GAATIAA 208

RESULT 49

US-11-188-298-1962
; Sequence 1962, Application US/11188298
; Publication No. US20060075522A1

; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569

; SEQ ID NO 1962
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Thermoplasma acidophilum
US-11-188-298-1962

Query Match 78.8%; Score 26; DB 11; Length 467;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 221 GAATIAA 227

RESULT 50

US-11-188-298-5948
; Sequence 5948, Application US/11188298
; Publication No. US20060075522A1

; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569

; SEQ ID NO 5948
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-188-298-5948

Query Match 78.8%; Score 26; DB 11; Length 512;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATNLAA 7
Db 145 GATNLVS 151

Search completed: May 11, 2006, 16:50:27
Job time : 17.7213 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:15:30 ; Search time 83.2131 Seconds
(without alignments)
47.521 Million cell updates/sec

Title: US-10-808-538-6

Perfect score: 55

Sequence: 1 LHSEYPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	9	2	Aaw23435 CDR-3 of
2	55	100.0	108	2	Aaw23439 Modified
3	55	100.0	108	2	Aaw23440 Modified
4	55	100.0	108	2	Aaw23442 Modified
5	55	100.0	108	2	Aaw23436 rW12 ligh
6	43	78.2	976	4	Abb68735 Drosophil
7	43	78.2	976	8	Ado00983 Fruit fly
8	42	76.4	508	4	Abb71345 Drosophil
9	41	74.5	113	4	Aae03749 Murine PS
10	41	74.5	238	4	Aae03754 Chimeric
11	40	72.7	101	5	Abb07177 Mouse 09
12	40	72.7	101	8	Adi26670 Mouse ant
13	40	72.7	107	9	Adv66159 Human BpC
14	40	72.7	107	9	Adv83517 AntiEpCam
15	40	72.7	108	8	Adi26700 Mouse ant
16	40	72.7	242	2	Aay17957 Mouse scF
17	40	72.7	242	2	Aay17961 Mouse scF
18	40	72.7	242	2	Aay17959 Mouse scF
19	40	72.7	491	9	Adz83409 C-termina
20	40	72.7	494	9	Adv66089 Anti-CD3
21	40	72.7	497	9	Adv66123 Anti-CD3
22	40	72.7	497	9	Adv66125 Anti-CD3
23	40	72.7	506	9	Adz83427 Deimmuniz
24	40	72.7	515	9	Adv66113 Anti-CD3

25	40	72.7	2346	5	AD116955	Adi16955	Murine NO
26	39	70.9	9	8	ADR38871	ADR38871	Mouse lig
27	39	70.9	9	9	AEA44021	AEA44021	Anti-TPO
28	39	70.9	9	9	AEA44003	AEA44003	Anti-TPO
29	39	70.9	9	9	AEA44012	AEA44012	Anti-TPO
30	39	70.9	9	9	AEA44042	AEA44042	Anti-TPO
31	39	70.9	9	9	AEA44018	AEA44018	Anti-TPO
32	39	70.9	9	9	AEA44024	AEA44024	Anti-TPO
33	39	70.9	9	9	AEA44015	AEA44015	Anti-TPO
34	39	70.9	9	9	AEA44027	AEA44027	Anti-TPO
35	39	70.9	9	9	AEA44036	AEA44036	Anti-TPO
36	39	70.9	9	9	AEA44009	AEA44009	Anti-TPO
37	39	70.9	9	9	AEA44033	AEA44033	Anti-TPO
38	39	70.9	9	9	AEA44000	AEA44000	Anti-TPO
39	39	70.9	9	9	AEA44006	AEA44006	Anti-TPO
40	39	70.9	14	2	Aay14406	Aay14406	Peptide C
41	39	70.9	112	2	Aay24099	Aay24099	Figure 11
42	39	70.9	112	9	AEA89804	AEA89804	Antibody
43	39	70.9	112	9	AEA89802	AEA89802	Antibody
44	39	70.9	112	9	AEA89801	AEA89801	Antibody
45	39	70.9	112	9	AEA44068	AEA44068	Anti-TPO
46	39	70.9	112	9	AEA44070	AEA44070	Anti-TPO
47	39	70.9	112	9	AEA44072	AEA44072	Anti-TPO
48	39	70.9	112	9	AEA44062	AEA44062	Anti-TPO
49	39	70.9	112	9	AEA44074	AEA44074	Anti-TPO
50	39	70.9	112	9	AEA44080	AEA44080	Anti-TPO
51	39	70.9	112	9	AEA44084	AEA44084	Anti-TPO
52	39	70.9	112	9	AEA44082	AEA44082	Anti-TPO
53	39	70.9	112	9	AEA44088	AEA44088	Anti-TPO
54	39	70.9	112	9	AEA44076	AEA44076	Anti-TPO
55	39	70.9	112	9	AEA44064	AEA44064	Anti-TPO
56	39	70.9	112	9	AEA44078	AEA44078	Anti-TPO
57	39	70.9	112	9	AEA44066	AEA44066	Anti-TPO
58	39	70.9	115	8	ADI26477	ADI26477	Protein o
59	39	70.9	132	9	AEA51617	AEA51617	Human Mpl
60	39	70.9	147	2	Aay74025	Aay74025	Human pro
61	39	70.9	157	2	Aay60541	Aay60541	Human nor
62	39	70.9	167	2	Aay14356	Aay14356	Anti-HCV
63	39	70.9	236	5	ABG77160	ABG77160	Germline
64	39	70.9	236	8	ADR28582	ADR28582	Human ant
65	39	70.9	447	6	ADA36096	ADA36096	Acinetoba
66	39	70.9	744	8	ADR89397	ADR89397	AXMI-007.
67	39	70.9	1747	8	ADO17146	ADO17146	Novel exp
68	39	70.9	2136	4	AAM78695	AAM78695	Human pro
69	39	70.9	2725	5	ABG61913	ABG61913	Prostate
70	39	70.9	2725	7	ADJ69881	ADJ69881	Human hea
71	39	70.9	2725	7	ADN39610	ADN39610	Cancer/an
72	39	70.9	2725	8	ADQ21282	ADQ21282	Human sof
73	39	70.9	2725	8	ADU06625	ADU06625	Novel bro
74	38	69.1	9	9	ADU94321	ADU94321	Antibody
75	38	69.1	9	9	ADV21403	ADV21403	Human ant
76	38	69.1	18	8	ADS84935	ADS84935	Beta-site
77	38	69.1	107	9	ADV21397	ADV21397	Human ant
78	38	69.1	119	4	AAU56089	AAU56089	Propionib
79	38	69.1	119	6	ABM52608	ABM52608	Propionib
80	38	69.1	128	8	ADS94332	ADS94332	Antibody
81	38	69.1	243	9	ADV21484	ADV21484	Mature fo
82	38	69.1	328	6	ABU15017	ABU15017	Protein e
83	38	69.1	336	4	ABG25968	ABG25968	Novel hum
84	38	69.1	496	9	ADV21523	ADV21523	Mature fo
85	38	69.1	496	9	ADV21533	ADV21533	Mature fo
86	38	69.1	498	9	ADV21503	ADV21503	Mature fo
87	38	69.1	498	9	ADV21513	ADV21513	Mature fo
88	38	69.1	633	8	ADH72176	ADH72176	Human pro
89	38	69.1	633	8	ADH72182	ADH72182	Human pro
90	38	69.1	653	2	AAAR27259	AAAR27259	Penicilli
91	38	69.1	659	2	AAAR27262	AAAR27262	Penicilli
92	38	69.1	717	2	AAW06109	AAW06109	Scytalidi
93	38	69.1	717	8	ADT89624	ADT89624	Aspergill
94	38	69.1	717	8	ADT89640	ADT89640	Scytalidi
95	38	69.1	879	6	ABR40109	ABR40109	Human cel
96	38	69.1	959	5	ABP43938	ABP43938	FLJ20047
97	38	69.1	959	8	ADH72178	ADH72178	Human pro

98	38	69.1	1021	8	ADH72180	Adh72180 Human pro	171	36	65.5	2397	8	ADJ76266	Adj76266 Marker ge
99	38	69.1	1025	8	ADH72174	Adh72174 Human pro	172	36	65.5	9913	8	ADT40977	Adt40977 hSARS vir
100	38	69.1	1025	8	ADH72172	Adh72172 Human pro	173	36	65.5	9913	8	ADT38507	Adt38507 hSARS vir
101	38	69.1	1063	5	ABP70110	Abp70110 Human NOV	174	36	65.5	9913	8	AEBO0352	Aeb00352 SARS coro
102	38	69.1	1063	5	ABP70110	Abp70110 Human NOV	175	35	63.6	9	3	ABAB11390	Aab11390 Murine II
103	38	69.1	1289	7	ADH72170	Adh72170 Human pro	176	35	63.6	9	8	ADOM43568	Ado43568 Complemen
104	38	69.1	3003	5	ADH72184	Adh72184 Human pro	177	35	63.6	9	8	ADOM43562	Ado43562 Complemen
105	38	69.1	3003	5	ADH72184	Adh72184 Human pro	178	35	63.6	9	8	ADR38865	Adr38865 Mouse lig
106	38	69.1	3361	5	ABP70111	Abp70111 Human NOV	179	35	63.6	9	9	AEAM45564	Aea45564 Apolipop
107	38	69.1	3361	5	ADH72186	Adh72186 Human pro	180	35	63.6	9	9	AEAM44030	Aea44030 Anti-TPO
108	37	67.3	9	2	AA30450	Aar30450 C242:11 M	181	35	63.6	9	9	AEAM44039	Aea44039 Anti-TPO
109	37	67.3	138	8	ADM87819	Adm87819 Human EST	182	35	63.6	9	9	AEAM44212	Aea44212 Anti-TPO
110	37	67.3	139	5	ABP43157	Abp43157 Human ova	183	35	63.6	9	9	AEAM43997	Aea43997 Anti-TPO
111	37	67.3	141	2	AA30454	Aar30454 C242:11 M	184	35	63.6	9	9	AEAM44179	Aea44179 Anti-TPO
112	37	67.3	141	2	AA30454	Aar30454 C242:11 M	185	35	63.6	88	4	AAU39918	Aau39918 Propionib
113	37	67.3	153	8	ADY11687	Ady11687 Plant ful	186	35	63.6	88	6	ABM36437	Abm36437 Propionib
114	37	67.3	219	8	ADI35160	Adi35160 Humanised	187	35	63.6	96	4	ABB68925	Abb68925 Drosophil
115	37	67.3	257	5	AAU87032	Aau87032 Adenoviru	188	35	63.6	107	7	ADKI8596	Adk18596 Anti-huma
116	37	67.3	261	5	ABB9937	Abb9937 Human zin	189	35	63.6	107	7	ADKI8867	Adk18867 Anti-huma
117	37	67.3	262	9	AB343167	Aeb43167 Zea mays	190	35	63.6	107	7	ADKI8804	Adk18804 Anti-huma
118	37	67.3	302	8	ADX88450	Adx88450 Plant ful	191	35	63.6	107	8	ADL25410	Adl25410 Human mAb
119	37	67.3	350	2	AAW41164	Aaw41164 Metal-reg	192	35	63.6	108	2	AA34019	Aar34019 BW 835 VK
120	37	67.3	353	5	ABB93880	Abb93880 Herbicida	193	35	63.6	108	3	ABAB11392	Aab11392 Murine II
121	37	67.3	353	8	ADT06024	Adt06024 Soil rest	194	35	63.6	108	3	ABAB52210	Abg52210 Human ant
122	37	67.3	367	5	AAU87035	Aau87035 Adenoviru	195	35	63.6	108	5	ABG92887	Abg92887 Human imm
123	37	67.3	385	6	ABU65246	Abu65246 Novel hum	196	35	63.6	108	8	ABM80818	Abm80818 Tumour-as
124	37	67.3	419	8	ADG22429	Adg22429 Cyanophag	197	35	63.6	112	9	ABAM89803	Abam89803 Antibody
125	37	67.3	465	5	AAU87036	Aau87036 Adenoviru	198	35	63.6	112	9	AEAM4055	Aea44055 Anti-TPO
126	37	67.3	499	8	ADM87382	Adm87382 Human pro	199	35	63.6	112	9	AEAM4086	Aea44086 Anti-TPO
127	37	67.3	519	7	ADM05082	Adm05082 Human pro	200	35	63.6	112	9	AEAM44232	Aea44232 Anti-TPO
128	37	67.3	539	3	AB211040	Aab211040 Human nuc	201	35	63.6	112	9	AEAM44060	Aea44060 Anti-TPO
129	37	67.3	616	6	AAE32888	Aae32888 Sulfolobu	202	35	63.6	112	9	AEAM44226	Aea44226 Anti-TPO
130	37	67.3	616	8	ADO05462	Ado05462 Sulfolobu	203	35	63.6	112	9	AEAM44173	Aea44173 Anti-TPO
131	37	67.3	980	8	ADS44784	Ads44784 Bacterial	204	35	63.6	112	9	AEAM44193	Aea44193 Anti-TPO
132	36	65.5	9	8	ADR38734	Adr38734 Mouse lig	205	35	63.6	130	3	RAY56738	Ray56738 Amino aci
133	36	65.5	9	8	ADR38733	Adr38733 Mouse lig	206	35	63.6	132	3	AEAM89785	Aea89785 Antibody
134	36	65.5	9	8	ADR38868	Adr38868 Mouse lig	207	35	63.6	132	2	AA33951	Aar33951 CTMO1 VL
135	36	65.5	9	8	ADR38862	Adr38862 Mouse lig	208	35	63.6	133	2	AA33954	Aar33954 gLI varia
136	36	65.5	9	8	ADR38735	Adr38735 Mouse lig	209	35	63.6	133	2	AAW29754	Aaw29754 CDR-graft
137	36	65.5	18	8	ADT41373	Adt41373 hSARS vir	210	35	63.6	133	3	AAW56878	Aaw56878 gL2 varia
138	36	65.5	18	8	ADS80788	Ads80788 SARS viru	211	35	63.6	133	3	RAY56874	Ray56874 MAb CT-M-
139	36	65.5	18	8	ADT38903	Adt38903 hSARS vir	212	35	63.6	133	8	ADOM43553	Ado43553 Amino aci
140	36	65.5	49	2	AAW77664	Aaw77664 Oligopept	213	35	63.6	133	8	ADOM43549	Ado43549 Amino aci
141	36	65.5	80	9	ABE22971	Aeb22971 Artificia	214	35	63.6	152	8	ADK52390	Adk52390 Human ant
142	36	65.5	81	5	ABP51694	Abp51694 Plasmid p	215	35	63.6	163	4	AAU17739	Aam17739 Peptide #
143	36	65.5	81	5	ABE79463	Abb79463 Recombina	216	35	63.6	163	4	ABAB36765	Abb36765 Peptide #
144	36	65.5	81	8	ADQ16633	Adq16633 Plasmid p	217	35	63.6	163	4	AAU30254	Aam30254 Peptide #
145	36	65.5	81	9	ADV44371	Adv44371 Rationall	218	35	63.6	163	4	ABAB31548	Abb31548 Peptide #
146	36	65.5	81	9	ABE12844	Aeb12844 Jun dimer	219	35	63.6	163	4	ABAB22092	Abb22092 Protein #
147	36	65.5	107	8	ADH50830	Adh50830 Human lig	220	35	63.6	163	4	AAAM69916	Aam69916 Human bon
148	36	65.5	107	8	ADH50829	Adh50829 Human lig	221	35	63.6	163	4	AAAM57512	Aam57512 Human bra
149	36	65.5	107	8	ADH50889	Adh50889 Human lig	222	35	63.6	163	4	ABG51613	Abg51613 Human liv
150	36	65.5	108	8	ADH50825	Adh50825 Human lig	223	35	63.6	163	4	AAAM05399	Aam05399 Peptide #
151	36	65.5	108	8	ADH50837	Adh50837 Human lig	224	35	63.6	163	5	ABG39547	Abg39547 Human pep
152	36	65.5	128	2	AAW08427	Aaw08427 Vector ex	225	35	63.6	169	8	ADL91140	Adl91140 Human fic
153	36	65.5	128	2	AAW30055	Aaw30055 Amino aci	226	35	63.6	169	8	ADT77829	Adt77829 Human fic
154	36	65.5	159	4	AAW96718	Aaw96718 Purative	227	35	63.6	207	6	ABU24967	Abu24967 Protein e
155	36	65.5	229	8	ADH50828	Adh50828 Human hea	228	35	63.6	219	6	ABU02291	Abu02291 S. pneumo
156	36	65.5	252	4	ABE67266	Abb67266 Drosophil	229	35	63.6	219	6	ABP81455	Abp81455 Streptoco
157	36	65.5	252	4	ABE66827	Abb66827 Drosophil	230	35	63.6	219	8	ADK46530	Adk46530 Streptoco
158	36	65.5	271	4	AAU37334	Aau37334 Staphyloc	231	35	63.6	221	8	ADR96217	Adr96217 Novel S.
159	36	65.5	271	4	AAU34355	Aau34355 Staphyloc	232	35	63.6	221	9	AEAM60087	Aea60087 Streptoco
160	36	65.5	271	6	AAU16453	Abu16453 Protein e	233	35	63.6	234	2	AAAR64819	Aar64819 OMVU10 SC
161	36	65.5	271	6	ABM72498	Abm72498 Staphyloc	234	35	63.6	236	2	AAAR42065	Aar42065 Human ant
162	36	65.5	282	6	ABE12930	Aeb12930 Antibody	235	35	63.6	239	2	AAAR66757	Aar66757 Anti-toba
163	36	65.5	294	6	ABU16035	Abu16035 Protein e	236	35	63.6	254	9	AEAM44057	Aea44057 Anti-TFO
164	36	65.5	294	6	ABM72932	Abm72932 Staphyloc	237	35	63.6	278	6	ABM65334	Abm65334 Propionib
165	36	65.5	303	5	AAO22539	Aao22539 CH1, His6	238	35	63.6	323	6	ABU25642	Abu25642 Protein e
166	36	65.5	459	9	ADV44459	Adv44459 Anti-teta	239	35	63.6	330	6	ABM69861	Abm69861 Photorhab
167	36	65.5	614	6	ADA33217	Ada33217 Acinetoba	240	35	63.6	334	4	AAAG81594	Aag81594 S. epider
168	36	65.5	653	2	AAAR27258	Aar27258 Penicilli	241	35	63.6	335	5	ABP69393	Abp69393 Human pol
169	36	65.5	756	7	ABM85925	Abm85925 Rice abio	242	35	63.6	336	7	ADP06250	Adp06250 Bacterial
170	36	65.5	1537	4	AAAB83971	Aab83971 Amino aci	243	35	63.6	338	5	ABP40310	Abp40310 Staphyloc

244	35	63.6	338	8	ADS07466	Ado07466 Staphyloc	317	34	61.8	107	7	ADK18916	Adk18916 Anti-huma
245	35	63.6	350	8	ADN60366	Adn60366 B. lichen	318	34	61.8	107	7	ADK18885	Adk18885 Anti-huma
246	35	63.6	368	8	ADN25990	Adn25990 Bacterial	319	34	61.8	107	7	ADK18840	Adk18840 Anti-huma
247	35	63.6	402	2	AAW26651	Aaw26651 Chimeric	320	34	61.8	107	7	ADK18892	Adk18892 Anti-huma
248	35	63.6	383	2	AAW26648	Aaw26648 Chimeric	321	34	61.8	107	7	ADK18841	Adk18841 Anti-huma
249	35	63.6	450	5	ABP95637	Abp95637 Human GPC	322	34	61.8	107	7	ADK18879	Adk18879 Anti-huma
250	35	63.6	450	8	ADN20942	Adn20942 Bacterial	323	34	61.8	107	7	ADK18612	Adk18612 Anti-huma
251	35	63.6	451	4	ABB67864	Abb67864 Drosophil	324	34	61.8	107	7	ADK18602	Adk18602 Anti-huma
252	35	63.6	460	4	AAW17418	Aaw17418 Peptide #	325	34	61.8	107	7	ADK18810	Adk18810 Anti-huma
253	35	63.6	460	4	ABB36447	Abb36447 Peptide #	326	34	61.8	107	7	ADK18844	Adk18844 Anti-huma
254	35	63.6	460	4	AAW29945	Aaw29945 Peptide #	327	34	61.8	107	7	ADK18806	Adk18806 Anti-huma
255	35	63.6	460	4	ABB311237	Abb311237 Peptide #	328	34	61.8	107	7	ADK18808	Adk18808 Anti-huma
256	35	63.6	460	4	ABB21791	Abb21791 Protein #	329	34	61.8	107	7	ADK18807	Adk18807 Anti-huma
257	35	63.6	460	4	AAW69607	Aaw69607 Human bon	330	34	61.8	107	7	ADK18604	Adk18604 Anti-huma
258	35	63.6	460	4	AAW57201	Aaw57201 Human bra	331	34	61.8	107	7	ADK18600	Adk18600 Anti-huma
259	35	63.6	460	4	ABG51281	Abg51281 Human liv	332	34	61.8	107	7	ADP03912	Adp03912 Murine-ex
260	35	63.6	460	4	AAW05102	Aaw05102 Peptide #	333	34	61.8	107	7	ADP03908	Adp03908 Murine-ex
261	35	63.6	460	5	ABG39229	Abg39229 Human pep	334	34	61.8	107	7	ADP03996	Adp03996 Murine-ex
262	35	63.6	473	2	AAW26646	Aaw26646 Chimeric	335	34	61.8	107	8	ADL25422	Adl25422 Human mab
263	35	63.6	498	2	ADW18218	Adw18218 Eucalyptu	336	34	61.8	107	8	ADL25418	Adl25418 Human mab
264	35	63.6	514	2	AAW26647	Aaw26647 Chimeric	337	34	61.8	107	8	ADL25426	Adl25426 Human mab
265	35	63.6	524	9	AEA44228	Aea44228 Anti-TPO	338	34	61.8	107	8	ADL25442	Adl25442 Human mab
266	35	63.6	524	9	AEA41189	Aea41189 Anti-TPO	339	34	61.8	107	8	ADO07289	Ado07289 Human pro
267	35	63.6	524	9	AEA44199	Aea44199 Anti-TPO	340	34	61.8	107	8	ADO07291	Ado07291 Human pro
268	35	63.6	524	9	AEA44222	Aea44222 Anti-TPO	341	34	61.8	107	8	ADP22368	Adp22368 Human ant
269	35	63.6	524	9	AEA43937	Aea43937 Anti-TPO	342	34	61.8	107	8	ADP22401	Adp22401 Human ant
270	35	63.6	524	9	AEA44195	Aea44195 Anti-TPO	343	34	61.8	107	8	ADP22158	Adp22158 Human ant
271	35	63.6	569	7	ADF07078	Adf07078 Bacterial	344	34	61.8	107	8	ADP22354	Adp22354 Human ant
272	35	63.6	551	2	AAW26649	Aaw26649 Chimeric	345	34	61.8	108	2	AAW10229	Aaw10229 CDR-graft
273	35	63.6	692	2	AAW26650	Aaw26650 Chimeric	346	34	61.8	108	2	AAW10231	Aaw10231 CDR-graft
274	35	63.6	702	7	ADG42183	Adg42183 Human bra	347	34	61.8	108	2	AEA45100	Aea45100 Apolipop
275	35	63.6	766	3	AAW51248	Aaw51248 Rat actin	348	34	61.8	108	9	ABE11691	Abe11691 Anti-Pseu
276	35	63.6	766	5	AAW26351	Aaw26351 Ras-like	349	34	61.8	112	4	AAW84296	Aaw84296 Amino aci
277	35	63.6	828	4	ABW58368	Abw58368 Drosophil	350	34	61.8	113	5	ABP03161	Abp03161 Human ORF
278	35	63.6	830	8	ADR09134	Adr09134 Human pro	351	34	61.8	113	7	ADD28269	Add28269 Human het
279	35	63.6	924	5	ABW71323	Abw71323 Human GCR	352	34	61.8	123	4	ABW67419	Abw67419 Drosophil
280	35	63.6	1131	4	ABG11655	Abg11655 Novel hum	353	34	61.8	127	6	AAO16818	Aao16818 Mouse H c
281	35	63.6	1171	4	ABB64387	Abb64387 Drosophil	354	34	61.8	127	6	AAO16812	Aao16812 Blood flo
282	35	63.6	1413	4	ABB60857	Abb60857 Drosophil	355	34	61.8	127	6	AAO16815	Aao16815 Blood flo
283	35	63.6	1424	4	ABB60854	Abb60854 Drosophil	356	34	61.8	127	6	AAO16813	Aao16813 Blood flo
284	35	63.6	1872	8	ADO17147	Ado17147 Novel exp	357	34	61.8	127	6	AAO16816	Aao16816 Blood flo
285	35	63.6	1892	5	ABE18302	Abel18302 Venezuela	358	34	61.8	127	6	AAO16814	Aao16814 Blood flo
286	35	63.6	2492	9	ADY26147	Ady26147 Venezuela	359	34	61.8	129	3	AAW25290	Aaw25290 Eucalyptu
287	34	61.8	9	2	AAW10227	Aaw10227 CDR-graft	360	34	61.8	129	4	ABG21984	Abg21984 Novel hum
288	34	61.8	9	2	AAW52754	Aaw52754 Humanised	361	34	61.8	131	2	AAW04387	Aaw04387 Colon can
289	34	61.8	9	9	AEA45570	Aea45570 Apolipop	362	34	61.8	131	3	AAW57052	Aaw57052 Amino aci
290	34	61.8	9	9	AEA45074	Aea45074 Apolipop	363	34	61.8	131	3	AAW90720	Aaw90720 CC83 VL r
291	34	61.8	25	7	ADL66782	Adl66782 Shg prote	364	34	61.8	131	4	AAU02139	Aau02139 Mouse par
292	34	61.8	58	4	AAU50462	Aau50462 Propionib	365	34	61.8	131	5	ABP51320	Abp51320 Human MDD
293	34	61.8	58	6	ABW46981	Abw46981 Propionib	366	34	61.8	131	7	ADK66826	Adk66826 Mouse CC8
294	34	61.8	69	3	ABG60932	Abg60932 Arabidops	367	34	61.8	143	9	ADY21937	Ady21937 Human ant
295	34	61.8	69	3	ABG56755	Abg56755 Arabidops	368	34	61.8	152	8	ADK52354	Adk52354 Human ant
296	34	61.8	82	5	ADH32377	Adh32377 Yeast emc	369	34	61.8	154	6	ABU22863	Abu22863 Protein e
297	34	61.8	96	5	ABU05606	Abu05606 M. tuberc	370	34	61.8	164	7	ADD28242	Add28242 Human het
298	34	61.8	106	7	ABW74494	Abw74494 Mycobacte	371	34	61.8	164	9	ADW86829	Adw86829 Bacillus
299	34	61.8	107	2	AAW52724	Aaw52724 Humanised	372	34	61.8	172	4	ABU53238	Abu53238 Human tes
300	34	61.8	107	2	AAW52722	Aaw52722 Humanised	373	34	61.8	182	4	AAU16434	Aau16434 Human nov
301	34	61.8	107	2	AAW52763	Aaw52763 Anti-tiss	374	34	61.8	182	6	ABU55503	Abu55503 Human nov
302	34	61.8	107	2	AAW52764	Aaw52764 Anti-tiss	375	34	61.8	186	4	AAU66855	Aau66855 Propionib
303	34	61.8	107	2	AAW52721	Aaw52721 Humanised	376	34	61.8	186	6	ABM63374	Abm63374 Propionib
304	34	61.8	107	2	AAW52723	Aaw52723 Humanised	377	34	61.8	212	4	AAU15998	Aau15998 Human nov
305	34	61.8	107	2	AAW52725	Aaw52725 Humanised	378	34	61.8	212	4	AAW94424	Aaw94424 Human pro
306	34	61.8	107	4	ABW74982	Abw74982 Humanised	379	34	61.8	212	6	ABU55067	Abu55067 Human nov
307	34	61.8	107	4	ABW74985	Abw74985 Humanised	380	34	61.8	214	7	ADC73235	Adc73235 Protein s
308	34	61.8	107	4	ABW74984	Abw74984 Humanised	381	34	61.8	214	8	ADF69630	Adf69630 Humanized
309	34	61.8	107	4	ABW74986	Abw74986 Humanised	382	34	61.8	234	2	AAW10233	Aaw10233 TF8-5G9 C
310	34	61.8	107	4	ABW74983	Abw74983 Humanised	383	34	61.8	236	5	ABG77164	Abg77164 Germline
311	34	61.8	107	4	ABW74988	Abw74988 Anti-TF m	384	34	61.8	236	8	ADR28586	Adr28586 Human ant
312	34	61.8	107	6	ABO16821	Abol16821 Blood flo	385	34	61.8	236	9	ABW57906	Abw57906 Human ger
313	34	61.8	107	7	ADC99789	Adc99789 Anti-huma	386	34	61.8	237	5	ABW47562	Abw47562 Listeria
314	34	61.8	107	7	ADD05393	Add05393 Anti-MUC1	387	34	61.8	241	4	ABW65660	Abw65660 Novel pro
315	34	61.8	107	7	ADF09831	Adf09831 Human ant	388	34	61.8	241	8	ADL29267	Adl29267 Human MAR
316	34	61.8	107	7	ADK18842	Adk18842 Anti-huma	389	34	61.8	242	6	ABR62131	AbR62131 Single ch

390	34	61.8	242	8	ADT91207	Adt91207 Single ch	463	34	61.8	862	7	ADC27568	Adc27568 Human col
391	34	61.8	251	5	AAU72868	Aau72868 P5-10 sin	464	34	61.8	939	4	ABBS58143	Abbs58143 Drosophil
392	34	61.8	259	5	ABG31023	Abg31023 Mouse sin	465	34	61.8	1070	4	AAW17789	Aaw17789 Green flu
393	34	61.8	259	7	ADD25452	Add25452 Binding d	466	34	61.8	1663	5	ABB05714	Abb05714 Human tes
394	34	61.8	259	7	ADM42727	Adm42727 Synthetic	467	34	61.8	2133	8	ADP25432	Adp25432 Plasmodiu
395	34	61.8	259	9	ABE95395	AbE95395 Mouse G28	468	34	61.8	2214	8	ADS43717	Ads43717 Bacterial
396	34	61.8	259	9	ABE94429	AbE94429 Mouse ant	469	34	61.8	3587	2	AAR34713	Aar34713 Bacillus
397	34	61.8	261	9	ADY21943	Ady21943 Human ant	470	34	61.8	3588	2	AAR34712	Aar34712 Bacillus
398	34	61.8	261	9	ADY21939	Ady21939 Human sin	471	33-5	60.9	83	4	AAO12664	Aao12664 Human pol
399	34	61.8	287	3	AAU76749	Aau76749 Human pro	472	33	60.9	83	4	ADS18660	Ads18660 Peptide s
400	34	61.8	287	3	AAE06207	Aae06207 Human pro	473	33	60.0	12	8	ADS84879	Ads84879 Beta-site
401	34	61.8	287	4	AAE62587	Aae62587 Cell cycl	474	33	60.0	18	8	ADS84959	Ads84959 Beta-site
402	34	61.8	287	5	ABB84434	Abb84434 Human pro	475	33	60.0	18	8	ADS84921	Ads84921 Beta-site
403	34	61.8	288	7	ADH88428	Adh88428 Enterococ	476	33	60.0	56	4	AAI15159	Aai15159 Peptide #
404	34	61.8	293	9	ADW17766	Adw17766 Pinus rad	477	33	60.0	56	4	ABB34152	Abb34152 Peptide #
405	34	61.8	296	9	ADY22011	Ady22011 Antibody	478	33	60.0	56	4	AAW27616	Aaw27616 Peptide #
406	34	61.8	315	6	ABU41521	Abu41521 Protein e	479	33	60.0	56	4	ABB28984	Abb28984 Peptide #
407	34	61.8	320	7	ABO84003	AbO84003 Pseudomon	480	33	60.0	56	4	ABBI19596	Abbi19596 Protein #
408	34	61.8	324	4	ABB63895	Abb63895 Drosophil	481	33	60.0	56	4	AAW67324	Aaw67324 Human bon
409	34	61.8	328	6	ABM73204	Abm73204 Staphyloc	482	33	60.0	56	4	AAW54944	Aaw54944 Human bra
410	34	61.8	337	7	ADD30817	Add30817 Plant vie	483	33	60.0	56	4	ABG48986	Abg48986 Human liv
411	34	61.8	337	8	ADI41857	Adi41857 Plant tra	484	33	60.0	56	4	AAW02897	Aaw02897 Peptide #
412	34	61.8	358	7	ADM25683	Adm25683 Hyperther	485	33	60.0	56	5	ABG36967	Abg36967 Human pep
413	34	61.8	359	7	ADM04511	Adm04511 Human pro	486	33	60.0	72	4	AAU65559	Aau65559 Propionib
414	34	61.8	360	4	AAU64532	Aau64532 Propionib	487	33	60.0	72	6	ABM62078	Abm62078 Propionib
415	34	61.8	360	6	ABM61051	Abm61051 Propionib	488	33	60.0	73	4	AAW99722	Aaw99722 Human exc
416	34	61.8	372	7	ABO60821	AbO60821 Klebsiell	489	33	60.0	73	4	AAW42537	Aaw42537 Human kid
417	34	61.8	384	7	ADH87954	Adh87954 Enterococ	490	33	60.0	80	7	ADC00271	Adc00271 Enterohae
418	34	61.8	420	8	ADN19118	Adn19118 Bacterial	491	33	60.0	80	7	ADR72413	Adr72413 Human end
419	34	61.8	429	6	ABP96244	Abp96244 Human nuc	492	33	60.0	89	2	AAW80080	Aaw80080 Mouse der
420	34	61.8	430	8	ADJ37221	Adj37221 Human nuc	493	33	60.0	92	2	AAW95477	Aaw95477 Mouse der
421	34	61.8	430	8	ADM87363	Adm87363 Human pro	494	33	60.0	104	9	AEA64466	Aea64466 Monoclon
422	34	61.8	442	8	ADU06573	Adu06573 Novel bro	495	33	60.0	106	4	AAW93409	Aaw93409 Human pro
423	34	61.8	453	6	ABU02300	Abu02300 S. pneumo	496	33	60.0	107	6	ABG74718	Abg74718 Murine hu
424	34	61.8	463	8	ADM92219	Adm92219 S. pneumo	497	33	60.0	107	6	ABG74702	Abg74702 Murine hu
425	34	61.8	467	7	ADB80139	Adb80139 Mycobacte	498	33	60.0	107	6	ABG74710	Abg74710 Murine hu
426	34	61.8	467	7	ABO83856	AbO83856 Pseudomon	499	33	60.0	107	7	ABR83149	AbR83149 Hu007 ant
427	34	61.8	471	4	AAW71966	Aaw71966 Human TGF	500	33	60.0	107	7	ABR83156	AbR83156 Hu007 ant
428	34	61.8	471	4	ABW85792	Abw85792 Human kin	501	33	60.0	107	7	ABR83157	AbR83157 Hu007 ant
429	34	61.8	471	7	ADB64482	Adb64482 Human pro	502	33	60.0	107	8	ADE25833	Ade25833 Anti-alpha
430	34	61.8	471	8	ADR58901	Adr58901 Human Elk	503	33	60.0	107	8	ADR73589	Adr73589 Anti-AR a
431	34	61.8	471	8	ADR58899	Adr58899 Human Elk	504	33	60.0	107	8	ADR73600	Adr73600 Humanised
432	34	61.8	487	8	ADK46519	Adk46519 Streptoco	505	33	60.0	110	4	AAW66519	Aaw66519 Human NF-
433	34	61.8	487	8	ADR94719	Adr94719 Novel S.	506	33	60.0	115	3	AAG33413	Aag33413 Zee may
434	34	61.8	487	9	AEA58589	Aea58589 Streptoco	507	33	60.0	125	4	AAW64963	Aaw64963 Human gap
435	34	61.8	493	9	ADY22001	Ady22001 Antibody	508	33	60.0	127	8	ADR73597	Adr73597 Anti-AR a
436	34	61.8	493	9	ADY22003	Ady22003 Antibody	509	33	60.0	127	8	ADR73605	Adr73605 HuPAR34 s
437	34	61.8	493	9	ADY21999	Ady21999 Antibody	510	33	60.0	140	4	AAW92162	Aaw92162 Human dig
438	34	61.8	493	9	ADY21953	Ady21953 Antibody	511	33	60.0	140	4	AAW99930	Aaw99930 Human pol
439	34	61.8	493	9	ADY21951	Ady21951 Antibody	512	33	60.0	142	3	AAW34762	Aaw34762 Human sec
440	34	61.8	493	9	ADY21955	Ady21955 Antibody	513	33	60.0	153	5	ADH32556	Adh32556 Yeast smo
441	34	61.8	495	9	ADY21945	Ady21945 Antibody	514	33	60.0	159	3	AAW12282	Aaw12282 Zee may
442	34	61.8	495	9	ADY21949	Ady21949 Antibody	515	33	60.0	170	3	AAW34717	Aaw34717 Human sec
443	34	61.8	499	9	ADY21947	Ady21947 Antibody	516	33	60.0	170	5	ABG72184	Abg72184 Membrane-
444	34	61.8	500	9	ADY22007	Ady22007 Antibody	517	33	60.0	174	8	ADK99017	Adk99017 Streptoco
445	34	61.8	505	3	AAW69159	Aaw69159 Peptide Q	518	33	60.0	187	6	ABP79296	Abp79296 N. gonorr
446	34	61.8	506	3	AAW53165	Aaw53165 Arabidops	519	33	60.0	214	6	ABG74711	Abg74711 Murine hu
447	34	61.8	515	3	AAW53164	Aaw53164 Arabidops	520	33	60.0	214	7	ABR83150	AbR83150 Hu007 ant
448	34	61.8	524	4	ABG20141	AbG20141 Novel hum	521	33	60.0	216	2	AAW15935	Aaw15935 Antibody
449	34	61.8	549	4	ABW71550	Abw71550 Drosophil	522	33	60.0	216	7	ABO62710	AbO62710 Klebsiell
450	34	61.8	586	9	ADY22009	Ady22009 Antibody	523	33	60.0	221	4	AAW72779	Aaw72779 Dictyoste
451	34	61.8	590	5	ABG34140	AbG34140 Antibody	524	33	60.0	228	6	ABR40633	AbR40633 Glycine m
452	34	61.8	590	7	ADC66319	Adc66319 Chinese h	525	33	60.0	228	7	ADC23565	Adc23565 Polypepti
453	34	61.8	590	7	ADL18099	Adl18099 Anti-lect	526	33	60.0	236	8	ADP07905	Adp07905 Human imm
454	34	61.8	590	7	ADL35263	Adl35263 Chinese h	527	33	60.0	243	4	ABW70500	Abw70500 Drosophil
455	34	61.8	592	9	ADY22005	Ady22005 Antibody	528	33	60.0	262	4	ABW65789	Abw65789 Drosophil
456	34	61.8	621	7	ABM87014	Abm87014 Rice abio	529	33	60.0	266	4	ABW70016	Abw70016 Drosophil
457	34	61.8	669	5	ABP66110	Abp66110 Bifidobac	530	33	60.0	275	8	ADW72828	Adw72828 Plant ful
458	34	61.8	713	4	ABW58892	Abw58892 Drosophil	531	33	60.0	277	4	AAU59754	Aau59754 Propionib
459	34	61.8	731	6	ABR52843	AbR52843 Protein s	532	33	60.0	277	6	ABW56273	Abw56273 Propionib
460	34	61.8	731	6	ADK62286	Adk62286 Disease t	533	33	60.0	278	7	ADE08738	Ade08738 Novel pro
461	34	61.8	759	8	ADS28664	Ads28664 Bacterial	534	33	60.0	286	4	AAW72761	Aaw72761 Dictyoste
462	34	61.8	819	8	ADH72314	Adh72314 Human pro	535	33	60.0	291	5	ABP29739	Abp29739 Streptoco

536	33	60.0	291	7	ABO61655	Abob1655 Klebsiell	609	33	60.0	478	6	ADA87269	Ada87269 Novel hum
537	33	60.0	301	8	ADS30011	Ads30011 Bacterial	610	33	60.0	478	6	ADB16471	Adb16471 Human PRO
538	33	60.0	309	2	Aaw32798	Aaw32798 Polypepti	611	33	60.0	478	6	ADA91563	Ada91563 Novel hum
539	33	60.0	309	2	Aaw32799	Aaw32799 Polypepti	612	33	60.0	478	6	ADB14626	Adb14626 Human PRO
540	33	60.0	309	2	Aaw27722	Aaw27722 Amino aci	613	33	60.0	478	6	ADB18587	Adb18587 Novel hum
541	33	60.0	309	8	ADN05882	Adno5882 Antipsori	614	33	60.0	478	6	ADA93802	Ada93802 Human PRO
542	33	60.0	310	9	AEA39559	Aear3959 Nematode	615	33	60.0	478	6	ADB19698	Adb19698 Novel hum
543	33	60.0	314	2	AAR75200	Aar75200 Rat P-F4M	616	33	60.0	478	6	ADB13010	Adb13010 Human PRO
544	33	60.0	314	2	AAR75199	Aar75199 Mouse P-F	617	33	60.0	478	6	ABO43217	Abob43217 Novel hum
545	33	60.0	336	6	ABU44621	Abu44621 Protein e	618	33	60.0	478	6	ADA74264	Ada74264 Human PRO
546	33	60.0	341	7	ADF04470	Adf04470 Bacterial	619	33	60.0	478	6	ADB24497	Adb24497 Human PRO
547	33	60.0	350	2	AAR75198	Aar75198 Rat Gal-b	620	33	60.0	478	6	ADA82021	Ada82021 Human PRO
548	33	60.0	350	2	AAR75197	Aar75197 Mouse Gal	621	33	60.0	478	6	ADA74984	Ada74984 Human PRO
549	33	60.0	350	7	ADE59126	Ades9126 Rat Prote	622	33	60.0	478	6	ADA85062	Ada85062 Novel hum
550	33	60.0	350	7	ADE59130	Ades9130 Rat Prote	623	33	60.0	478	6	ADA84510	Ada84510 Novel hum
551	33	60.0	350	7	ADB64099	Adbe64099 Human Pro	624	33	60.0	478	6	ADB29766	Adb29766 Human PRO
552	33	60.0	350	7	ADB64097	Adbe64097 Rat Prote	625	33	60.0	478	6	ADA80294	Ada80294 Human PRO
553	33	60.0	350	7	ADP45580	Adp45580 Rat Prote	626	33	60.0	478	6	ADA75536	Ada75536 Human PRO
554	33	60.0	350	7	ABM85655	Abm85655 Human pro	627	33	60.0	478	6	ADA46761	Ada46761 Human PRO
555	33	60.0	350	9	ADY27625	Ady27625 Mouse alp	628	33	60.0	478	6	ADB25057	Adb25057 Human PRO
556	33	60.0	351	7	ADB59132	Adbe59132 Human Pro	629	33	60.0	478	6	ADA93233	Ada93233 Human PRO
557	33	60.0	351	7	ADP45582	Adp45582 Human Pro	630	33	60.0	478	6	ADB26583	Adb26583 Human PRO
558	33	60.0	351	7	ADP59128	Adp59128 Human Pro	631	33	60.0	478	6	ADB30870	Adb30870 Human PRO
559	33	60.0	355	2	AAW35125	Aaw35125 R. pipien	632	33	60.0	478	6	ADA60798	Ada60798 Homo sapi
560	33	60.0	355	2	AAW35129	Aaw35129 R. pipien	633	33	60.0	478	6	ADB23945	Adb23945 Human PRO
561	33	60.0	358	2	AAW35127	Aaw35127 R. pipien	634	33	60.0	478	7	ADA77295	Ada77295 Human PRO
562	33	60.0	358	2	AAW35130	Aaw35130 R. pipien	635	33	60.0	478	6	ADA96274	Ada96274 Human PRO
563	33	60.0	360	2	AAW35128	Aaw35128 R. pipien	636	33	60.0	478	6	ADA80846	Ada80846 Human PRO
564	33	60.0	374	4	ABP95711	Abp95711 Human pro	637	33	60.0	478	6	ADA95722	Ada95722 Human PRO
565	33	60.0	379	2	AAW35126	Aaw35126 R. pipien	638	33	60.0	478	6	ADB26031	Adb26031 Human PRO
566	33	60.0	379	7	ABM85654	Abm85654 Mouse pro	639	33	60.0	478	6	ADB23945	Adb23945 Human PRO
567	33	60.0	379	9	AEA20393	Aea20393 Novel hum	640	33	60.0	478	7	ADA18035	Ada18035 Human PRO
568	33	60.0	388	7	ADP72407	Adp72407 Human end	641	33	60.0	478	7	ADA86718	Ada86718 Novel hum
569	33	60.0	390	5	ABG96365	Abg96365 Human ova	642	33	60.0	478	7	ADA87821	Ada87821 Novel hum
570	33	60.0	390	7	ADP75434	Adp75434 Prostate	643	33	60.0	478	7	ADA46209	Ada46209 Novel hum
571	33	60.0	390	7	ADP75434	Adp75434 Prostate	644	33	60.0	478	7	ADB28239	Adb28239 Human PRO
572	33	60.0	390	9	ADX07777	Adx07777 Cyclin-de	645	33	60.0	478	7	ADB28791	Adb28791 Human PRO
573	33	60.0	406	7	ADP72408	Adp72408 Human end	646	33	60.0	478	7	ADA76743	Ada76743 Human PRO
574	33	60.0	435	8	ADG98234	Adg98234 Acyl1-spec	647	33	60.0	478	7	ADA88373	Ada88373 Novel hum
575	33	60.0	455	2	AAR89136	Aar89136 Bombyx mo	648	33	60.0	478	7	ADA97378	Ada97378 Human PRO
576	33	60.0	458	4	ABP74696	Abp74696 Human mem	649	33	60.0	478	7	ADB27135	Adb27135 Human PRO
577	33	60.0	458	7	ADM04634	Adm04634 Human pro	650	33	60.0	478	7	ADB22068	Adb22068 Novel hum
578	33	60.0	458	7	ADM87308	Adm87308 Human pro	651	33	60.0	478	7	ADA66759	Ada66759 Human PRO
579	33	60.0	459	5	AAE18218	Aae18218 Human MOL	652	33	60.0	478	7	ADB22620	Adb22620 Human PRO
580	33	60.0	459	7	ADD18214	Add18214 Human mol	653	33	60.0	478	7	ADB23393	Adb23393 Human PRO
581	33	60.0	466	4	ABP67567	Abp67567 Drosophil	654	33	60.0	478	7	ADA92115	Ada92115 Novel hum
582	33	60.0	467	2	AAR89137	Aar89137 Bombyx mo	655	33	60.0	478	7	ADB15178	Adb15178 Human PRO
583	33	60.0	474	3	AAI32427	Aai32427 Human leu	656	33	60.0	478	7	ADB38430	Adb38430 Novel hum
584	33	60.0	474	3	AAI32427	Aai32427 Human leu	657	33	60.0	478	7	ADB37878	Adb37878 Novel hum
585	33	60.0	474	4	ABG15118	Abg15118 Novel hum	658	33	60.0	478	7	ADB89430	Adb89430 Human PRO
586	33	60.0	474	7	ADJ70304	Adj70304 Human hea	659	33	60.0	478	7	ADB89430	Adb89430 Human PRO
587	33	60.0	478	4	AAU12240	Aau12240 Human PRO	660	33	60.0	478	7	ADB90162	Adb90162 Human PRO
588	33	60.0	478	5	AAU09862	Aau09862 Novel hum	661	33	60.0	478	7	ADB39263	Adb39263 Novel hum
589	33	60.0	478	6	ABO17684	Abol7684 Novel hum	662	33	60.0	478	7	ADB46886	Adb46886 Novel hum
590	33	60.0	478	6	ABU80938	Abu80938 Human PRO	663	33	60.0	478	7	ADB86493	Adb86493 Human PRO
591	33	60.0	478	6	ABU66638	Abu66638 Human PRO	664	33	60.0	478	7	ADB77098	Adb77098 Novel hum
592	33	60.0	478	6	ABU59719	Abu59719 Novel sec	665	33	60.0	478	7	ADB34255	Adb34255 Human PRO
593	33	60.0	478	6	ABU24909	Abu24909 Human sec	666	33	60.0	478	7	ADB35359	Adb35359 Human PRO
594	33	60.0	478	6	ABU66914	Abu66914 Human sec	667	33	60.0	478	7	ADB33703	Adb33703 Human PRO
595	33	60.0	478	6	ADA45657	Ada45657 Novel hum	668	33	60.0	478	7	ADB34807	Adb34807 Human PRO
596	33	60.0	478	6	ADA76088	Ada76088 Human PRO	669	33	60.0	478	7	ADB35911	Adb35911 Human PRO
597	33	60.0	478	6	ADA18738	Ada18738 Human PRO	670	33	60.0	478	7	ADB46306	Adb46306 Novel hum
598	33	60.0	478	6	ADA61361	Ada61361 Homo sapi	671	33	60.0	478	7	ADC50179	Adc50179 Novel hum
599	33	60.0	478	6	ADB19146	Adb19146 Novel hum	672	33	60.0	478	7	ADC71726	Adc71726 Novel hum
600	33	60.0	478	6	ADB27687	Adb27687 Human PRO	673	33	60.0	478	7	ADC59705	Adc59705 Novel hum
601	33	60.0	478	6	ADA86166	Ada86166 Novel hum	674	33	60.0	478	7	ADC52712	Adc52712 Novel hum
602	33	60.0	478	6	ADB15730	Adb15730 Human PRO	675	33	60.0	478	7	ADC57066	Adc57066 Novel hum
603	33	60.0	478	6	ADA47516	Ada47516 Human PRO	676	33	60.0	478	7	ADC60257	Adc60257 Novel hum
604	33	60.0	478	6	ADA67311	Ada67311 Human PRO	677	33	60.0	478	7	ADC50732	Adc50732 Novel hum
605	33	60.0	478	6	ADB30318	Adb30318 Human PRO	678	33	60.0	478	7	ADC65259	Adc65259 Human PRO
606	33	60.0	478	6	ADA85614	Ada85614 Novel hum	679	33	60.0	478	7	ADC54357	Adc54357 Novel hum
607	33	60.0	478	6	ADA96826	Ada96826 Human PRO	680	33	60.0	478	7	ADC53318	Adc53318 Novel hum
608	33	60.0	478	6	ADA79130	Ada79130 Human PRO	681	33	60.0	478	7	ADC58841	Adc58841 Novel hum

682	33	60.0	478	7	ADC55719	Novel	hum	Adc55719	Novel	hum	755	33	60.0	478	8	ADE89001	Human	PRO
683	33	60.0	478	7	ADC58289	Novel	hum	Adc58289	Novel	hum	756	33	60.0	478	8	ADE18140	Human	PRO
684	33	60.0	478	7	ADC02963	Novel	hum	Adc02963	Novel	hum	757	33	60.0	478	8	ADE88449	Human	PRO
685	33	60.0	478	7	ADC89955	Novel	hum	Adc89955	Novel	hum	758	33	60.0	478	8	ADE94469	Human	PRO
686	33	60.0	478	7	ADC69374	Human	PRO	Adc69374	Human	PRO	759	33	60.0	478	8	ADE90880	Human	PRO
687	33	60.0	478	7	ADC48263	Human	PRO	Adc48263	Human	PRO	760	33	60.0	478	8	ADE95021	Human	PRO
688	33	60.0	478	7	ADD09792	Human	PRO	Add09792	Human	PRO	761	33	60.0	478	8	ADE93131	Human	PRO
689	33	60.0	478	7	ADD04367	Novel	hum	AdD04367	Novel	hum	762	33	60.0	478	8	ADF34712	Human	PRO
690	33	60.0	478	7	ADC80323	Novel	hum	AdC80323	Novel	hum	763	33	60.0	478	8	ADE92027	Novel	hum
691	33	60.0	478	7	ADD10830	Human	PRO	AdD10830	Human	PRO	764	33	60.0	478	8	ADE90328	Human	PRO
692	33	60.0	478	7	ADC47711	Human	PRO	AdC47711	Human	PRO	765	33	60.0	478	8	ADE91475	Novel	hum
693	33	60.0	478	7	ADC79771	Novel	hum	AdC79771	Novel	hum	766	33	60.0	478	8	ADE92054	Human	PRO
694	33	60.0	478	7	ADD09240	Human	PRO	AdD09240	Human	PRO	767	33	60.0	478	8	ADG21840	Novel	hum
695	33	60.0	478	7	ADD40953	Novel	hum	AdD40953	Novel	hum	768	33	60.0	478	8	ADG19910	Human	PRO
696	33	60.0	478	7	ADD52092	Human	PRO	AdD52092	Human	PRO	769	33	60.0	478	8	ADF97816	Human	PRO
697	33	60.0	478	7	ADD52832	Human	PRO	AdD52832	Human	PRO	770	33	60.0	478	8	ADG24033	Novel	hum
698	33	60.0	478	7	ADD53384	Novel	hum	AdD53384	Novel	hum	771	33	60.0	478	8	ADP98387	Human	PRO
699	33	60.0	478	7	ADD51540	Human	PRO	AdD51540	Human	PRO	772	33	60.0	478	8	ADG03218	Human	PRO
700	33	60.0	478	7	ADD02339	Human	PRO	AdD02339	Human	PRO	773	33	60.0	478	8	ADP98939	Human	PRO
701	33	60.0	478	7	ADD01773	Human	PRO	AdD01773	Human	PRO	774	33	60.0	478	8	ADG16524	Human	PRO
702	33	60.0	478	7	ADD53955	Novel	hum	AdD53955	Novel	hum	775	33	60.0	478	8	ADG04983	Human	PRO
703	33	60.0	478	7	ADD92272	Human	PRO	AdD92272	Human	PRO	776	33	60.0	478	8	ADG19250	Human	PRO
704	33	60.0	478	7	ADD91168	Human	PRO	AdD91168	Human	PRO	777	33	60.0	478	8	ADG13087	Human	PRO
705	33	60.0	478	7	ADE03782	Human	PRO	AdE03782	Human	PRO	778	33	60.0	478	8	ADG08144	Novel	hum
706	33	60.0	478	7	ADE32079	Novel	hum	AdE32079	Novel	hum	779	33	60.0	478	8	ADG15314	Human	PRO
707	33	60.0	478	7	ADE22011	Human	PRO	AdE22011	Human	PRO	780	33	60.0	478	8	ADF96712	Human	PRO
708	33	60.0	478	7	ADD79235	Human	PRO	AdD79235	Human	PRO	781	33	60.0	478	8	ADG05897	Human	PRO
709	33	60.0	478	7	ADE41771	Human	PRO	AdE41771	Human	PRO	782	33	60.0	478	8	ADG23481	Novel	hum
710	33	60.0	478	7	ADE17588	Human	PRO	AdE17588	Human	PRO	783	33	60.0	478	8	ADG03770	Human	PRO
711	33	60.0	478	7	ADD91720	Human	PRO	AdD91720	Human	PRO	784	33	60.0	478	8	ADG24671	Novel	hum
712	33	60.0	478	7	ADE33183	Novel	hum	AdE33183	Novel	hum	785	33	60.0	478	8	ADG06968	Novel	hum
713	33	60.0	478	7	ADE33735	Novel	hum	AdE33735	Novel	hum	786	33	60.0	478	8	ADG07520	Novel	hum
714	33	60.0	478	7	ADD79787	Human	PRO	AdD79787	Human	PRO	787	33	60.0	478	8	ADG55015	Novel	hum
715	33	60.0	478	7	ADD92824	Human	PRO	AdD92824	Human	PRO	788	33	60.0	478	8	ADG60679	Novel	hum
716	33	60.0	478	7	ADE19244	Human	PRO	AdE19244	Human	PRO	789	33	60.0	478	8	ADG61783	Novel	hum
717	33	60.0	478	7	ADE18692	Human	PRO	AdE18692	Human	PRO	790	33	60.0	478	8	ADG81984	Human	PRO
718	33	60.0	478	7	ADE42888	Human	PRO	AdE42888	Human	PRO	791	33	60.0	478	8	ADG57223	Novel	hum
719	33	60.0	478	7	ADD95677	Human	PRO	AdD95677	Human	PRO	792	33	60.0	478	8	ADG56671	Novel	hum
720	33	60.0	478	7	ADE22563	Human	PRO	AdE22563	Human	PRO	793	33	60.0	478	8	ADG55567	Novel	hum
721	33	60.0	478	7	ADD78681	Human	PRO	AdD78681	Human	PRO	794	33	60.0	478	8	ADG58327	Novel	hum
722	33	60.0	478	7	ADE32631	Novel	hum	AdE32631	Novel	hum	795	33	60.0	478	8	ADG70693	Novel	hum
723	33	60.0	478	7	ADE42323	Human	PRO	AdE42323	Human	PRO	796	33	60.0	478	8	ADG57775	Novel	hum
724	33	60.0	478	7	ADD80339	Human	PRO	AdD80339	Human	PRO	797	33	60.0	478	8	ADG53359	Novel	hum
725	33	60.0	478	7	ADD89367	Human	PRO	AdD89367	Human	PRO	798	33	60.0	478	8	ADG71245	Novel	hum
726	33	60.0	478	7	ADE40651	Human	PRO	AdE40651	Human	PRO	799	33	60.0	478	8	ADG81432	Human	PRO
727	33	60.0	478	7	ADE04450	Human	PRO	AdE04450	Human	PRO	800	33	60.0	478	8	ADH30394	Human	PRO
728	33	60.0	478	7	ADE92579	Human	PRO	AdE92579	Human	PRO	801	33	60.0	478	8	ADH11761	Novel	hum
729	33	60.0	478	7	ADG21288	Novel	hum	AdG21288	Novel	hum	802	33	60.0	478	8	ADG52183	Novel	hum
730	33	60.0	478	7	ADG22929	Novel	hum	AdG22929	Novel	hum	803	33	60.0	478	8	ADG53911	Novel	hum
731	33	60.0	478	7	ADP97264	Human	PRO	AdP97264	Human	PRO	804	33	60.0	478	8	ADG80880	Human	PRO
732	33	60.0	478	7	ADG80328	Human	PRO	AdG80328	Human	PRO	805	33	60.0	478	8	ADG56119	Novel	hum
733	33	60.0	478	7	ADG79776	Human	PRO	AdG79776	Human	PRO	806	33	60.0	478	8	ADH12385	Novel	hum
734	33	60.0	478	7	ADH55068	Novel	hum	AdH55068	Novel	hum	807	33	60.0	478	8	ADG61231	Novel	hum
735	33	60.0	478	7	ADH55620	Novel	hum	AdH55620	Novel	hum	808	33	60.0	478	8	ADH28318	Human	PRO
736	33	60.0	478	7	ADI63839	Novel	hum	AdI63839	Novel	hum	809	33	60.0	478	8	ADG54463	Novel	hum
737	33	60.0	478	7	ADI64788	Novel	hum	AdI64788	Novel	hum	810	33	60.0	478	8	ADG59503	Novel	hum
738	33	60.0	478	7	ADI63287	Novel	hum	AdI63287	Novel	hum	811	33	60.0	478	8	ADI80927	Human	PRO
739	33	60.0	478	7	ADH81701	Novel	hum	AdH81701	Novel	hum	812	33	60.0	478	8	ADG09670	Novel	hum
740	33	60.0	478	7	ADH81149	Novel	hum	AdH81149	Novel	hum	813	33	60.0	478	8	ADH15141	Novel	hum
741	33	60.0	478	7	ADM82318	Novel	hum	AdM82318	Novel	hum	814	33	60.0	478	8	ADG09018	Novel	hum
742	33	60.0	478	7	ADN15717	Novel	hum	AdN15717	Novel	hum	815	33	60.0	478	8	ADI14473	Novel	hum
743	33	60.0	478	7	ADN16346	Novel	hum	AdN16346	Novel	hum	816	33	60.0	478	8	ADI18068	Novel	hum
744	33	60.0	478	7	ADN15165	Novel	hum	AdN15165	Novel	hum	817	33	60.0	478	8	ADJ63349	Novel	hum
745	33	60.0	478	7	ADN14613	Novel	hum	AdN14613	Novel	hum	818	33	60.0	478	8	ADJ77244	Human	PRO
746	33	60.0	478	8	ADC80875	Novel	hum	AdC80875	Novel	hum	819	33	60.0	478	8	ADJ65366	Human	PRO
747	33	60.0	478	8	ADD76323	Human	PRO	AdD76323	Human	PRO	820	33	60.0	478	8	ADM27502	Human	PRO
748	33	60.0	478	8	ADD87687	Human	PRO	AdD87687	Human	PRO	821	33	60.0	478	8	ADM42226	Human	PRO
749	33	60.0	478	8	ADD86091	Human	PRO	AdD86091	Human	PRO	822	33	60.0	478	8	ADM28088	Human	PRO
750	33	60.0	478	8	ADE75539	Human	PRO	AdE75539	Human	PRO	823	33	60.0	478	8	ADI95570	Human	PRO
751	33	60.0	478	8	ADE23115	Human	PRO	AdE23115	Human	PRO	824	33	60.0	478	8	ADI96122	Novel	hum
752	33	60.0	478	8	ADE23667	Human	PRO	AdE23667	Human	PRO	825	33	60.0	478	8	ADS10656	Human	the
753	33	60.0	478	8	ADE24310	Human	PRO	AdE24310	Human	PRO	826	33	60.0	478	8	ADS32074	Novel	hum
754	33	60.0	478	8	ADD87135	Human	PRO	AdD87135	Human	PRO	827	33	60.0	478	8	ADT03058	Human	PRO

828	33	60.0	478	9	AD2033109	Ad203109 Human sec	901	32.5	59.1	324	4	AAU16439	Aau16439 Human nov
829	33	60.0	478	9	AEb13855	Aeb13855 Cancer ce	902	32.5	59.1	324	6	ABU55508	Abu55508 Human nov
830	33	60.0	487	8	ADJ25978	Adj25978 Baeyer-Vi	903	32.5	59.1	378	4	AAU16003	Aau16003 Human nov
831	33	60.0	488	8	ADM87309	Adm87309 Human pro	904	32.5	59.1	378	6	ABU55072	Abu55072 Human nov
832	33	60.0	495	8	AD757452	Adt757452 Plant pol	905	32.5	59.1	383	4	AAU16048	Aau16048 Human nov
833	33	60.0	502	4	ABG17975	Abg17975 Novel hum	906	32.5	59.1	383	6	ABU55117	Abu55117 Human nov
834	33	60.0	510	4	ABG17976	Abg17976 Novel hum	907	32.5	59.1	394	4	AAW93790	Aam93790 Human pol
835	33	60.0	516	7	ABO71042	Abot71042 Pseudomon	908	32.5	59.1	394	8	ADL31782	Adl31782 Human pro
836	33	60.0	519	8	ADN99844	Adn99844 Novel hum	909	32.5	59.1	394	8	ADP12540	Adp12540 Protein e
837	33	60.0	523	6	ABR533260	Abf533260 Protein s	910	32.5	59.1	394	8	ABM82120	Abm82120 Tumour-as
838	33	60.0	523	7	ADK63168	Adk63168 Disease t	911	32.5	59.1	500	6	ABU29861	Abu29861 Protein e
839	33	60.0	523	8	ADN19079	Adn19079 Bacterial	912	32.5	59.1	545	8	ADV955983	Adv955983 Human can
840	33	60.0	525	4	ABE69653	Abbe69653 Drosophil	913	32.5	59.1	644	7	ADJ69390	Adj69390 Human hea
841	33	60.0	527	4	AAW78981	Aam78981 Human pro	914	32.5	59.1	811	5	ABP43842	Abp43842 DKFZP564M
842	33	60.0	527	4	ABG17973	Abg17973 Novel hum	915	32.5	59.1	896	8	ADQ67676	Adq67676 Novel hum
843	33	60.0	527	8	ADD01219	Ado01219 Human nuc	916	32.5	59.1	902	8	ABO58476	Abos58476 Human gen
844	33	60.0	527	8	ADX89867	Adx89867 Plant ful	917	32.5	59.1	986	8	ABO67538	Abog67538 Novel hum
845	33	60.0	530	4	AAW79965	Aam79965 Human pro	918	32	58.2	9	2	AAW62016	Aaw62016 Light cha
846	33	60.0	530	4	ABG16931	Abg16931 Novel hum	919	32	58.2	9	3	AAV82342	Aay82342 Humanised
847	33	60.0	570	2	AAW01669	Aaw01669 Influenza	920	32	58.2	9	3	AAV92163	Aay92163 Murine 15
848	33	60.0	570	2	AAW75441	Aaw75441 Influenza	921	32	58.2	9	8	ADE85732	Ades85732 Human Eph
849	33	60.0	570	4	ABE66046	Abbe66046 Drosophil	922	32	58.2	9	8	ADG39003	Adg39003 Humanised
850	33	60.0	570	4	ABE04951	Aae04951 Influenza	923	32	58.2	9	8	ADL23070	Adl23070 Human Eph
851	33	60.0	585	7	ADC31315	Adc31315 Human nov	924	32	58.2	9	8	ADR03423	Adr03423 Humanised
852	33	60.0	590	8	ADS22613	Ads22613 Bacterial	925	32	58.2	9	8	ADR03426	Adr03426 Humanised
853	33	60.0	650	8	ADN20002	Adn20002 Bacterial	926	32	58.2	9	8	ADU87723	Adu87723 Anti-CS1
854	33	60.0	653	2	AAW27263	Aar27263 Penicilli	927	32	58.2	9	8	ADU87707	Adu87707 Mouse Luc
855	33	60.0	662	8	ADK99014	Adk99014 Streptoco	928	32	58.2	9	9	ADY32305	Ady32305 Human Eph
856	33	60.0	662	8	ADK99013	Adk99013 Streptoco	929	32	58.2	9	9	AEA34927	Aea34927 Human ant
857	33	60.0	665	8	ADK99018	Adk99018 Streptoco	930	32	58.2	9	9	ABE17168	Aeb17168 EphA2-spe
858	33	60.0	665	8	ADK99010	Adk99010 Streptoco	931	32	58.2	9	9	AEA42968	Aea42968 EphA2 ant
859	33	60.0	668	8	ADK99019	Adk99019 Streptoco	932	32	58.2	10	6	ABM66259	Abm66259 Propionib
860	33	60.0	671	8	ADK99016	Adk99016 Streptoco	933	32	58.2	19	7	ADF79001	Adf79001 KLK2-EHTE
861	33	60.0	676	8	ADK99011	Adk99011 Streptoco	934	32	58.2	34	4	AAW18317	Aam18317 Peptide #
862	33	60.0	685	8	ADK99012	Adk99012 Streptoco	935	32	58.2	34	4	ABB37351	Abb37351 Peptide #
863	33	60.0	686	8	ADK99015	Adk99015 Streptoco	936	32	58.2	34	4	AAW30805	Aam30805 Peptide #
864	33	60.0	686	8	ADK99020	Adk99020 Streptoco	937	32	58.2	34	4	ABB32098	Abb32098 Peptide #
865	33	60.0	699	8	ADV89411	Adv89411 Streptoco	938	32	58.2	34	4	ABB22637	Abb22637 Protein #
866	33	60.0	699	8	ADV80664	Adv80664 Streptoco	939	32	58.2	34	4	AAW70481	Aam70481 Human bon
867	33	60.0	707	3	AAV95065	Aay95065 Candida a	940	32	58.2	34	4	AAW58041	Aam58041 Human bra
868	33	60.0	719	5	ABP26534	Abp26534 Streptoco	941	32	58.2	34	4	ABG52165	Abg52165 Human liv
869	33	60.0	719	8	ADV82831	Adv82831 Streptoco	942	32	58.2	34	4	AAW05925	Aam05925 Peptide #
870	33	60.0	729	4	ABG23306	Abg23306 Novel hum	943	32	58.2	34	5	ABG40120	Abg40120 Human pep
871	33	60.0	749	4	ABE62718	Abe62718 Drosophil	944	32	58.2	57	4	ABB37383	Abb37383 Peptide #
872	33	60.0	749	4	AAU38943	Aau38943 Drosophil	945	32	58.2	57	4	AAW38416	Aam38416 Peptide #
873	33	60.0	749	7	ADC35811	Adc35811 Drosophil	946	32	58.2	57	4	AAW65510	Aam65510 Human bra
874	33	60.0	761	4	ABG23321	Abg23321 Novel hum	947	32	58.2	65	5	ABP00737	Abp00737 Human ORF
875	33	60.0	801	4	ABE62287	Abbe62287 Drosophil	948	32	58.2	66	4	AAU59050	Aau59050 Propionib
876	33	60.0	805	8	ADM94430	Adm94430 Human pho	949	32	58.2	66	6	ABM55569	Abm55569 Propionib
877	33	60.0	858	9	ABE69227	Abe69227 Human mod	950	32	58.2	68	5	ABP32731	Abp32731 Human ORF
878	33	60.0	865	8	ADE52650	Ades2650 Murine dn	951	32	58.2	71	5	ABG40390	Abg40390 Human pep
879	33	60.0	881	4	AGS70761	Aag70761 S cerevis	952	32	58.2	71	7	ADP79000	Adp79000 KLK2-EHTE
880	33	60.0	967	8	ADRS2670	Adrs2670 Human pro	953	32	58.2	72	5	ADH32558	Adh32558 Yeast smO
881	33	60.0	1030	2	AAW90261	Aaw90261 A. tigrin	954	32	58.2	80	7	ADF05614	Adf05614 Bacterial
882	33	60.0	1051	5	AAO22157	Aao22157 Ramoplan	955	32	58.2	88	5	ADH32539	Adh32539 Yeast smO
883	33	60.0	1064	4	ABE66662	Abbe66662 Drosophil	956	32	58.2	88	4	ABB63347	Abb63347 Drosophil
884	33	60.0	1071	8	ADN46198	Adn46198 Thermococ	957	32	58.2	88	5	ABP06662	Abp06662 Human ORF
885	33	60.0	1118	8	ADU02820	Adu02820 Novel hum	958	32	58.2	88	4	ADS96706	Ads96706 Human ORF
886	33	60.0	1153	8	ABM83355	Abm83355 Human dia	959	32	58.2	103	5	ABP32015	Abp32015 Human ORF
887	33	60.0	1198	8	ABM83354	Abm83354 Human dia	960	32	58.2	105	8	ADT75007	Adt75007 Light cha
888	33	60.0	1207	8	ABM83353	Abm83353 Human dia	961	32	58.2	106	9	ABE12768	Aeb12768 Antibody
889	33	60.0	1225	8	ABM83352	Abm83352 Rice abio	962	32	58.2	107	3	AAV92157	Aay92157 Murine 15
890	33	60.0	1232	7	ADB80764	Adbe80764 Microsate	963	32	58.2	107	8	ABE85729	Abes85729 Human Eph
891	33	60.0	1232	8	ADU24093	Adu24093 Human eap	964	32	58.2	107	8	ABE25834	Abes25834 Anti-alpha
892	33	60.0	1234	8	ABM83351	Abm83351 Human dia	965	32	58.2	107	8	ADL23067	Adl23067 Human Eph
893	33	60.0	1259	7	ADJ70768	Adj70768 Human hea	966	32	58.2	107	8	ADU87730	Adu87730 Humanized
894	33	60.0	1382	7	ABM8630	Abm8630 Rice abio	967	32	58.2	107	8	ADU87728	Adu87728 Light cha
895	33	60.0	1781	4	ABG233291	Abg233291 Novel hum	968	32	58.2	107	8	ADU87734	Adu87734 VL region
896	33	60.0	5909	4	ABG233295	Abg233295 Novel hum	969	32	58.2	107	8	ADU87693	Adu87693 Mouse Luc
897	33	60.0	6619	4	ABG23329	Abg23329 Novel hum	970	32	58.2	107	8	ADU87736	Adu87736 Light cha
898	32.5	59.1	111	7	AD120695	Ad120695 Light cha	971	32	58.2	107	9	ADY32226	Ady32226 Human Eph
899	32.5	59.1	235	4	AAW94860	Aaw94860 Human pro	972	32	58.2	107	9	AEA34924	Aea34924 Human ant
900	32.5	59.1	291	7	AD120697	Ad120697 scFvG19-2	973	32	58.2	107	9	ABE17165	Aeb17165 EphA2-spe

974 32 58.2 107 9 AEA42965
 975 32 58.2 107 9 AEA62455
 976 32 58.2 108 2 AAW62017
 977 32 58.2 108 2 AAW63528
 978 32 58.2 108 2 AAW63529
 979 32 58.2 108 3 AAY82344
 980 32 58.2 108 3 AAY82343
 981 32 58.2 108 8 ADG38989
 982 32 58.2 108 8 ADG38990
 983 32 58.2 108 8 ABO57551
 984 32 58.2 108 8 ADP83455
 985 32 58.2 108 8 ADP83455
 986 32 58.2 108 8 ADR03365
 987 32 58.2 108 8 ADR03364
 988 32 58.2 108 8 ADM38457
 989 32 58.2 109 2 ADX80645
 990 32 58.2 109 2 AAY29449
 991 32 58.2 109 3 AAY77752
 992 32 58.2 109 3 AAB30309
 993 32 58.2 109 6 ABU13786
 994 32 58.2 109 6 ABU59499
 995 32 58.2 109 7 AAE33082
 996 32 58.2 110 4 AAM85655
 997 32 58.2 111 5 ABG93039
 998 32 58.2 115 9 AEB38360
 999 32 58.2 124 5 ABP39352
 1000 32 58.2 124 8 ADS04517
 ADU87781 Anti-CS1

ALIGNMENTS

RESULT 1
 AAW23435
 ID AAW23435 standard; peptide; 9 AA.

AC AAW23435;

DT 23-APR-1998 (first entry)

DE CDR-3 of rW12 light chain.

XX Antibody; complementarity determining region; CDR; light chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.

XX Rattus sp.

XX WO9734636-A1.

XX 25-SEP-1997.

XX 19-MAR-1997; 97WO-US004696.

XX 20-MAR-1996; 96US-0013708P.

XX (IMMU-) IMMUNOMEDICS INC.

XX Leung S, Loeman MJ, Hansen H;

XX WPI; 1997-479997/44.

XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotypic
 FT antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 FT stimulate immune response against cancer.

PS Claim 4; Page 30; 46pp; English.

XX This sequence represents the complementarity determining region-3 (CDR-3)
 CC of the rW12 light chain. This sequence is used in an antibody of the
 CC invention. The antibody of the invention is a chimeric or humanised anti-
 CC idiotype antibodies (cab and hab, respectively) or a fragment which
 CC specifically binds to the idiotype region of an anti-carcinoembryonic

CC antigen (CEA), where: (i) cab comprises the rW12 light (L) and heavy (H)
 CC chain variable regions, or silent mutations; and (ii) hab comprises rW12
 CC complementarity determining regions (CDR) and humanised framework (FR)
 CC regions. The hab is used as a vaccine to stimulate an immune response in
 CC a patient against cancers expressing CEA. The hab, can be used to clear
 CC non-targeted antibody in a method of diagnosis or treatment of a patient
 CC where a CEA antibody is used as a (pre-)targeting or therapy agent. The
 CC cab is used to detect the presence of an antibody that specifically binds
 CC to CEA in a sample

XX Sequence 9 AA;

Query Match 100.0%; Score 55; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9

Db 1 LHHSEYPT 9

RESULT 2

AAW23439

ID AAW23439 standard; protein; 108 AA.

XX AAW23439;

DT 23-APR-1998 (first entry)

XX Modified light chain variable region REIW12VKRS.

XX Antibody; complementarity determining region; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region; mutein; variable region.

OS Synthetic.

OS Rattus sp.

XX Key Location/Qualifiers

FT Misc-difference 4 /note= "L to M mutation"

FT Misc-difference 9 /note= "A to S mutation"

FT Misc-difference 12 /note= "P to S mutation"

FT Misc-difference 15 /note= "L to V mutation"

FT Region 24. .34

FT Misc-difference 39 /note= "complementarity determining region-1"

FT Misc-difference 43 /note= "K to T mutation"

FT Misc-difference 45 /note= "S to A mutation"

FT Misc-difference 45 /note= "R to K mutation"

FT Region 50. .56

FT Misc-difference 72 /note= "complementarity determining region-2"

FT Misc-difference 73 /note= "S to T mutation"

FT Misc-difference 76 /note= "L to F mutation"

FT Misc-difference 76 /note= "N to S mutation"

FT Misc-difference 79 /note= "B to Q mutation"

FT Misc-difference 80 /note= "S to P mutation"

FT Misc-difference 83 /note= "M to I mutation"

FT Misc-difference 85 /note= "I to T mutation"

FT Region 89. .97

FT /note= "complementarity determining region-3"

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 55; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LHHSEYPT 9
 |||||

Db 89 LHHSEYPT 97

RESULT 4
 AAW23442
 ID AAW23442 standard; protein; 108 AA.
 XX
 AC AAW23442;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE hW12 light chain.
 XX
 KW Antibody; complementarity determining region; light chain; human; CEA;
 KW hW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 89..97
 FT /note= "complementarity determining region-3"
 FT
 XX WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86304.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 XX antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 XX stimulate immune response against cancer.
 XX
 XX Disclosure; Fig 4; 46pp; English.
 XX
 XX This sequence represents the human hW12 light chain. This sequence is
 XX used in an antibody of the invention. The antibody of the invention is a
 XX chimeric or humanised anti-idiotype antibodies (cab and hab,
 XX respectively) or a fragment which specifically binds to the idiotype
 XX region of an anti-carcinoembryonic antigen (CEA), where: (i) cab
 XX comprises the hW12 light (L) and heavy (H) chain variable regions, or
 XX silent mutations; and (ii) hab comprises hW12 complementarity determining
 XX regions (CDR) and humanised framework (FR) regions. The hab is used as a
 XX vaccine to stimulate an immune response in a patient against cancers
 XX expressing CEA. The hab, can be used to clear non-targeted antibody in a
 XX method of diagnosis or treatment of a patient where a CEA antibody is
 XX used as a (pre-)targeting or therapy agent. The cab is used to detect the
 XX presence of an antibody that specifically binds to CEA in a sample
 XX
 XX Sequence 108 AA;

Query Match 100.0%; Score 55; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LHHSEYPT 9
 |||||

Db 89 LHHSEYPT 97

RESULT 5
 AAW23436
 ID AAW23436 standard; protein; 108 AA.
 XX
 AC AAW23436;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE rW12 light chain.
 XX
 KW Antibody; complementarity determining region; light chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /note= "complementarity determining region-1"
 FT Region 50..56
 FT /note= "complementarity determining region-2"
 FT Region 88..97
 FT /note= "complementarity determining region-3"
 FT
 XX WO9734636-A1.
 XX
 XX 25-SEP-1997.
 XX
 XX 19-MAR-1997; 97WO-US004696.
 XX
 XX 20-MAR-1996; 96US-0013708P.
 XX
 XX (IMMU-) IMMUNOMEDICS INC.
 XX
 XX Leung S, Losman MJ, Hansen H;
 XX
 XX WPI; 1997-479997/44.
 XX N-PSDB; AAT86287.
 XX
 XX Chimeric and humanised anti-carcinoembryonic antigen anti-idiotype
 XX antibodies - useful in detection of anti-CEA antibodies and as vaccine to
 XX stimulate immune response against cancer.
 XX
 XX Claim 6; Fig 7; 46pp; English.
 XX
 XX This sequence represents the rat rW12 light chain. This sequence is used
 XX in an antibody of the invention. The antibody of the invention is a
 XX chimeric or humanised anti-idiotype antibodies (cab and hab,
 XX respectively) or a fragment which specifically binds to the idiotype
 XX region of an anti-carcinoembryonic antigen (CEA), where: (i) cab
 XX comprises the rW12 light (L) and heavy (H) chain variable regions, or
 XX silent mutations; and (ii) hab comprises rW12 complementarity determining
 XX regions (CDR) and humanised framework (FR) regions. The hab is used as a
 XX vaccine to stimulate an immune response in a patient against cancers
 XX expressing CEA. The hab, can be used to clear non-targeted antibody in a
 XX method of diagnosis or treatment of a patient where a CEA antibody is
 XX used as a (pre-)targeting or therapy agent. The cab is used to detect the
 XX presence of an antibody that specifically binds to CEA in a sample
 XX
 XX Sequence 108 AA;

Query Match 100.0%; Score 55; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 07-AUG-2001 (first entry)
DE Chimeric 2403 IgG antibody light chain (SF2.4H4.1E3).
XX Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
KW human; immunoglobulin G; IgG; light chain region.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..131
FT /note= "Derived from mouse light chain variable region
FT (VL)"
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..238
FT /label= Mature_IgG_antibody_light_chain
FT Region 132..238
FT /note= "Derived from human light chain constant region
FT (CL)"
XX
PN WO200140309-A2.
XX
XX 07-JUN-2001.
XX
XX 27-OCT-2000; 2000WO-US029603.
XX
XX 29-OCT-1999; 99US-0162558P.
PR 16-FEB-2000; 2000US-0182872P.
XX
XX (GETH) GENENTECH INC.
XX
XX Devaux B, Keller G, Koeppen H, Lasky LA;
XX WPI; 2001-389954/41.
XX
XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-
PT expressing cancer cells in vivo, useful for killing PSCA-expressing
PT cancer cells.
XX
XX Claim 5; Fig 13; 112pp; English.
XX
XX The present chimeric sequence is full length 2403 immunoglobulin G (IgG)
CC antibody light chain (SF2.4H4.1E3) derived from murine light chain
CC variable region (VL) and human constant light chain region (CL). This
CC antibody binds to prostate stem cell antigen (PSCA) which is a single
CC subunit glycoprotein that is expressed on the cell surface as a
CC glycosylphosphatidylinositol (GPI)-anchored protein. The present
CC invention relates to anti-PSCA antibody composition and methods of
CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
CC killing the growth of PSCA-expressing cancer cells such as prostate
CC cancer, bladder cancer or lung cancer cells. Humanised antibody
CC conjugated to a toxin or a radioactive isotope is used for killing the
CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing
CC tumour cells in vivo and for inhibiting or killing these cells. The
CC antibodies are also useful for treating the above mentioned cancers and
CC for diagnosing and staging of PSCA-expressing cancer, for purification or
CC immunoprecipitation of PSCA from cells, and for detection and
CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC cancers by gene therapy techniques. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 238 AA;
Query Match 74.5%; Score 41; DB 4; Length 238;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 113 LQHLEPYT 121
| | | | |
RESULT 11
ABB07177
ID ABB07177 standard; protein; 101 AA.
XX
XX ABB07177;
AC
XX 13-MAR-2002 (first entry)
DT
XX Mouse 09 antibody kappa light chain 2 variable region.
DE
XX Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4;
KW ebvHIGM Msi19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; Msi19E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary; mouse.
XX
XX Mus sp.
OS
XX WO200185797-A1.
PN
XX 15-NOV-2001.
PD
XX 30-MAY-2000; 2000WO-US014902.
PF
XX 10-MAY-2000; 2000US-00568351.
PR
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
PA
XX Rodriguez M, Miller DJ, Pease LR;
PI
XX WPI; 2002-066596/09.
DR
XX N-PSDB; ABA94224.
XX
XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
XX Disclosure; Fig 36A-B; 219pp; English.
PS
XX The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHIGM22 (LYM 22), ebvHIGM Msi19D10, ebv HIGM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or Msi19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the mouse 09
XX antibody kappa light chain 2 variable region
SQ Sequence 101 AA;
Query Match 72.7%; Score 40; DB 5; Length 101;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
 Db 91 HNEYPYT 97

RESULT 12
 ADI26670
 ID ADI26670 standard; protein; 101 AA.
 AC ADI26670;
 XX
 DT 15-APR-2004 (first entry)
 DE Mouse anti oligodendrocyte antibody O9 V kappa 2 protein.
 XX Mouse; antibody; IgM; remyelination; neuronal growth; autoantibody;
 KW demyelination disease; multiple sclerosis; central nervous system; CNS;
 KW axon; glial cell proliferation;
 KW Theiler's murine encephalomyelitis virus infection; CNS injury;
 KW spinal cord injury.
 XX
 OS Mus sp.
 XX
 FN US2003185827-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 13-NOV-2001; 2001US-00010729.
 XX
 PR 29-APR-1994; 94US-00236520.
 PR 08-AUG-1996; 96US-00692084.
 PR 07-JAN-1997; 97US-00779784.
 PR 28-MAY-1999; 99US-00322862.
 PR 30-MAY-2000; 2000US-00580787.
 PR 05-DEC-2000; 2000US-00730473.
 XX
 PA (MAYO-) MAYO FOUND.
 XX
 PI Rodriguez M, Miller DU, Pease LR;
 XX
 DR WPI; 2004-119219/12.
 DR N-PSDB; ADI26671.
 XX
 PT New human immunoglobulin M antibody for treating or preventing a
 PT demyelinating disease of the central nervous system in a human or
 FT domestic animal, such as multiple sclerosis.
 XX
 PS Example 11; Fig 54; 159pp; English.
 XX
 CC The invention relates to an antibody (I) produced by injecting an
 CC immunocompetent host with an antibody peptide, and harvesting the
 CC antibody, where the peptide comprises a human anti-IgM antibody fragment
 CC given in the specification, or active fragments. Also included are
 CC stimulating remyelination of central nervous system (CNS) axons in a
 CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial
 CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs

and other agents for the ability to modulate the production or mimic the
 activities of mAb sHGM22, sHGM46, or combinations of them, a
 recombinant virus transformed with recombinant antibody nucleic acids or
 vector, imaging a portion of the CNS using the antibody and diagnosing or
 monitoring demyelination and/or remyelination of the CNS comprising using
 CNS image. The antibody is used to stimulate remyelination of CNS axons,
 and to stimulate the proliferation of glial cells in CNS axons,
 optionally in vitro. The antibody is used to treat or prevent a
 demyelinating disease of the CNS in a human or domestic animal, such as
 multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 preferably the mammal is a mouse infected with Strain DA of Theiler's
 murine encephalomyelitis virus. The antibody is used to treat a spinal
 cord injury and used to screen drugs and other agents for the ability to
 modulate the production or mimic the activities of the antibody. The
 antibody can be used to image a portion of the CNS which can be used to
 diagnose or monitor demyelination and/or remyelination of the CNS. The
 present sequence is a variable region of a mouse anti-IgM antibody (or
 fragment).

SQ Sequence 101 AA;
 Query Match 72.7%; Score 40; DB 8; Length 101;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
 Db 91 HNEYPYT 97
 :.|||||
 :.|||||

RESULT 13
 ADV66159
 ID ADV66159 standard; protein; 107 AA.
 XX
 AC ADV66159;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE Human EpCAM-specific antibody light chain variable domain - SEQ ID 82.
 XX
 KW bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EpCAM; tumor; cancer; cytostatic; light chain variable region.
 XX
 OS Unidentified.
 XX
 FN WO2004106383-A1.
 XX
 PD 09-DEC-2004.
 XX
 PF 26-MAY-2004; 2004WO-EP005687.
 XX
 PR 31-MAY-2003; 2003EP-00012133.
 PR 31-MAY-2003; 2003EP-00012134.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;
 XX
 DR WPI; 2005-021271/02.
 DR N-PSDB; ADV66158.
 XX
 PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX
 PS Claim 10; SEQ ID NO 82; 227pp; English.
 XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or

CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents an antibody
CC light chain variable domain that is specific for human EpcAM.

XX
XX
SQ Sequence 107 AA;

Query Match 72.7%; Score 40; DB 9; Length 107;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPVT 9
Db 91 HNEYPYT 97

RESULT 14
ADZ83517
ID ADZ83517 standard; protein; 107 AA.

XX AC ADZ83517;

XX DT 14-JUL-2005 (first entry)

XX DE AntiEpcam single chain antibody SEQ ID NO 139.

XX KW neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
KW Epcam; antibody.

XX OS Synthetic.

XX PN WO2005040220-A1.

XX PD 06-MAY-2005.

XX PF 15-OCT-2004; 2004WO-EP011646.

XX PR 16-OCT-2003; 2003EP-00023581.

XX PA (MICR-) MICROMET AG.

XX PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
XX Carr FU, Hamilton AA, Williams S;

XX DR WPI; 2005-333494/34.

XX DR N-PSDB; ADZ83516.

XX PT New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.

XX PS Example 8; SEQ ID NO 139; 639pp; English.

XX CC The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of an anti-Epcam single chain antibody.

XX SQ Sequence 107 AA;

Query Match 72.7%; Score 40; DB 9; Length 107;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPYT 9
Db 91 HNEYPYT 97

RESULT 15
ADI26700
ID ADI26700 standard; protein; 108 AA.

XX AC ADI26700;

XX DT 15-APR-2004 (first entry)

XX DE Mouse anti IgM antibody O1 kappa light chain protein.

XX KW Mouse; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW demyelination disease; multiple sclerosis; central nervous system; CNS;
KW axon; glial cell proliferation;
KW Theiler's murine encephalomyelitis virus infection; CNS injury;
KW spinal cord injury.

XX OS Mus sp.

XX PN US2003185827-A1.

XX PD 02-OCT-2003.

XX PF 13-NOV-2001; 2001US-00010729.

XX PR 29-APR-1994; 94US-00236520.

XX PR 08-AUG-1996; 96US-00692084.

XX PR 07-JAN-1997; 97US-00779784.

XX PR 28-MAY-1999; 99US-00322862.

XX PR 30-MAY-2000; 2000US-00580787.

XX PR 05-DEC-2000; 2000US-00730473.

XX PA (MAYO-) MAYO FOUND.

XX PI Rodriguez M, Miller DJ, Pease LR;

XX DR WPI; 2004-119219/12.

XX DR N-PSDB; ADI26701.

XX PT New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.

XX PS Example 19; Fig 58; 159pp; English.

XX CC The invention relates to an antibody (I) produced by injecting an
CC immunocompetent host with an antibody peptide, and harvesting the
CC antibody, where the peptide comprises a human anti-IgM antibody fragment
CC given in the specification, or active fragments. Also included are
CC stimulating remyelination of central nervous system (CNS) axons in a
CC mammal (comprising administering a monoclonal antibody, or mixtures,
CC monomers, active fragments, or recombinant antibodies derived from it,
CC characterised by their ability to bind structures and cells within the
CC CNS, including oligodendrocytes), stimulating the proliferation of glial
CC cells in CNS axons in a mammal (comprising administering a monoclonal
CC antibody, or mixtures, monomers, active fragments, or recombinant
CC antibodies derived from it, characterised by their ability to bind
CC structures and cells within the CNS), treating or preventing a
CC demyelinating disease of the CNS in a mammal (comprising administering a
CC monoclonal antibody, or mixtures, monomers, active fragments, or
CC recombinant antibodies derived from it, characterised by their ability to
CC bind structures and cells within the CNS, and to stimulate remyelination
CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
CC cells from mixed cell culture, stimulating remyelination of CNS axons in

CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of mAb sHlgM22, sHlgM46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-IgM antibody (or
 CC fragment).
 CC
 CC SQ Sequence 108 AA;

Query Match 72.7%; Score 40; DB 8; Length 108;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
 Db 91 HNEYPYT 97
 |:|||||

RESULT 16
 AAY17957
 ID AAY17957 standard; protein; 242 AA.
 XX
 AC AAY17957;
 XX
 XX
 XX 04-AUG-1999 (first entry)
 XX Mouse scFv fragment 3-1.
 XX
 XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 XX
 XX Mus sp.
 XX
 XX WO9925818-A1.
 XX
 XX 27-MAY-1999.
 XX
 XX 16-NOV-1998; 98WO-EP007313.
 XX
 XX 17-NOV-1997; 97EP-00120096.
 XX
 XX (KUFE/) KUFER P.
 XX
 XX Kufer P, Raum T, Borschert K, Zettl F, Lutterbues R;
 XX
 XX WPI; 1999-338004/28.
 XX N-PSDB; AAX77240.
 XX
 XX Phage display system for identification of binding site domains retaining
 XX capacity to bind an epitope.
 XX
 XX Claim 27; Fig 6.3; 152pp; English.
 XX
 XX The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or

CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences AAY17957-965 represent
 CC mouse scFv fragments
 CC
 CC SQ Sequence 242 AA;

Query Match 72.7%; Score 40; DB 2; Length 242;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
 Db 226 HNEYPYT 232
 |:|||||

RESULT 17
 AAY17961
 ID AAY17961 standard; protein; 242 AA.
 XX
 AC AAY17961;
 XX
 XX 04-AUG-1999 (first entry)
 XX Mouse scFv fragment 4-4.
 XX
 XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 XX
 XX Mus sp.
 XX
 XX WO9925818-A1.
 XX
 XX 27-MAY-1999.
 XX
 XX 16-NOV-1998; 98WO-EP007313.
 XX
 XX 17-NOV-1997; 97EP-00120096.
 XX
 XX (KUFE/) KUFER P.
 XX
 XX Kufer P, Raum T, Borschert K, Zettl F, Lutterbues R;
 XX
 XX WPI; 1999-338004/28.
 XX N-PSDB; AAX77244.
 XX
 XX Phage display system for identification of binding site domains retaining
 XX capacity to bind an epitope.
 XX
 XX Claim 27; Fig 6.7; 152pp; English.
 XX
 XX The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or

CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences AAV17957-965 represent
 CC mouse scFV fragments
 XX
 SQ Sequence 242 AA;

Query Match 72.7%; Score 40; DB 2; Length 242;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
 Db 226 HNEYPT 232
 |:|||||

RESULT 18
 AAV17959
 ID AAV17959 standard; protein; 242 AA.
 AC AAV17959;
 XX
 DT 04-AUG-1999 (first entry)
 XX
 DE Mouse scFV fragment 3-8.
 XX
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 XX

OS Mus sp.
 XX
 XX WO925818-A1.
 PN
 XX 27-MAY-1999.
 PD
 XX
 PF 16-NOV-1998; 98WO-EP007313.
 XX
 PR 17-NOV-1997; 97EP-00120096.
 XX
 XX (KUPE/) KUPER P.
 PA

PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbueser R;
 DR WPI; 1999-338004/28.
 DR N-PSDB; AAX77242.
 XX
 PT Phage display system for identification of binding site domains retaining
 PT capacity to bind an epitope.

PS Claim 27; Fig 6.5; 152pp; English.

XX
 CC The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences AAV17957-965 represent
 CC mouse scFV fragments

XX Sequence 242 AA;

Query Match 72.7%; Score 40; DB 2; Length 242;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
 Db 226 HNEYPT 232
 |:|||||

RESULT 19
 ADZ83409
 ID ADZ83409 standard; protein; 491 AA.

XX AC ADZ83409;

XX 14-JUL-2005 (first entry)

XX C-terminal EpCam binder SEQ ID NO 31.

XX neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
 KW EpCam.

XX Synthetic.

XX WO2005040220-A1.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011646.

XX 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FU, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.
 DR N-PSDB; ADZ83408.

XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.

PS Claim 20; SEQ ID NO 31; 639pp; English.

XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of an anti-EpCam binder.

XX Sequence 491 AA;

Query Match 72.7%; Score 40; DB 9; Length 491;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
 XX WPI: 2005-021271/02.
 DR N-PSDB; ADV66124.
 XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX Claim 12; SEQ ID NO 48; 227pp; English.
 XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.
 XX SQ Sequence 497 AA;
 Query Match 72.7%; Score 40; DB 9; Length 497;
 Best Local Similarity 85.7%; Pred. NO. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HSEYPYPT 9
 DB 475 HNEYPT 481
 RESULT 23
 AD283427
 ID AD283427 standard; protein; 506 AA.
 XX AC AD283427;
 XX 14-JUL-2005 (first entry)
 XX Deimmunized construct 3-1xanti-CD3.
 DE neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
 XX Synthetic.
 OS WO2005040220-A1.
 XX 06-MAY-2005.
 XX 15-OCT-2004; 2004WO-EP011646.
 XX 16-OCT-2003; 2003EP-00023581.
 XX (MICR-) MICROMET AG.
 XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FJ, Hamilton AA, Williams S;
 XX WPI: 2005-333494/34.
 DR N-PSDB; AD283426.
 XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX Claim 20; SEQ ID NO 49; 639pp; English.
 XX The invention relates to a cytotoxically active CD3 specific binding

CC construct comprises a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of deimmunized construct 3-1xanti-CD3.
 XX SQ Sequence 506 AA;
 Query Match 72.7%; Score 40; DB 9; Length 506;
 Best Local Similarity 85.7%; Pred. NO. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HSEYPYPT 9
 DB 110 HNEYPT 116
 RESULT 24
 ADV66113
 ID ADV66113 standard; protein; 515 AA.
 XX AC ADV66113;
 XX 24-FEB-2005 (first entry)
 XX Anti-CD3-anti-EPCAM bispecific single chain antibody - SEQ ID 36.
 DE bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EPCAM; CD3; tumor; cancer; cytostatic.
 XX Unidentified.
 OS WO2004106383-A1.
 XX 09-DEC-2004.
 XX 26-MAY-2004; 2004WO-EP005687.
 XX 31-MAY-2003; 2003EP-00012133.
 XX 31-MAY-2003; 2003EP-00012134.
 XX (MICR-) MICROMET AG.
 XX Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
 XX WPI: 2005-021271/02.
 DR N-PSDB; ADV66112.
 XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX Claim 12; SEQ ID NO 36; 227pp; English.
 XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

```

XX SQ Sequence 515 AA;
Query Match 72.7%; Score 40; DB 9; Length 515;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
Db 110 HNEYPT 116

RESULT 25
ADI16955
ID ADI16955 standard; protein; 2346 AA.
XX AC ADI16955;
XX DT 15-APR-2004 (first entry)
XX DE Murine NOVX protein homologue SeqID 491.
XX KW mouse; murine; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infect.
XX OS Mus musculus.
XX PN WO200268649-A2.
XX PD 06-SEP-2002.
XX PF 31-JAN-2002; 2002WO-US002785.
XX PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273045P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.

30-MAY-2001; 2001US-0294473P.
08-JUN-2001; 2001US-0296964P.
18-JUN-2001; 2001US-0298959P.
19-JUN-2001; 2001US-0299324P.
13-AUG-2001; 2001US-0312020P.
16-AUG-2001; 2001US-0312889P.
21-AUG-2001; 2001US-0312908P.
28-AUG-2001; 2001US-0313390P.
31-AUG-2001; 2001US-0315470P.
07-SEP-2001; 2001US-0316447P.
07-SEP-2001; 2001US-0318115P.
12-SEP-2001; 2001US-0318118P.
19-SEP-2001; 2001US-0318740P.
18-OCT-2001; 2001US-0323379P.
18-OCT-2001; 2001US-0330245P.
18-OCT-2001; 2001US-0330308P.
14-NOV-2001; 2001US-0332701P.
XX PA (CURA-) CURAGEN CORP.
XX PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RU, Gusev VI, Colman SD, Wolenc AR, Pena CEA;
XX Furtak K, Grosse WM, Alcobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX Disclosure; SEQ ID NO 491; 1498pp; English.
XX This invention relates to a novel nucleic acids, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments of
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
XX and epilepsy. Accordingly, these molecules have many activities including
XX cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
XX haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
XX antiathmatic, nephrotropic, antiarthritic, hepatotropic,
XX neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
XX relaxant and anticonvulsant. In addition, they are useful in screening
XX assays to identify small molecules that modulate or inhibit, for example,
XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX used as in chromosome mapping, tissue typing, preventive medicine and
XX pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
XX of the invention.
SQ Sequence 2346 AA;

Query Match 72.7%; Score 40; DB 5; Length 2346;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSSEYPT 9
Db 534 LHYSEYGT 542

RESULT 26

```


ADR38971
ID ADR38971 standard; peptide; 9 AA.
XX
AC ADR38971;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse light chain anti-BoNT-antibody CD3 seqid 273.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; light chain;
KW CDR3; complementarity determining region 1.
XX
OS Mus sp.
XX
XX US2004175385-A1.
XX
XX 09-SEP-2004.
XX
XX 01-AUG-2003; 2003US-00632706.
XX
XX 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX Marks JD, Amersdorfer P;
PI WPI; 2004-652009/63.
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX Example 4; SEQ ID NO 273; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (i) binds to and neutralises botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C39, IC6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
XX 3-8, 3-10 and INGI, where (i) binds to and neutralizes botulinum
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
XX comprising BoNT/A neutralising epitope having an epitope that is
XX specifically bound by an antibody expressed by clones as mentioned in (I)
XX ; producing (I); and a composition (III) comprising several anti-
XX botulinum neurotoxin antibodies, where each antibody is specific for a
XX different epitope of a botulinum neurotoxin and the combination of
XX antibodies shows greater toxin neutralisation than the single antibodies
XX in surplus. The following are disclosed: a pharmaceutical composition
XX comprising (I); and a kit comprising (I). (I) is useful for neutralising
XX BoNT/A antibody and for neutralising a botulinum neurotoxin which
XX involves contacting neurotoxin with (I) in surplus, where each of (I) is
XX specific for a different epitope of the botulinum neurotoxin and the
XX combination of antibodies shows greater toxin neutralisation than the
XX single antibodies in surplus. (I) is useful for diagnosing the botulism
XX or for treating pathologies associated with botulinum neurotoxin
XX poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
XX enables rapid detection or diagnosis of botulism. This is the amino acid
XX sequence of mouse light chain anti-BoNT-antibody CDR3.
SQ Sequence 9 AA;

Query Match 70.9%; Score 39; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 HSEVPT 9
|:|:|:|:|
DB 2 HYSTVPT 9

RESULT 27
AEA44021
ID AEA44021 standard; peptide; 9 AA.
XX
AC AEA44021;
XX
DT 25-AUG-2005 (first entry)
XX
DE Anti-TPO antibody CDR 3 SEQ ID NO 86.
XX
XX hemostatic; single chain antibody; protein purification;
KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
KW hematological disease.
XX
XX Unidentified.
XX WO2005056604-A1.
XX
XX 23-JUN-2005.
XX
XX 10-DEC-2004; 2004WO-JP018506.
XX
XX 12-DEC-2003; 2003JP-00415746.
PR 12-MAR-2004; 2004JP-00071763.
PR 27-AUG-2004; 2004JP-00248323.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
XX
XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
PI WPI; 2005-445149/45.
XX
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
XX genetically-engineered antihuman Mpl diabody, applicable in drug
XX compositions for use in chemotherapy of thrombocytopenia and other
XX diseases associated with Mpl mutation.
XX
XX Claim 17; SEQ ID NO 86; 106pp; Japanese.
XX
XX The invention describes an antibody is a single-chain polypeptide with
XX TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
XX heavy-chain variable regions and 2 light-chain variable regions. Also
XX described are: a chimeric antibody for binding with Mpl; an antibody for
XX binding with soluble Mpl; antibodies for binding with human Mpl and
XX monkey Mpl; antibodies with agonistic activity against human Mpl and
XX monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
XX with TPO agonistic activity; antibodies containing a heavy-chain variable
XX region with CDR (complementary-determinant regions 1, 2 and 3);
XX antibodies containing a light-chain variable region with CDR 1 2 and 3;
XX antibodies containing heavy and light-chain variable regions with CDR 1,
XX 2 and 3 selected from the already-specified groups in 18 combinations;
XX antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4;
XX antibodies containing a light-chain variable region with FR1, 2, 3 and 4;
XX epitope-recognizing antibodies that can recognize the antibodies with the
XX heavy and light-chain variable regions and amino acid sequences;
XX antibodies that can recognize the amino acid moiety in human Mpl from
XX positions 26-274; polynucleotides encoding these antibodies;
XX polynucleotides hybridizable with the polynucleotides that encode the
XX antibodies under stringent conditions and the antibodies encoded by which
XX have equivalent activity as such antibodies; vectors containing these
XX polynucleotides; host cells carrying such polynucleotides or vectors; and
XX drug compositions containing these antibodies. The antibodies are
XX applicable in drug compositions for use in chemotherapy of
XX thrombocytopenia and other diseases associated with Mpl mutation such as
XX congenital amegakaryocytic thrombocytopenia. These antibodies can include
XX antihuman Mpl antibody and variants like genetically-engineered antihuman
XX Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
XX soluble to enhance binding ability. The diabody and sc(Fv)2 show high
XX agonistic activity against antihuman Mpl antibody, such activity of which
XX is comparable or superior to that of the natural ligand, human TPO. This
XX is the amino acid sequence of an anti-TPO antibody complementarity
XX determining region (CDR).

XX SQ Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LHHSEYPT 9
 : |||||
 Db 1 MQHVEYPT 9

RESULT 28
 AEA44003
 ID AEA44003 standard; peptide; 9 AA.
 XX AEA44003;
 XX 25-AUG-2005 (first entry)
 XX Anti-TPO antibody CDR 3 SEQ ID NO 68.
 XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 XX WO2005056604-A1.
 XX 23-JUN-2005.
 XX 10-DEC-2004; 2004WO-JP018506.
 XX 12-DEC-2003; 2003JP-00415746.
 PR 12-MAR-2004; 2004JP-00071763.
 PR 27-AUG-2004; 2004JP-00248323.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 XX WPI; 2005-445149/45.
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 XX Disclosure; SEQ ID NO 68; 106pp; Japanese.

XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups with CDR 1,
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and

CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).

XX SQ Sequence 9 AA;
 Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LHHSEYPT 9
 : |||||
 Db 1 MQHVEYPT 9

RESULT 29
 AEA44012
 ID AEA44012 standard; peptide; 9 AA.
 XX AEA44012;
 XX 25-AUG-2005 (first entry)
 XX Anti-TPO antibody CDR 3 SEQ ID NO 77.
 XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 XX WO2005056604-A1.
 XX 23-JUN-2005.
 XX 10-DEC-2004; 2004WO-JP018506.
 XX 12-DEC-2003; 2003JP-00415746.
 PR 12-MAR-2004; 2004JP-00071763.
 PR 27-AUG-2004; 2004JP-00248323.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 XX WPI; 2005-445149/45.
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 XX Disclosure; SEQ ID NO 77; 106pp; Japanese.

XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups with CDR 1,
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and

CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).

XX Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. NO. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9

DB : | |||||
 1 MQHLEYPYT 9

RESULT 30

AEA44042
 ID AEA44042 standard; peptide; 9 AA.

AC AEA44042;

DT 25-AUG-2005 (first entry)

XX Anti-TPO antibody CDR 3 SEQ ID NO 107.

XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.

XX Unidentified.

XX WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX WPI; 2005-445149/45.

XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.

PS Disclosure; SEQ ID NO 107; 106pp; Japanese.

XX

CC The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).

XX Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. NO. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9

DB : | |||||
 1 MQHLEYPYT 9

RESULT 31

AEA44018

ID AEA44018 standard; peptide; 9 AA.

AC AEA44018;

XX 25-AUG-2005 (first entry)

XX Anti-TPO antibody CDR 3 SEQ ID NO 83.

XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.

XX Unidentified.

XX WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.

XX (CHUS) CHUGAI SEIYAKU KK.

XX

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PI Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
XX WPI; 2005-445149/45.
XX
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
XX genetically-engineered antihuman Mpl diabody, applicable in drug
XX compositions for use in chemotherapy of thrombocytopenia and other
XX diseases associated with Mpl mutation.
XX
XX Disclosure; SEQ ID NO 83; 106pp; Japanese.
XX
XX The invention describes an antibody is a single-chain polypeptide with
XX TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
XX heavy-chain variable regions and 2 light-chain variable regions. Also
XX described are: a chimeric antibody for binding with Mpl; an antibody for
XX binding with soluble Mpl; antibodies for binding with human Mpl and
XX monkey Mpl; antibodies with agonistic activity against human Mpl and
XX monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
XX with TPO agonistic activity; antibodies containing a heavy-chain variable
XX region with CDR (complementary-determinant regions 1, 2 and 3);
XX antibodies containing a light-chain variable region with CDR 1, 2 and 3;
XX antibodies containing a heavy-chain variable region with CDR 1, 2 and 3;
XX antibodies containing a light-chain variable region with FRI, 2, 3 and 4;
XX epitope-recognizing antibodies that can recognize the antibodies with the
XX heavy and light-chain variable regions and amino acid sequences;
XX antibodies that can recognize the amino acid moiety in human Mpl from
XX positions 26-274; polynucleotides encoding these antibodies;
XX polynucleotides hybridizable with the polynucleotides that encode the
XX antibodies under stringent conditions and the antibodies encoded by which
XX have equivalent activity as such antibodies; vectors containing these
XX polynucleotides; host cells carrying such polynucleotides or vectors; and
XX drug compositions containing these antibodies. The antibodies are
XX applicable in drug compositions for use in chemotherapy of
XX thrombocytopenia and other diseases associated with Mpl mutation such as
XX congenital amegakaryocytic thrombocytopenia. These antibodies can include
XX antihuman Mpl antibody and variants like genetically-engineered antihuman
XX Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
XX soluble to enhance binding ability. The diabody and sc(Fv)2 show high
XX agonistic activity against antihuman Mpl antibody, such activity of which
XX is comparable or superior to that of the natural ligand, human TPO. This
XX is the amino acid sequence of an anti-TPO antibody complementarity
XX determining region (CDR).
XX
XX Sequence 9 AA;
XX
XX Query Match 70.9%; Score 39; DB 9; Length 9;
XX Best Local Similarity 66.7%; Pred. NO. 2e+06;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 LHHSEYPT 9
XX : | |||||
XX Db 1 MQHLEYPT 9
XX
XX RESULT 32
XX AEA44024
XX ID AEA44024 standard; peptide; 9 AA.
XX AC AEA44024;
XX
XX DT 25-AUG-2005 (first entry)
XX
XX DE Anti-TPO antibody CDR 3 SEQ ID NO 89.
XX
XX KW hemostatic; single chain antibody; protein purification;
XX antibody engineering; antibody production; thrombocytopenia; hemostatic;
XX hematological disease.
XX
XX OS Unidentified.
XX
XX FN WO2005056604-A1.

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XX 23-JUN-2005.
XX
XX 10-DEC-2004; 2004WO-JP018506.
XX
XX 12-DEC-2003; 2003JP-00415746.
XX
XX 12-MAR-2004; 2004JP-00071763.
XX
XX 27-AUG-2004; 2004JP-00248323.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
XX WPI; 2005-445149/45.
XX
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
XX genetically-engineered antihuman Mpl diabody, applicable in drug
XX compositions for use in chemotherapy of thrombocytopenia and other
XX diseases associated with Mpl mutation.
XX
XX Disclosure; SEQ ID NO 89; 106pp; Japanese.
XX
XX The invention describes an antibody is a single-chain polypeptide with
XX TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
XX heavy-chain variable regions and 2 light-chain variable regions. Also
XX described are: a chimeric antibody for binding with Mpl; an antibody for
XX binding with soluble Mpl; antibodies for binding with human Mpl and
XX monkey Mpl; antibodies with agonistic activity against human Mpl and
XX monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
XX with TPO agonistic activity; antibodies containing a heavy-chain variable
XX region with CDR (complementary-determinant regions 1, 2 and 3);
XX antibodies containing a light-chain variable region with CDR 1, 2 and 3;
XX antibodies containing a heavy-chain variable region with CDR 1, 2 and 3;
XX antibodies containing a light-chain variable region with FRI, 2, 3 and 4;
XX epitope-recognizing antibodies that can recognize the antibodies with the
XX heavy and light-chain variable regions and amino acid sequences;
XX antibodies that can recognize the amino acid moiety in human Mpl from
XX positions 26-274; polynucleotides encoding these antibodies;
XX polynucleotides hybridizable with the polynucleotides that encode the
XX antibodies under stringent conditions and the antibodies encoded by which
XX have equivalent activity as such antibodies; vectors containing these
XX polynucleotides; host cells carrying such polynucleotides or vectors; and
XX drug compositions containing these antibodies. The antibodies are
XX applicable in drug compositions for use in chemotherapy of
XX thrombocytopenia and other diseases associated with Mpl mutation such as
XX congenital amegakaryocytic thrombocytopenia. These antibodies can include
XX antihuman Mpl antibody and variants like genetically-engineered antihuman
XX Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
XX soluble to enhance binding ability. The diabody and sc(Fv)2 show high
XX agonistic activity against antihuman Mpl antibody, such activity of which
XX is comparable or superior to that of the natural ligand, human TPO. This
XX is the amino acid sequence of an anti-TPO antibody complementarity
XX determining region (CDR).
XX
XX Sequence 9 AA;
XX
XX Query Match 70.9%; Score 39; DB 9; Length 9;
XX Best Local Similarity 66.7%; Pred. NO. 2e+06;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 LHHSEYPT 9
XX : | |||||
XX Db 1 MQHLEYPT 9
XX
XX RESULT 33
XX AEA44015
XX ID AEA44015 standard; peptide; 9 AA.
XX
XX AC AEA44015;
XX
XX
XX
XX

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DT 25-AUG-2005 (first entry)
 XX Anti-TPO antibody CDR 3 SEQ ID NO 80.
 XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 OS WO2005056604-A1.
 XX 23-JUN-2005.
 XX 10-DEC-2004; 2004WO-JP018506.
 PF 12-DEC-2003; 2003JP-00415746.
 PR 12-MAR-2004; 2004JP-00071763.
 PR 27-AUG-2004; 2004JP-00248323.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 XX WPI; 2005-445149/45.
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 XX Claim 17; SEQ ID NO 80; 106pp; Japanese.
 PS The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FR1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX Sequence 9 AA;
 SQ
 Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
 : | |||||
 Db 1 MQHLEYPYT 9
 RESULT 34
 AEA44027
 ID AEA44027 standard; peptide; 9 AA.
 XX AEA44027;
 XX 25-AUG-2005 (first entry)
 XX Anti-TPO antibody CDR 3 SEQ ID NO 92.
 DE hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 OS WO2005056604-A1.
 XX 23-JUN-2005.
 XX 10-DEC-2004; 2004WO-JP018506.
 PF 12-DEC-2003; 2003JP-00415746.
 PR 12-MAR-2004; 2004JP-00071763.
 PR 27-AUG-2004; 2004JP-00248323.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 XX WPI; 2005-445149/45.
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 XX Disclosure; SEQ ID NO 92; 106pp; Japanese.
 PS The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FR1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX Sequence 9 AA;
 SQ

CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).

XX Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2;

Qy 1 LHHSEYPYT 9
 : | |||||
 Db 1 MQHLEYPYT 9

RESULT 35
 AEA44036
 ID AEA44036 standard; peptide; 9 AA.

XX AC AEA44036;

XX DT 25-AUG-2005 (first entry)

XX DE Anti-TPO antibody CDR 3 SEQ ID NO 101.

XX KW hemostatic; single chain antibody; protein purification;
 XX KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 XX KW hematological disease.

XX OS Unidentified.

XX PN WO2005056604-A1.

XX PD 23-JUN-2005.

XX PF 10-DEC-2004; 2004WO-JP018506.

XX PR 12-DEC-2003; 2003JP-00415746.

XX PR 12-MAR-2004; 2004JP-00071763.

XX PR 27-AUG-2004; 2004JP-00248323.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX DR WPI; 2005-445149/45.

XX PT Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 XX PT genetically-engineered antihuman Mpl diabody, applicable in drug
 XX PT compositions for use in chemotherapy of thrombocytopenia and other
 XX PT diseases associated with Mpl mutation.

XX PS Disclosure; SEQ ID NO 101; 106pp; Japanese.

XX CC The invention describes an antibody is a single-chain polypeptide with
 XX CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 XX CC heavy-chain variable regions and 2 light-chain variable regions. Also
 XX CC described are: a chimeric antibody for binding with Mpl; an antibody for
 XX CC binding with soluble Mpl; antibodies for binding with human Mpl and
 XX CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 XX CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 XX CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 XX CC region with CDR (complementary-determinant regions 1, 2 and 3);
 XX CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 XX CC antibodies containing heavy and light-chain variable regions with CDR 1,
 XX CC 2 and 3 selected from the already-specified groups in 18 combinations;
 XX CC antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4;
 XX CC antibodies containing a light-chain variable region FR1, 2, 3 and 4;
 XX CC epitope-recognizing antibodies that can recognize the antibodies with the
 XX CC heavy and light-chain variable regions and amino acid sequences;
 XX CC antibodies that can recognize the amino acid moiety in human Mpl from
 XX CC positions 26-274; polynucleotides encoding these antibodies;

CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).

XX SQ Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2;

Qy 1 LHHSEYPYT 9
 : | |||||
 Db 1 MQHLEYPYT 9

RESULT 36
 AEA44009
 ID AEA44009 standard; peptide; 9 AA.

XX AC AEA44009;

XX DT 25-AUG-2005 (first entry)

XX DE Anti-TPO antibody CDR 3 SEQ ID NO 74.

XX KW hemostatic; single chain antibody; protein purification;
 XX KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 XX KW hematological disease.

XX OS Unidentified.

XX PN WO2005056604-A1.

XX PD 23-JUN-2005.

XX PF 10-DEC-2004; 2004WO-JP018506.

XX PR 12-DEC-2003; 2003JP-00415746.

XX PR 12-MAR-2004; 2004JP-00071763.

XX PR 27-AUG-2004; 2004JP-00248323.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX DR WPI; 2005-445149/45.

XX PT Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 XX PT genetically-engineered antihuman Mpl diabody, applicable in drug
 XX PT compositions for use in chemotherapy of thrombocytopenia and other
 XX PT diseases associated with Mpl mutation.

XX PS Disclosure; SEQ ID NO 74; 106pp; Japanese.

XX CC The invention describes an antibody is a single-chain polypeptide with
 XX CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 XX CC heavy-chain variable regions and 2 light-chain variable regions. Also
 XX CC described are: a chimeric antibody for binding with Mpl; an antibody for
 XX CC binding with soluble Mpl; antibodies for binding with human Mpl and
 XX CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 XX CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies

CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRL 1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRL 1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC anti-human Mpl antibody and variants like genetically-engineered anti-human
 CC Mpl diabody and (humanized) anti-human Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against anti-human Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEVPYT 9
 : | |||||
 Db 1 MQHLEYPYT 9

RESULT 37
 AEA44033
 ID AEA44033 standard; peptide; 9 AA.
 XX AEA44033;
 AC AEA44033;

25-AUG-2005 (first entry)

DE Anti-TPO antibody CDR 3 SEQ ID NO 98.

KW hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.

OS Unidentified.

PN WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX WPI; 2005-445149/45.

XX Anti-Mpl antibodies including anti-human Mpl antibody and variants like

PT genetically-engineered anti-human Mpl diabody, applicable in drug

PT compositions for use in chemotherapy of thrombocytopenia and other

PT diseases associated with Mpl mutation.
 XX Claim 17; SEQ ID NO 98; 106pp; Japanese.

CC The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRL 1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRL 1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC anti-human Mpl antibody and variants like genetically-engineered anti-human
 CC Mpl diabody and (humanized) anti-human Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against anti-human Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX Sequence 9 AA;

Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEVPYT 9
 : | |||||
 Db 1 MQHLEYPYT 9

RESULT 38
 AEA44000
 ID AEA44000 standard; peptide; 9 AA.
 XX AEA44000;
 AC AEA44000;

25-AUG-2005 (first entry)

DE Anti-TPO antibody CDR 3 SEQ ID NO 65.

KW hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.

OS Unidentified.

PN WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 XX WPI; 2005-445149/45.
 XX
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 XX
 XX Claim 17; SEQ ID NO 65; 106pp; Japanese.
 XX
 XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC epitopes recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPT 9
 : | |||||
 Db 1 MQHLEYPT 9
 : | |||||
 RESULT 39
 AEA44006
 ID AEA44006 standard; peptide; 9 AA.
 XX
 AC AEA44006;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Anti-TPO antibody CDR 3 SEQ ID NO 71.
 XX
 KW hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.

XX Unidentified.
 OS
 FN WO200505604-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-JP018506.
 XX
 PR 12-DEC-2003; 2003JP-00415746.
 PR 12-MAR-2004; 2004JP-00071763.
 PR 27-AUG-2004; 2004JP-00248323.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 PI WPI; 2005-445149/45.
 DR
 DR
 XX
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.
 PT
 XX
 XX Disclosure; SEQ ID NO 71; 106pp; Japanese.
 PS
 XX
 XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC epitopes recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC is the amino acid sequence of an anti-TPO antibody complementarity
 CC determining region (CDR).
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 70.9%; Score 39; DB 9; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPT 9
 : | |||||
 Db 1 MQHLEYPT 9
 : | |||||
 RESULT 40
 AAY14406

ID AAY14406 standard; peptide; 14 AA.
 AC AAY14406;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Peptide CDR-L3 derived from anti-HCV Ser/Thr protease MAb 8D4.
 XX
 KW Complementarity determining region; CDR; monoclonal antibody; MAb;
 KW hepatitis C virus; HCV; protease; binding site.
 XX
 OS Synthetic.
 XX
 PN JP11127861-A.
 XX
 PD 18-MAY-1999.
 XX
 PF 29-OCT-1997; 97JP-00297451.
 XX
 PR 29-OCT-1997; 97JP-00297451.
 XX
 PA (NIHA) JAPAN ENERGY CORP.
 XX
 DR WPI; 1999-350322/30.
 XX
 XX Neutralized antibody partial peptide derived from hepatitis C virus -
 PT useful for inhibiting Hepatitis C Virus (HCV) serine protease activity.
 XX
 PS Example 1; Page 13; 32pp; Japanese.
 XX
 CC This sequence represents a peptide derived for the sequence of the light
 CC chain variable region complementarity determining region (CDR)-3 of the
 CC anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (MAb)
 CC 8D4 protein. The invention relates to the use of partial peptides
 CC (AAY14348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease
 CC activity
 XX
 SQ Sequence 14 AA;
 Query Match 70.9%; Score 39; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 6.4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPYT 9
 : | |||||
 Db 4 MQHLEYPYT 12
 RESULT 41
 AAY24099
 ID AAY24099 standard; protein; 112 AA.
 XX
 AC AAY24099;
 XX
 DT 09-SEP-1999 (first entry)
 XX
 DE Figure 11 protein from WO9933968.
 XX
 KW HIV; surface protein; gp41; antibody catalyst; monoclonal antibody;
 KW anti-viral; anti-cancer; anti-thrombotic.
 XX
 OS Unidentified.
 XX
 PN WO9933968-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 25-DEC-1998; 98WO-JP005961.
 XX
 PR 26-DEC-1997; 97JP-00359799.
 PR 25-JUN-1998; 98JP-00177921.
 XX
 PA (UDAT/) UDA T.
 XX
 XX Uda T;
 PI WPI; 1999-419103/35.
 DR
 XX
 XX Production of antibody catalysts, useful as anti-virals, anti-cancer
 PT agents, anti-thrombotics, and general enzymes.
 XX
 XX Example 14; Fig 11; 44pp; Japanese.
 PS
 XX The present invention describes a new process for producing an antibody
 CC catalyst capable of cleaving and/or decomposing a target protein or
 CC peptide. The process comprises the construction of a monoclonal antibody
 CC with use of the protein, peptide or peptide fragment as antigen, and
 CC recovering the antibody catalyst from the produced monoclonal antibody.
 CC The antibody catalysts can be used as anti-virals, anti-cancer agents,
 CC anti-thrombotics, and general enzymes, for example, the anti-gp 41
 CC antibody light chain is capable of cleaving the peptide YP41-I and
 CC protein gp41 of HIV which is therefore a good anti-HIV agent. The present
 CC sequence represents a protein used in an example from the present
 CC invention
 XX
 SQ Sequence 112 AA;
 Query Match 70.9%; Score 39; DB 2; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPYT 9
 : | |||||
 Db 94 MQHLEYPYT 102
 RESULT 42
 AEA89804
 ID AEA89804 standard; protein; 112 AA.
 XX
 AC AEA89804;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Antibody activity-related mouse Vb16 protein region SeqID27.
 XX
 KW antibody engineering; cytostatic; apoptosis stimulation; cancer;
 KW therapeutic.
 XX
 OS Mus musculus.
 XX
 PN WO2005056798-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-JP018493.
 XX
 PR 12-DEC-2003; 2003JP-00415760.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Yabuta N, Tsunoda H, Tsuchiya M;
 XX
 DR WPI; 2005-479085/48.
 XX
 XX Reinforcing activity of antibody e.g. antihuman Mpl antibody by coupling
 PT heavy chain variable domains to light chain variable domains by linker,
 PT to produce single chain polypeptide.
 XX
 PS Example 2; SEQ ID NO 27; 44pp; Japanese.
 XX
 XX This invention relates to a novel method of reinforcing activity of an
 CC antibody, for example antihuman Mpl antibody. The method comprises
 CC coupling 2 or more heavy chain variable domains to 2 or more light chain
 CC variable domains by a linker to produce a single chain polypeptide, or
 CC coupling a first polypeptide having a heavy chain and light chain

CC variable domain of an antibody and a second polypeptide having a heavy
 CC chain and light chain variable domain of an antibody by a linker. The
 CC invention may be useful for the development of compounds with a
 CC cytosolic activity acting as a stimulator of apoptosis. The method is
 CC useful for reinforcing activity of an antibody which may be useful for
 CC treating cancer. The method enables an increase in the agonistic activity
 CC of the antibody, which is highly stable. The present sequence is that of
 CC a region of a mouse protein which was used in the exemplification of the
 CC invention.

XX
 XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHMSEYPT 9
 : | |||||
 Db 94 MQHLEYPT 102

RESULT 43
 AEA89802
 ID AEA89802 standard; protein; 112 AA.
 XX
 AC AEA89802;
 DT 25-AUG-2005 (first entry)
 XX
 DE Antibody activity-related mouse VB45B protein region SeqID25.
 XX
 KW antibody engineering; cytostatic; apoptosis stimulation; cancer;
 KW therapeutic.
 XX
 OS Mus musculus.
 XX
 PN WO2005056798-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-JP018493.
 XX
 PR 12-DEC-2003; 2003JP-00415760.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Yabuta N, Tsunoda H, Tsuchiya M;
 XX
 DR WPI; 2005-479085/48.
 XX
 PT Reinforcing activity of antibody e.g. antihuman Mpl antibody by coupling
 PT heavy chain variable domains to light chain variable domains by linker,
 PT to produce single chain polypeptide.
 XX
 PS Example 2; SEQ ID NO 25; 44pp; Japanese.
 XX
 CC This invention relates to a novel method of reinforcing activity of an
 CC antibody, for example antihuman Mpl antibody. The method comprises
 CC coupling 2 or more heavy chain variable domains to 2 or more light chain
 CC variable domains by a linker to produce a single chain polypeptide, or
 CC coupling a first polypeptide having a heavy chain and light chain
 CC variable domain of an antibody and a second polypeptide having a heavy
 CC chain and light chain variable domain of an antibody by a linker. The
 CC invention may be useful for the development of compounds with a
 CC cytosolic activity acting as a stimulator of apoptosis. The method is
 CC useful for reinforcing activity of an antibody which may be useful for
 CC treating cancer. The method enables an increase in the agonistic activity
 CC of the antibody, which is highly stable. The present sequence is that of
 CC a region of a mouse protein which was used in the exemplification of the
 CC invention.

XX
 XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHMSEYPT 9
 : | |||||
 Db 94 MQHLEYPT 102

RESULT 44
 AEA89801
 ID AEA89801 standard; protein; 112 AA.
 XX
 AC AEA89801;
 DT 25-AUG-2005 (first entry)
 XX
 DE Antibody activity-related mouse VB140 protein region SeqID24.
 XX
 KW antibody engineering; cytostatic; apoptosis stimulation; cancer;
 KW therapeutic.
 XX
 OS Mus musculus.
 XX
 PN WO2005056798-A1.
 XX
 PD 23-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-JP018493.
 XX
 PR 12-DEC-2003; 2003JP-00415760.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ohtomo T, Yabuta N, Tsunoda H, Tsuchiya M;
 XX
 DR WPI; 2005-479085/48.
 XX
 PT Reinforcing activity of antibody e.g. antihuman Mpl antibody by coupling
 PT heavy chain variable domains to light chain variable domains by linker,
 PT to produce single chain polypeptide.
 XX
 PS Example 2; SEQ ID NO 24; 44pp; Japanese.
 XX
 CC This invention relates to a novel method of reinforcing activity of an
 CC antibody, for example antihuman Mpl antibody. The method comprises
 CC coupling 2 or more heavy chain variable domains to 2 or more light chain
 CC variable domains by a linker to produce a single chain polypeptide, or
 CC coupling a first polypeptide having a heavy chain and light chain
 CC variable domain of an antibody and a second polypeptide having a heavy
 CC chain and light chain variable domain of an antibody by a linker. The
 CC invention may be useful for the development of compounds with a
 CC cytosolic activity acting as a stimulator of apoptosis. The method is
 CC useful for reinforcing activity of an antibody which may be useful for
 CC treating cancer. The method enables an increase in the agonistic activity
 CC of the antibody, which is highly stable. The present sequence is that of
 CC a region of a mouse protein which was used in the exemplification of the
 CC invention.

XX
 XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHMSEYPT 9
 : | |||||
 Db 94 MQHLEYPT 102

RESULT 45
 AEA44068
 ID AEA44068 standard; protein; 112 AA.

XX AEA44068;
AC 25-AUG-2005 (first entry)
XX Anti-TPO antibody associated polypeptide SEQ ID NO 133.
XX hemostatic; single chain antibody; protein purification;
KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
KW hematological disease.
XX Unidentified.
XX WO2005056604-A1.
XX 23-JUN-2005.
XX 10-DEC-2004; 2004WO-JP018506.
XX 12-DEC-2003; 2003JP-00415746.
PR 12-MAR-2004; 2004JP-00071763.
PR 27-AUG-2004; 2004JP-00248323.
XX (CHUS) CHUGAI SEIYAKU KK.
XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
XX WPI; 2005-445149/45.
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
PT genetically-engineered antihuman Mpl diabody, applicable in drug
PT compositions for use in chemotherapy of thrombocytopenia and other
PT diseases associated with Mpl mutation.
XX Claim 22; SEQ ID NO 133; 106pp; Japanese.
XX The invention describes an antibody is a single-chain polypeptide with
CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
CC heavy-chain variable regions and 2 light-chain variable regions. Also
CC described are: a chimeric antibody for binding with Mpl; an antibody for
CC binding with soluble Mpl; antibodies for binding with human Mpl and
CC monkey Mpl; antibodies with agonistic activity against human Mpl and
CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
CC with TPO agonistic activity; antibodies containing a heavy-chain variable
CC region with CDR (complementary-determinant regions 1, 2 and 3);
CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
CC antibodies containing heavy and light-chain variable regions with CDR 1,
CC 2 and 3 selected from the already-specified groups in 18 combinations;
CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
CC epitope-recognizing antibodies that can recognize the antibodies with the
CC heavy and light-chain variable regions and amino acid sequences;
CC antibodies that can recognize the an amino acid moiety in human Mpl from
CC positions 26-274; polynucleotides encoding these antibodies;
CC polynucleotides hybridizable with the polynucleotides that encode the
CC antibodies under stringent conditions and the antibodies encoded by which
CC have equivalent activity as such antibodies; vectors containing these
CC polynucleotides; host cells carrying such polynucleotides or vectors; and
CC drug compositions containing these antibodies. The antibodies are
CC applicable in drug compositions for use in chemotherapy of
CC thrombocytopenia and other diseases associated with Mpl mutation such as
CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
CC antihuman Mpl antibody and variants like genetically-engineered antihuman
CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
CC agonistic activity against antihuman Mpl antibody, such activity of which
CC is comparable or superior to that of the natural ligand, human TPO. This
CC sequence represents an anti-TPO antibody associated polypeptide.
XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
Best Local Similarity 66.7%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LHSEYPT 9
: | |||||
Db 94 MQHLEYPY 102

RESULT 46
AEA44070
ID AEA44070 standard; protein; 112 AA.
XX AEA44070;
XX 25-AUG-2005 (first entry)
XX Anti-TPO antibody associated variable light chain SEQ ID NO 135.
XX hemostatic; single chain antibody; protein purification;
KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
KW hematological disease; light chain variable region.
XX Unidentified.
XX WO2005056604-A1.
XX 23-JUN-2005.
XX 10-DEC-2004; 2004WO-JP018506.
PR 12-DEC-2003; 2003JP-00415746.
PR 12-MAR-2004; 2004JP-00071763.
PR 27-AUG-2004; 2004JP-00248323.
XX (CHUS) CHUGAI SEIYAKU KK.
XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
XX WPI; 2005-445149/45.
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
PT genetically-engineered antihuman Mpl diabody, applicable in drug
PT compositions for use in chemotherapy of thrombocytopenia and other
PT diseases associated with Mpl mutation.
XX Claim 22; SEQ ID NO 135; 106pp; Japanese.
XX The invention describes an antibody is a single-chain polypeptide with
CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
CC heavy-chain variable regions and 2 light-chain variable regions. Also
CC described are: a chimeric antibody for binding with Mpl; an antibody for
CC binding with soluble Mpl; antibodies for binding with human Mpl and
CC monkey Mpl; antibodies with agonistic activity against human Mpl and
CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
CC with TPO agonistic activity; antibodies containing a heavy-chain variable
CC region with CDR (complementary-determinant regions 1, 2 and 3);
CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
CC antibodies containing heavy and light-chain variable regions with CDR 1,
CC 2 and 3 selected from the already-specified groups in 18 combinations;
CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
CC antibodies containing a light-chain variable region FRI, 2, 3 and 4;
CC epitope-recognizing antibodies that can recognize the antibodies with the
CC heavy and light-chain variable regions and amino acid sequences;
CC antibodies that can recognize the an amino acid moiety in human Mpl from
CC positions 26-274; polynucleotides encoding these antibodies;
CC polynucleotides hybridizable with the polynucleotides that encode the
CC antibodies under stringent conditions and the antibodies encoded by which
CC have equivalent activity as such antibodies; vectors containing these
CC polynucleotides; host cells carrying such polynucleotides or vectors; and
CC drug compositions containing these antibodies. The antibodies are
CC applicable in drug compositions for use in chemotherapy of
CC thrombocytopenia and other diseases associated with Mpl mutation such as
CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
CC antihuman Mpl antibody and variants like genetically-engineered antihuman
CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
CC agonistic activity against antihuman Mpl antibody, such activity of which
CC is comparable or superior to that of the natural ligand, human TPO. This
CC sequence represents an anti-TPO antibody associated polypeptide.
XX Sequence 112 AA;

CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC sequence represents an anti-TPO antibody light chain variable region.

XX SQ Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
 : |||||
 Db 94 MQHLEYPT 102

RESULT 47
 AEA44072
 ID AEA44072 standard; protein; 112 AA.

XX AEA44072;

XX 25-AUG-2005 (first entry)

XX Anti-TPO antibody associated variable light chain SEQ ID NO 137.

XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease; light chain variable region.

XX Unidentified.

XX WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX WPI; 2005-445149/45.

XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.

XX Claim 22; SEQ ID NO 137; 106pp; Japanese.

XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl) -binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRI, 2, 3 and 4;
 CC antibodies containing a light-chain variable region with FRI, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the amino acid moiety in human Mpl from

CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC sequence represents an anti-TPO antibody light chain variable region.

XX SQ Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
 : |||||
 Db 94 MQHLEYPT 102

RESULT 48

AEA44062
 ID AEA44062 standard; protein; 112 AA.

XX AEA44062;

XX 25-AUG-2005 (first entry)

XX Anti-TPO antibody associated variable light chain SEQ ID NO 127.

XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease; light chain variable region.

XX Unidentified.

XX WO2005056604-A1.

XX 23-JUN-2005.

XX 10-DEC-2004; 2004WO-JP018506.

XX 12-DEC-2003; 2003JP-00415746.

PR 12-MAR-2004; 2004JP-00071763.

PR 27-AUG-2004; 2004JP-00248323.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;

XX WPI; 2005-445149/45.

XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.

XX Claim 22; SEQ ID NO 127; 106pp; Japanese.

XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl) -binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies

CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRL 1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRL 1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC sequence represents an anti-TPO antibody light chain variable region.
 XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPYT 9
 : | | | | |
 Db 94 MQHLEYPYT 102

RESULT 49
 AEA44074
 ID AEA44074 standard; protein; 112 AA.
 AC AEA44074;
 XX
 XX
 XX 25-AUG-2005 (first entry)
 XX
 XX Anti-TPO antibody associated polypeptide SEQ ID NO 139.
 XX
 XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 OS
 XX WO2005056604-A1.
 FN
 XX 23-JUN-2005.
 PD
 XX 10-DEC-2004; 2004WO-JP018506.
 PF
 XX 12-DEC-2003; 2003JP-00415746.
 PR
 XX 12-MAR-2004; 2004JP-00071763.
 PR
 XX 27-AUG-2004; 2004JP-00248323.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
 PI
 XX WPI; 2005-445149/45.
 DR
 XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
 PT genetically-engineered antihuman Mpl diabody, applicable in drug
 PT compositions for use in chemotherapy of thrombocytopenia and other
 PT diseases associated with Mpl mutation.

XX Claim 22; SEQ ID NO 139; 106pp; Japanese.
 PS
 XX The invention describes an antibody is a single-chain polypeptide with
 CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
 CC heavy-chain variable regions and 2 light-chain variable regions. Also for
 CC described are: a chimeric antibody for binding with Mpl; an antibody for
 CC binding with soluble Mpl; antibodies for binding with human Mpl and
 CC monkey Mpl; antibodies with agonistic activity against human Mpl and
 CC with TPO agonistic activity; antibodies containing a heavy-chain variable
 CC region with CDR (complementary-determinant regions 1, 2 and 3);
 CC antibodies containing a light-chain variable region with CDR 1 2 and 3;
 CC antibodies containing heavy and light-chain variable regions with CDR 1,
 CC 2 and 3 selected from the already-specified groups in 18 combinations;
 CC antibodies containing a heavy-chain variable region with FRL 1, 2, 3 and 4;
 CC antibodies containing a light-chain variable region FRL 1, 2, 3 and 4;
 CC epitope-recognizing antibodies that can recognize the antibodies with the
 CC heavy and light-chain variable regions and amino acid sequences;
 CC antibodies that can recognize the an amino acid moiety in human Mpl from
 CC positions 26-274; polynucleotides encoding these antibodies;
 CC polynucleotides hybridizable with the polynucleotides that encode the
 CC antibodies under stringent conditions and the antibodies encoded by which
 CC have equivalent activity as such antibodies; vectors containing these
 CC polynucleotides; host cells carrying such polynucleotides or vectors; and
 CC drug compositions containing these antibodies. The antibodies are
 CC applicable in drug compositions for use in chemotherapy of
 CC thrombocytopenia and other diseases associated with Mpl mutation such as
 CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
 CC antihuman Mpl antibody and variants like genetically-engineered antihuman
 CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
 CC soluble to enhance binding ability. The diabody and sc(Fv)2 show high
 CC agonistic activity against antihuman Mpl antibody, such activity of which
 CC is comparable or superior to that of the natural ligand, human TPO. This
 CC sequence represents an anti-TPO antibody associated polypeptide.
 XX Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LHHSEYPYT 9
 : | | | | |
 Db 94 MQHLEYPYT 102

RESULT 50
 AEA44080
 ID AEA44080 standard; protein; 112 AA.
 XX
 AC AEA44080;
 XX
 XX 25-AUG-2005 (first entry)
 XX
 XX Anti-TPO antibody associated polypeptide SEQ ID NO 145.
 XX
 XX hemostatic; single chain antibody; protein purification;
 KW antibody engineering; antibody production; thrombocytopenia; hemostatic;
 KW hematological disease.
 XX Unidentified.
 OS
 XX WO2005056604-A1.
 FN
 XX 23-JUN-2005.
 PD
 XX 10-DEC-2004; 2004WO-JP018506.
 PF
 XX 12-DEC-2003; 2003JP-00415746.
 PR
 XX 12-MAR-2004; 2004JP-00071763.
 PR
 XX 27-AUG-2004; 2004JP-00248323.
 XX

PA (CHUS) CHUGAI SEIYAKU KK.
XX
XX
PI Tsunoda H, Nakano K, Orita T, Tsuchiya M, Hirata Y;
XX
XX MPI; 2005-445149/45.
DR
XX
XX Anti-Mpl antibodies including antihuman Mpl antibody and variants like
PT genetically-engineered antihuman Mpl diabody, applicable in drug
PT compositions for use in chemotherapy of thrombocytopenia and other
PT diseases associated with Mpl mutation.
XX
XX Claim 22; SEQ ID NO 145; 106pp; Japanese.
PS
XX
XX The invention describes an antibody is a single-chain polypeptide with
CC TPO (thrombopoietin) receptor (Mpl)-binding activity that contains the 2
CC heavy-chain variable regions and 2 light-chain variable regions. Also
CC described are: a chimeric antibody for binding with Mpl; an antibody for
CC binding with soluble Mpl; antibodies for binding with human Mpl and
CC monkey Mpl; antibodies with agonistic activity against human Mpl and
CC monkey Mpl; antibodies with binding activity for soluble Mpl; antibodies
CC with TPO agonistic activity; antibodies containing a heavy-chain variable
CC region with CDR (complementary-determinant regions 1, 2 and 3);
CC antibodies containing a light-chain variable region with CDR 1, 2 and 3;
CC antibodies containing heavy and light-chain variable regions with CDR 1,
CC 2 and 3 selected from the already-specified groups in 18 combinations;
CC antibodies containing a heavy-chain variable region with FR1, 2, 3 and 4;
CC antibodies containing a light-chain variable region FR1, 2, 3 and 4;
CC epitope-recognizing antibodies that can recognize the antibodies with the
CC heavy and light-chain variable regions and amino acid sequences;
CC antibodies that can recognize the amino acid moiety in human Mpl from
CC positions 26-274; polynucleotides encoding these antibodies;
CC polynucleotides hybridizable with the polynucleotides that encode the
CC antibodies under stringent conditions and the antibodies encoded by which
CC have equivalent activity as such antibodies; vectors containing these
CC polynucleotides; host cells carrying such polynucleotides or vectors; and
CC drug compositions containing these antibodies. The antibodies are
CC applicable in drug compositions for use in chemotherapy of
CC thrombocytopenia and other diseases associated with Mpl mutation such as
CC congenital amegakaryocytic thrombocytopenia. These antibodies can include
CC antihuman Mpl antibody and variants like genetically-engineered antihuman
CC Mpl diabody and (humanized) antihuman Mpl sc(Fv)2. Such antibodies are
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CC agonistic activity against antihuman Mpl antibody, such activity of which
CC is comparable or superior to that of the natural ligand, human TPO. This
CC sequence represents an anti-TPO antibody associated polypeptide.
XX
SQ Sequence 112 AA;

Query Match 70.9%; Score 39; DB 9; Length 112;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db : | | | | |
94 MQHLEYPYT 102

Search completed: May 11, 2006, 16:28:19
Job time : 113.213 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:28:47 ; Search time 13.2787 Seconds
(without alignments)
65.214 Million cell updates/sec

Title: US-10-808-538-6
Perfect score: 55
Sequence: 1 LHSEYPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	76.4	508	S59870	fork head domain p
2	41	74.5	98	PH1065	Ig kappa chain v r
3	41	74.5	1289	T31344	GP80 precursor - s
4	40	72.7	335	H90165	hypothetical prote
5	39	70.9	112	E26275	Ig kappa chain v r
6	39	70.9	112	E26317	Ig kappa chain v r
7	39	70.9	112	A26317	Ig kappa chain v r
8	39	70.9	112	PL0274	Ig kappa chain v r
9	39	70.9	112	F26317	Ig kappa chain v r
10	39	70.9	112	G26317	Ig kappa chain v r
11	39	70.9	112	B26317	Ig kappa chain v r
12	39	70.9	197	S29593	Ig kappa chain (WM
13	39	70.9	240	B87409	hypothetical prote
14	39	70.9	291	D82491	hypothetical prote
15	39	70.9	865	A53186	flUG protein - Eme
16	39	70.9	1747	T43162	vitellogenin - gyp
17	38	69.1	99	D38601	Ig kappa chain v r
18	38	69.1	129	B23986	Ig kappa chain pre
19	38	69.1	328	H90889	hypothetical prote
20	38	69.1	328	G64901	ABC-type transport
21	38	69.1	328	A85728	hypothetical prote
22	38	69.1	399	T19115	hypothetical prote
23	37	67.3	189	C82483	hypothetical prote
24	37	67.3	195	A99240	anthranilate synth
25	37	67.3	195	B40635	anthranilate synth
26	37	67.3	326	D84719	hypothetical prote
27	37	67.3	353	T52184	zinc transporter 2
28	37	67.3	980	D69974	formate dehydrogen
29	36	65.5	157	S57451	cysteine proteinas

molybdenum cofacto
spore germination
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
protein T30816.23
protein C38C10.5b
protein C38C10.5b
versican precursor
hypothetical prote
hypothetical prote
Ig kappa chain v r
Ig kappa chain v r
Ig kappa chain pre
hypothetical prote
type IV prepilin p
hypothetical prote
squamosa promoter
Rf4 protein - yeas
hypothetical prote
anthranilate synth
vitellogenin - Ach
nonstructural poly
nonstructural poly
nonstructural poly
Ig heavy chain v r
hypothetical prote
probable membrane
Ig kappa chain v r
Ig kappa chain v r
probable membrane
hypothetical prote
hypothetical prote
transcription regu
transcription regu
bidirectional hydr
transcription aci
probable transcrip
porin thermoregula
hypothetical prote
protein F1504.21
protein C18A11.3
hypothetical prote
hypothetical prote
hemagglutinin - in
hemagglutinin - in
hemagglutinin - in
hemagglutinin - in
hemagglutinin - in
hypothetical prote
hypothetical prote
hemagglutinin - in
conserved hypothet
hypothetical prote
anthranilate synth
hypothetical prote
anthranilate synth
related to PR9 pr
T48730
hypothetical prote
ATP-dependent DNA
ribonucleoside-dip
pyrimidine synthe
surfactin syntheta
surfactin syntheta
probable outer mem
hypothetical prote
hypothetical prote
hypothetical prote

103	33	60.0	112	2	B49060	Ig light chain V r	176	32	58.2	320	2	T04934	hypothetical prote
104	33	60.0	187	2	B81903	hypothetical prote	177	32	58.2	324	2	AH3134	hypothetical prote
105	33	60.0	205	2	A82169	hypothetical prote	178	32	58.2	329	2	F84105	oligopeptide ABC t
106	33	60.0	218	2	C81118	hypothetical prote	179	32	58.2	332	2	S60935	hypothetical prote
107	33	60.0	225	2	C70045	two-component resp	180	32	58.2	339	2	S76619	hypothetical prote
108	33	60.0	235	2	D89101	protein F25E5.8 [i	181	32	58.2	354	2	T48321	hypothetical prote
109	33	60.0	241	2	T17798	hypothetical prote	182	32	58.2	355	2	D98153	oligopeptide ABC t
110	33	60.0	252	2	S06567	finger protein (cl	183	32	58.2	378	2	A25399	homeotic protein A
111	33	60.0	268	2	G82042	bioH protein VC271	184	32	58.2	391	2	T39673	probable mannosylt
112	33	60.0	271	2	S18730	aminoglycoside N3'	185	32	58.2	394	2	S26492	homeotic protein A
113	33	60.0	281	2	E70975	probable IS1552 tr	186	32	58.2	425	2	F98350	hypothetical prote
114	33	60.0	318	2	A82363	hypothetical prote	187	32	58.2	426	2	D71367	conserved hypotHet
115	33	60.0	323	2	JX0240	antihemorrhagic fa	188	32	58.2	471	2	T33787	hypothetical prote
116	33	60.0	330	2	B95262	probable formate d	189	32	58.2	496	2	B71489	probable exodeoxyr
117	33	60.0	347	2	S52173	hemagglutinin - in	190	32	58.2	517	2	T06274	probable lipoxysen
118	33	60.0	350	2	J52251	beta-galactoside a	191	32	58.2	519	2	S76850	hypothetical prote
119	33	60.0	350	2	A54420	beta-galactoside a	192	32	58.2	524	2	T08931	hypothetical prote
120	33	60.0	350	2	B54420	beta-galactoside a	193	32	58.2	568	2	S15008	gene disco protein
121	33	60.0	375	2	T00565	geranylgeranyl-dip	194	32	58.2	574	2	G83794	hypothetical prote
122	33	60.0	394	2	A81068	probable membrane	195	32	58.2	577	2	F86414	hypothetical prote
123	33	60.0	424	2	S76359	hypothetical prote	196	32	58.2	611	2	T38908	probable gamma-glu
124	33	60.0	439	2	F71656	hypothetical prote	197	32	58.2	616	2	T32753	hypothetical prote
125	33	60.0	440	2	H97794	hypothetical prote	198	32	58.2	643	2	B59436	Rho GTPase activat
126	33	60.0	453	2	A13613	glutamate-1-semial	199	32	58.2	647	2	T19307	hypothetical prote
127	33	60.0	467	2	JC6150	Gram-negative bact	200	32	58.2	688	2	AH2294	proteinnase II (imp
128	33	60.0	482	2	S55950	hypothetical prote	201	32	58.2	762	2	H71916	DNA mismatch repai
129	33	60.0	519	2	A38073	transcription acti	202	32	58.2	817	2	T21336	hypothetical prote
130	33	60.0	523	2	S50479	26S proteasome reg	203	32	58.2	855	2	A34810	3',5'-cyclic-GMP p
131	33	60.0	583	1	RDZQTB	dihydrofolate redu	204	32	58.2	889	2	T32299	hypothetical prote
132	33	60.0	604	2	T37870	RNA-binding / Ran	205	32	58.2	941	2	S09851	hypothetical prote
133	33	60.0	650	2	S75333	oligopeptide trans	206	32	58.2	959	2	T03053	ribonucleoside-dip
134	33	60.0	695	2	T37667	probable cytochrom	207	32	58.2	1033	2	T71256	conserved hypotHet
135	33	60.0	858	2	JC4520	3',5'-cyclic-GMP p	208	32	58.2	1784	2	C96615	hypothetical prote
136	33	60.0	881	2	S46633	probable membrane	209	32	58.2	1797	2	A55677	laminin beta-2 cha
137	33	60.0	1030	2	A42497	anion exchanger 3,	210	32	58.2	1798	2	S53869	laminin beta-2 cha
138	33	60.0	1227	2	A33638	erythrocyte anion	211	32	58.2	1801	1	NWRTS	laminin beta-2 cha
139	33	60.0	1227	2	B34911	band 3-related pro	212	32	58.2	1807	2	T30940	vitellogenin - Pim
140	33	60.0	1227	2	T20370	hypothetical prote	213	31-5	57.3	494	2	AD3255	1-sorbose dehydrog
141	33	60.0	1232	2	T38496	anion exchanger 3	214	31	56.4	50	2	C82725	hypothetical prote
142	33	60.0	2591	2	T30288	pristinamycin I sy	215	31	56.4	52	2	F43284	finger protein ZNF
143	32.5	59.1	111	2	S37202	Ig kappa chain V r	216	31	56.4	100	2	PH1075	Ig light chain V r
144	32.5	59.1	150	2	D69081	deoxyuridine 5-tri	217	31	56.4	103	2	PH1056	Ig light chain V r
145	32.5	59.1	644	2	T46277	hypothetical prote	218	31	56.4	112	2	H26317	Ig kappa chain V r
146	32	58.2	84	2	C81037	hypothetical prote	219	31	56.4	125	2	S40353	Ig kappa chain V-J
147	32	58.2	97	1	NDBPT4	ndd protein - phag	220	31	56.4	132	2	E82403	hypothetical prote
148	32	58.2	103	2	H30502	Ig kappa chain V r	221	31	56.4	142	2	C75344	conserved hypotHet
149	32	58.2	106	2	S26345	Ig light chain V r	222	31	56.4	144	2	S23661	superoxide dismuta
150	32	58.2	108	1	KIHUKU	Ig kappa chain V-I	223	31	56.4	163	2	T23691	hypothetical prote
151	32	58.2	108	1	KWMS06	Ig kappa chain V r	224	31	56.4	181	2	AG1853	sucrose-phosphatas
152	32	58.2	108	1	KWMS09	Ig kappa chain V r	225	31	56.4	192	2	T29645	hypothetical prote
153	32	58.2	108	1	KWMS61	Ig kappa chain V r	226	31	56.4	214	2	B86156	hypothetical prote
154	32	58.2	111	2	S70302	hypothetical prote	227	31	56.4	226	2	T23054	hypothetical prote
155	32	58.2	112	2	B84559	probable auxin-reg	228	31	56.4	241	2	T50406	hypothetical prote
156	32	58.2	113	1	KWMS7S	Ig kappa chain V r	229	31	56.4	264	2	T52104	GATA-binding trans
157	32	58.2	117	2	S42466	Ig kappa chain V r	230	31	56.4	269	2	E75526	hypothetical prote
158	32	58.2	129	2	S67075	probable membrane	231	31	56.4	271	2	A99411	conserved hypotHet
159	32	58.2	164	2	S18038	homeotic protein S	232	31	56.4	271	2	JC6553	transcription fact
160	32	58.2	177	2	T37444	probable 20.7K pro	233	31	56.4	277	2	T21330	hypothetical prote
161	32	58.2	182	2	JQ1801	B7R 21.3K protein	234	31	56.4	277	2	E71545	probable oligopept
162	32	58.2	182	2	T23259	hypothetical prote	235	31	56.4	279	2	B81705	conserved hypotHet
163	32	58.2	207	2	D84980	guanylate kinase (236	31	56.4	280	2	A10483	conserved hypotHet
164	32	58.2	209	2	S55887	CCHH finger protei	237	31	56.4	283	2	G84457	probable multi doma
165	32	58.2	229	2	H82043	guanylate kinase V	238	31	56.4	286	2	G82698	ABC transporter AT
166	32	58.2	234	2	S46642	probable membrane	239	31	56.4	288	2	B70715	hypothetical prote
167	32	58.2	237	2	T07820	hypothetical prote	240	31	56.4	290	2	F69456	signal sequence pe
168	32	58.2	249	2	S41374	single chain Fv an	241	31	56.4	302	2	AH0191	probable polysacch
169	32	58.2	249	2	AD2341	hypothetical prote	242	31	56.4	311	2	A56235	transcription acti
170	32	58.2	251	2	S20893	homeotic protein c	243	31	56.4	323	2	B69471	dipeptide transpor
171	32	58.2	256	2	C83474	hypothetical prote	244	31	56.4	325	2	I48765	slah-2 protein - m
172	32	58.2	303	2	S23440	hypothetical prote	245	31	56.4	331	2	JQ2377	hemagglutinin - in
173	32	58.2	312	2	B23705	cysteine proteinas	246	31	56.4	331	2	D82301	peptide ABC transp
174	32	58.2	312	2	A23705	cysteine proteinas	247	31	56.4	333	2	AE0266	oligopeptide trans
175	32	58.2	312	2	T21992	hypothetical prote	248	31	56.4	335	2	S21954	type II site-speci

249	31	56.4	340	1	OKBYR1	protein kinase byr	322	31	56.4	1132	2	C75259	probable iron-sulf
250	31	56.4	347	2	T28059	hypothetical prote	323	31	56.4	1132	2	T49403	related to protein
251	31	56.4	358	1	A49511	transcription fact	324	31	56.4	1137	2	A98276	hypothetical prote
252	31	56.4	358	1	JC5121	transcription fact	325	31	56.4	1153	2	T31080	nitric-oxide synth
253	31	56.4	358	1	S25464	transcription fact	326	31	56.4	1350	2	S00647	finger protein - A
254	31	56.4	359	2	S14028	type II site-speci	327	31	56.4	1584	2	T18276	protein-tyrosine k
255	31	56.4	365	1	JC1168	transcription fact	328	31	56.4	1877	2	T40550	probable phosphati
256	31	56.4	370	2	JC5130	paired box transcr	329	31	56.4	1879	2	T15962	hypothetical prote
257	31	56.4	379	1	S41834	ubiquinol-cytochro	330	31	56.4	2137	2	T05244	hypothetical prote
258	31	56.4	381	2	T22334	hypothetical prote	331	31	56.4	2139	2	S46404	vitellogenin - yel
259	31	56.4	384	1	S54484	probable fatty aci	332	30.5	55.5	363	2	AD1304	carbamoyl-phosphat
260	31	56.4	384	2	H90026	hypothetical prote	333	30.5	55.5	490	1	S71776	calcium-dependent
261	31	56.4	385	1	WZWC6E	pectate lyase (EC	334	30	54.5	35	2	R38601	ig kappa chain v r
262	31	56.4	385	2	D71873	GTPase in circumfe	335	30	54.5	40	2	A23098	larvicidal toxin -
263	31	56.4	385	2	C64642	cell division prote	336	30	54.5	53	2	I43284	zinc finger protei
264	31	56.4	397	2	T35609	whfE protein I - s	337	30	54.5	71	2	AC3411	hypothetical prote
265	31	56.4	397	2	H81744	conserved hypotet	338	30	54.5	78	2	A97974	degenerate transpo
266	31	56.4	399	2	A95091	conserved hypotet	339	30	54.5	83	2	H85523	hypothetical prote
267	31	56.4	399	2	E97958	conserved hypotet	340	30	54.5	98	2	PH1061	ig light chain v r
268	31	56.4	412	2	T50519	hypothetical prote	341	30	54.5	98	2	A82603	hypothetical prote
269	31	56.4	415	2	S77471	adenylosuccinate s	342	30	54.5	100	2	H71133	hypothetical prote
270	31	56.4	419	2	AH2403	adenylosuccinate s	343	30	54.5	104	2	F72489	hypothetical prote
271	31	56.4	424	2	T31978	hypothetical prote	344	30	54.5	106	2	S20652	ig kappa chain v r
272	31	56.4	425	2	S66043	serine-tRNA ligase	345	30	54.5	112	2	C26317	ig kappa chain v r
273	31	56.4	426	2	S44953	lmbF protein - Scr	346	30	54.5	112	2	A90881	hypothetical prote
274	31	56.4	427	2	A12785	seryl-tRNA synthet	347	30	54.5	113	1	KVMS17	ig kappa chain v r
275	31	56.4	428	2	A81705	peptide ABC transp	348	30	54.5	122	2	H85737	hypothetical prote
276	31	56.4	435	2	C97565	seryl-tRNA synthet	349	30	54.5	127	2	S52447	ig kappa chain v r
277	31	56.4	437	2	T50415	ada2-like protein	350	30	54.5	129	2	D32513	ig kappa chain pre
278	31	56.4	459	2	I60717	streptothricin-ace	351	30	54.5	137	2	A83751	hypothetical prote
279	31	56.4	461	2	A56239	mannose-6-phosphat	352	30	54.5	142	2	B75463	conserved hypotet
280	31	56.4	467	2	H84538	hypothetical prote	353	30	54.5	149	2	D84181	hypothetical prote
281	31	56.4	474	2	T51103	2,3-dehydratase [v	354	30	54.5	151	1	S73506	pi1B homolog K05_o
282	31	56.4	476	2	T52157	hypothetical prote	355	30	54.5	168	2	T25749	hypothetical prote
283	31	56.4	502	2	D65057	hypothetical prote	356	30	54.5	168	2	S06570	finger protein (cl
284	31	56.4	506	2	A54190	cerebroside-sulfat	357	30	54.5	178	2	C87677	degenerate transpo
285	31	56.4	506	2	A86169	hypothetical prote	358	30	54.5	182	2	S79233	hypothetical prote
286	31	56.4	507	1	KJHUA	cerebroside-sulfat	359	30	54.5	185	2	T34286	CCHH finger protei
287	31	56.4	516	2	D64563	single-stranded-DN	360	30	54.5	197	2	S55886	anthranilate synth
288	31	56.4	516	2	B71946	probable single-st	361	30	54.5	201	2	C75356	hypothetical prote
289	31	56.4	519	2	G84598	probable bZIP tran	362	30	54.5	203	2	T25222	cytochrome c oxida
290	31	56.4	524	2	T23907	hypothetical prote	363	30	54.5	207	2	A81925	finger protein (cl
291	31	56.4	525	2	B84028	oligopeptide ABC t	364	30	54.5	216	2	S06781	hypothetical prote
292	31	56.4	527	2	F70543	probable L-asparta	365	30	54.5	217	2	T15482	Glutathione transf
293	31	56.4	550	1	A40449	protein-tyrosine-p	366	30	54.5	219	2	T48065	hypothetical prote
294	31	56.4	563	2	A47153	iduronate-2-sulfat	367	30	54.5	223	2	T30147	hypothetical prote
295	31	56.4	569	2	C69422	hydrogenase (EC 1.	368	30	54.5	233	2	T18453	hypothetical prote
296	31	56.4	571	2	T08930	hypothetical prote	369	30	54.5	238	2	H95105	pinin gene inverti
297	31	56.4	616	2	A13102	hypothetical prote	370	30	54.5	258	2	E97613	probable DNA bindi
298	31	56.4	616	2	A98184	hypothetical ABC t	371	30	54.5	268	2	T17657	hypothetical prote
299	31	56.4	636	1	TVMSMB	transforming prote	372	30	54.5	273	2	B48820	homeobox protein (
300	31	56.4	648	2	F82290	soluble lytic mure	373	30	54.5	274	2	T48296	hypothetical prote
301	31	56.4	705	2	AC0424	polyribonucleotide	374	30	54.5	275	2	D72801	gp15 protein - Myc
302	31	56.4	715	4	TVMSMY	transforming prote	375	30	54.5	276	1	BVECGG	gipE protein - Bsc
303	31	56.4	731	2	B83904	hypothetical prote	376	30	54.5	276	2	D86008	protein of gip reg
304	31	56.4	734	2	T43408	cullin-4 - fission	377	30	54.5	276	2	C91162	protein of gip reg
305	31	56.4	742	2	T38001	probable phosphati	378	30	54.5	278	2	C83552	hypothetical prote
306	31	56.4	768	2	T18461	hypothetical prote	379	30	54.5	279	2	B82353	conserved hypotet
307	31	56.4	785	2	T51203	related to ser/thr	380	30	54.5	280	2	C86021	hypothetical prote
308	31	56.4	804	2	A96494	protein F7F22.16 [381	30	54.5	280	2	C91175	hypothetical prote
309	31	56.4	842	2	S60402	protein kinase CIA	382	30	54.5	280	2	S47719	hypothetical prote
310	31	56.4	904	2	AF2304	polyA polymerase (383	30	54.5	281	2	E64068	transformation com
311	31	56.4	908	2	T16057	hypothetical prote	384	30	54.5	290	2	B81746	peptide ABC transp
312	31	56.4	941	2	T49136	protein kinase-lik	385	30	54.5	294	2	S30960	gene 15 protein -
313	31	56.4	959	2	C82392	oxidoreductase/lro	386	30	54.5	294	2	S75521	hypothetical prote
314	31	56.4	963	2	B70524	probable PPE prote	387	30	54.5	297	2	A84338	spermidine/puressc
315	31	56.4	963	2	T43676	hunchback-related	388	30	54.5	305	2	T16121	hypothetical prote
316	31	56.4	1091	2	AF2953	DNA polymerase III	389	30	54.5	307	2	T09923	cytidine deaminase
317	31	56.4	1091	2	G98329	probable DNA polym	390	30	54.5	314	2	D71410	hypothetical prote
318	31	56.4	1092	2	S77546	cobN protein - Syn	391	30	54.5	323	1	A28396	prostaglandin-F sy
319	31	56.4	1093	2	T18672	hypothetical prote	392	30	54.5	323	1	JH0575	prostaglandin-F sy
320	31	56.4	1110	2	I59370	guanylate cyclase	393	30	54.5	324	2	T39175	aldolase and adduc
321	31	56.4	1128	2	AD3008	peptide synthetase	394	30	54.5	326	2	T36497	probable branched-

395 30 54.5 326 2 S43991 cathepsin L-like p
396 30 54.5 327 2 AC0156 probable cobalamin
397 30 54.5 334 2 AD2321 phosphoribulokinas
398 30 54.5 335 2 S72197 adenosylmethionine
399 30 54.5 337 2 I48682 NEX-1 - mouse
400 30 54.5 337 2 I57038 gene Dlx-3 protein
401 30 54.5 339 2 T46713 hypothetical prote
402 30 54.5 339 2 C86536 hypothetical prote
403 30 54.5 339 2 E72086 hypothetical prote
404 30 54.5 343 1 KH00 cysteine proteinas
405 30 54.5 344 2 C81581 hypothetical prote
406 30 54.5 344 2 T46680 probable O-methyla
407 30 54.5 347 2 S00549 development cont
408 30 54.5 347 2 S10571 mucin 1 precursor,
409 30 54.5 350 2 F70139 exported prote in (
410 30 54.5 352 2 T22384 hypothetical prote
411 30 54.5 360 2 G02064 g protein-coupled
412 30 54.5 361 2 B84601 cysteine proteinas
413 30 54.5 362 1 S12581 cysteine proteinas
414 30 54.5 364 2 S58871 homeotic protein K
415 30 54.5 366 2 T33885 hypothetical prote
416 30 54.5 367 2 AC2469 hypothetical prote
417 30 54.5 368 2 S75234 hypothetical prote
418 30 54.5 368 2 A82846 cpaa protein (A700
419 30 54.5 368 2 B97623 alanine dehydrogen
420 30 54.5 372 2 A89955 alanine dehydrogen
421 30 54.5 372 2 G89921 prestalk cathepsin
422 30 54.5 376 1 KH00P cysteine proteinas
423 30 54.5 377 2 T12042 oligopeptide trans
424 30 54.5 377 2 AF3534 cysteine proteinas
425 30 54.5 380 2 S55923 cysteine proteinas
426 30 54.5 390 2 T21367 hypothetical prote
427 30 54.5 391 2 T32429 hypothetical prote
428 30 54.5 396 2 C84797 hypothetical prote
429 30 54.5 401 1 C71310 conserved hypothet
430 30 54.5 409 2 A70563 probable transposa
431 30 54.5 411 2 D75408 phosphoglycerate k
432 30 54.5 411 2 A49127 homeotic protein A
433 30 54.5 422 2 G71913 udp-n-acetylglucos
434 30 54.5 426 2 G02277 creatine transport
435 30 54.5 426 2 D71552 probable oligopept
436 30 54.5 430 2 T05980 hypothetical prote
437 30 54.5 433 1 ITHUC alpha-1-antichymot
438 30 54.5 435 2 T71857 hypothetical prote
439 30 54.5 435 2 B64658 hypothetical prote
440 30 54.5 437 2 AG0111 X-Pro aminopeptida
441 30 54.5 438 2 AH0873 proline aminopepti
442 30 54.5 439 2 T01270 hypothetical prote
443 30 54.5 441 1 DPECP X-Pro aminopeptida
444 30 54.5 441 2 C91101 proline aminopepti
445 30 54.5 441 2 G85946 proline aminopepti
446 30 54.5 442 2 B89783 hypothetical prote
447 30 54.5 447 2 S61875 hydroxymethylgluta
448 30 54.5 449 2 S65243 probable membrane
449 30 54.5 453 2 T39155 glycosyl hydrolase
450 30 54.5 453 2 G96573 protein Fl2M16.27
451 30 54.5 454 2 T49718 probable hydroxyme
452 30 54.5 463 2 H87280 adenosylhomocystei
453 30 54.5 466 1 DCBYO ornithine decarbox
454 30 54.5 468 2 E70839 probable PE protei
455 30 54.5 472 2 T19490 hypothetical prote
456 30 54.5 474 2 I54338 zinc finger protei
457 30 54.5 475 2 S03679 finger protein (cl
458 30 54.5 476 2 S79963 methyl CpG binding
459 30 54.5 477 2 JC2041 glucagon receptor
460 30 54.5 483 2 G81745 conserved hypothet
461 30 54.5 483 2 H71482 probable ABC trans
462 30 54.5 491 2 S58202 hydroxymethylgluta
463 30 54.5 491 2 A32584 Add-B protein - fr
464 30 54.5 493 2 A34220 homeotic protein A
465 30 54.5 498 2 AB0405 L-xyulokinase (EC
466 30 54.5 500 2 JC4709 steroid 11beta-mon
467 30 54.5 501 2 G72206 GMP synthase - The

468 30 54.5 504 2 JC5830 myocilin - human
469 30 54.5 518 2 AG3135 NADH dehydrogenase
470 30 54.5 518 2 E98152 NAD-dependent form
471 30 54.5 541 2 D82302 iron(III) ABC tran
472 30 54.5 541 2 C48717 glutamate formid
473 30 54.5 544 2 C96943 uncharacterized me
474 30 54.5 550 2 AB2000 ATP-binding protei
475 30 54.5 551 2 T39092 hypothetical ser-p
476 30 54.5 556 2 S22634 sphingomyelin phos
477 30 54.5 574 2 T04249 hypothetical prote
478 30 54.5 588 2 AB0927 terminase, Arpase
479 30 54.5 588 2 AH1037 probable terminase
480 30 54.5 595 2 G02075 transcription repr
481 30 54.5 595 2 H95006 beta-galactosidase
482 30 54.5 595 2 C97879 beta-galactosidase
483 30 54.5 606 2 S43118 finger protein - m
484 30 54.5 609 2 AH0388 alpha-glucosidase
485 30 54.5 611 2 F98325 hypothetical ABC t
486 30 54.5 612 2 AH2957 hypothetical prote
487 30 54.5 612 2 S62930 hypothetical prote
488 30 54.5 612 2 S62956 hypothetical prote
489 30 54.5 613 2 JC7952 negatively regulat
490 30 54.5 616 2 A99969 anaerobic ribonuc
491 30 54.5 622 2 G86371 hypothetical prote
492 30 54.5 624 2 T02289 probable polygalac
493 30 54.5 626 2 T01485 probable polygalac
494 30 54.5 635 2 A46081 Na(+)-dependent cr
495 30 54.5 635 2 JC2386 creatine transport
496 30 54.5 635 2 G02095 choline transport
497 30 54.5 635 2 S23431 fibroblast growth
498 30 54.5 641 2 T29991 DNA topoisomerase
499 30 54.5 650 1 JC1450 Pts enzyme II, ABC
500 30 54.5 663 2 B84194 hypothetical prote
501 30 54.5 665 2 B96970 probable type II D
502 30 54.5 673 2 T15551 hypothetical prote
503 30 54.5 678 2 H71816 hypothetical prote
504 30 54.5 686 2 T08919 anaerobic ribonuc
505 30 54.5 710 2 AH1109 anaerobic ribonuc
506 30 54.5 716 2 AB1471 hypothetical prote
507 30 54.5 729 2 E70333 anaerobic ribonuc
508 30 54.5 735 2 E95023 anaerobic ribonuc
509 30 54.5 737 2 G97894 ribonucleoside-tri
510 30 54.5 744 2 S65669 biotin sulfoxide r
511 30 54.5 747 2 A86659 anaerobic ribonuc
512 30 54.5 762 2 E64597 DNA mismatch repai
513 30 54.5 763 2 AG1460 alpha-glucosidase
514 30 54.5 763 2 AH1097 alpha-glucosidase
515 30 54.5 767 1 WMBEP6 ribonucleoside-dip
516 30 54.5 783 2 A55817 cyclin-dependent k
517 30 54.5 803 2 S26823 zinc finger protei
518 30 54.5 817 2 T16697 hypothetical prote
519 30 54.5 819 1 TNBR11 91.8K alpha trans-
520 30 54.5 847 2 T04772 hypothetical prote
521 30 54.5 859 2 T06352 lipoxigenase (EC 1
522 30 54.5 859 2 T06339 lipoxigenase (EC 1
523 30 54.5 862 2 S57964 lipoxigenase (EC 1
524 30 54.5 868 2 A30817 serendipity (sry h
525 30 54.5 876 2 E89949 valine-tRNA ligase
526 30 54.5 974 2 AC2076 two-component hybr
527 30 54.5 982 2 S09810 hypothetical prote
528 30 54.5 1001 2 T28897 hypothetical prote
529 30 54.5 1018 2 T40253 hypothetical prote
530 30 54.5 1021 2 F82230 conserved hypothet
531 30 54.5 1023 2 T31669 neural zinc finger
532 30 54.5 1032 2 T41424 neural zinc finger
533 30 54.5 1077 2 D45029 crml+ protein - fi
534 30 54.5 1078 2 T50137 chromosome region
535 30 54.5 1078 2 T43511 CRM1/exportin 1 -
536 30 54.5 1079 2 C96772 probable receptor
537 30 54.5 1148 2 A28614 nonstructural poly
538 30 54.5 1171 2 T42372 probable guanylate
539 30 54.5 1190 2 T28316 ORF MSV155 probabl
540 30 54.5 1247 2 E71616 hypothetical prote

541	30	54.5	1256	2	JE0209	brain-specific ang	614	29	52.7	207	1	KIECGU	guanylate kinase (
542	30	54.5	1279	2	T18312	hypothetical prote	615	29	52.7	207	2	AI0969	5'-guanylate kinase
543	30	54.5	1302	2	AC2017	cobalamin biosynth	616	29	52.7	207	2	D86041	guanylate kinase [
544	30	54.5	1330	2	S49010	embryonic receptor	617	29	52.7	207	2	C91194	guanylate kinase [
545	30	54.5	1344	1	A35175	mucin 1 precursor,	618	29	52.7	207	2	AI0005	guanylate kinase (
546	30	54.5	1538	2	S73296	glutamate synthase	619	29	52.7	215	2	T44861	probable hydroxyla
547	30	54.5	1782	2	S45289	vitellogenin precu	620	29	52.7	220	2	S40931	hypothetical prote
548	30	54.5	1844	2	D71612	hypothetical prote	621	29	52.7	223	2	S06576	finger protein (cl
549	30	54.5	2140	2	F95074	serine proteinase,	622	29	52.7	224	2	T14474	MADS box protein 2
550	30	54.5	2210	1	RRXP04	genome polyprotein	623	29	52.7	224	2	T14473	MADS box protein a
551	30	54.5	2301	1	GNNVTN	genome polyprotein	624	29	52.7	224	2	T33202	hypothetical prote
552	30	54.5	2303	1	GNNVTM	genome polyprotein	625	29	52.7	225	1	CYFEGE	epsilon-crystallin
553	30	54.5	2303	1	GNNVTP	genome polyprotein	626	29	52.7	228	2	S55888	CCHH finger protei
554	30	54.5	2303	2	S13554	genome polyprotein	627	29	52.7	233	2	S38899	ig kappa chain pre
555	30	54.5	2391	2	G89779	hypothetical prote	628	29	52.7	234	2	S14237	site-specific DNA-
556	30	54.5	2413	2	S34670	splicing factor PR	629	29	52.7	235	2	S64695	conserved hypothet
557	30	54.5	2479	1	MNWMRA	nonstructural poly	630	29	52.7	235	2	D71808	hypothetical prote
558	30	54.5	2573	2	D71614	hypothetical prote	631	29	52.7	236	2	C72343	conserved hypothet
559	29.5	53.6	346	2	T51551	quinone oxidoreduc	632	29	52.7	236	2	S65985	yybL protein - Bac
560	29.5	53.6	505	2	B95196	PTS system, IIBC c	633	29	52.7	237	2	G70066	capsular polysacch
561	29.5	53.6	510	2	G98062	phosphotransferase	634	29	52.7	246	2	T31020	hypothetical prote
562	29.5	53.6	523	2	S38186	hypothetical prote	635	29	52.7	251	2	AD1131	hypothetical prote
563	29.5	53.6	653	2	F75005	aldehyde-ferredoxi	636	29	52.7	253	2	G75350	conserved hypothet
564	29.5	53.6	653	2	B71157	hypothetical prote	637	29	52.7	257	2	A84848	probable C2H2-type
565	29	52.7	64	2	A86551	hypothetical prote	638	29	52.7	262	2	T05084	hypothetical prote
566	29	52.7	64	2	A72074	CT382.1 hypothetical	639	29	52.7	263	2	A75280	phenylacetic acid
567	29	52.7	64	2	E96976	hypothetical prote	640	29	52.7	266	2	A12431	hypothetical prote
568	29	52.7	69	2	E96976	hypothetical prote	641	29	52.7	266	2	C84963	extragenic suppres
569	29	52.7	74	2	D61600	segmentation prote	642	29	52.7	266	2	E83045	hypothetical prote
570	29	52.7	74	2	T06397	isoprenylated prot	643	29	52.7	267	2	AD1835	hypothetical prote
571	29	52.7	83	2	QJ1962	hypothetical 9.3K	644	29	52.7	275	2	C69904	hypothetical prote
572	29	52.7	92	2	S38622	ig kappa chain V r	645	29	52.7	277	2	AF0425	dihydropteroate sy
573	29	52.7	107	2	A28195	ig kappa chain V r	646	29	52.7	278	2	S41425	cysteine proteinas
574	29	52.7	107	2	D90955	hypothetical prote	647	29	52.7	279	2	T20443	hypothetical prote
575	29	52.7	107	2	A85804	hypothetical prote	648	29	52.7	282	2	C71444	probable thioester
576	29	52.7	107	2	H64953	hypothetical prote	649	29	52.7	285	2	E86835	maltese ABC transp
577	29	52.7	107	2	T08707	hypothetical prote	650	29	52.7	289	2	A48913	KRAB zinc finger p
578	29	52.7	108	1	K1HUBN	hypothetical prote	651	29	52.7	291	2	F71522	probable metal dep
579	29	52.7	108	1	K2DGM	ig kappa chain V-I	652	29	52.7	292	2	F83827	hypothetical prote
580	29	52.7	108	1	KWMS82	ig kappa chain V r	653	29	52.7	292	2	G72706	hypothetical prote
581	29	52.7	108	1	PL0204	anti-DNA autoantib	654	29	52.7	294	2	B85729	hypothetical prote
582	29	52.7	110	2	B90416	LSU ribosomal prot	655	29	52.7	294	2	G90888	hypothetical prote
583	29	52.7	112	2	C81123	hypothetical prote	656	29	52.7	294	2	J80629	formate dehydrogen
584	29	52.7	122	2	S41443	larval serum prote	657	29	52.7	295	2	D96648	hypothetical prote
585	29	52.7	124	2	T05574	hypothetical prote	658	29	52.7	296	2	T20726	hypothetical prote
586	29	52.7	125	2	C86490	F28L22.5 protein -	659	29	52.7	307	2	A29993	carbonate dehydrat
587	29	52.7	129	2	S40369	ig kappa chain - h	660	29	52.7	310	1	A70481	acetoin utilizatio
588	29	52.7	131	2	S55027	ig light chain pre	661	29	52.7	312	1	CRHU4	carbonate dehydrat
589	29	52.7	146	2	B64246	ribosomal protein	662	29	52.7	312	1	F71646	sfhB protein homol
590	29	52.7	146	2	S73551	ribosomal protein	663	29	52.7	313	2	T29691	hypothetical prote
591	29	52.7	152	2	S57422	cysteine proteinas	664	29	52.7	314	2	S41428	cysteine proteinas
592	29	52.7	152	2	S57423	cysteine proteinas	665	29	52.7	319	2	F82348	hypothetical prote
593	29	52.7	153	2	AG0795	conserved hypothet	666	29	52.7	319	2	I51569	UVS 2 protein - Af
594	29	52.7	153	2	D85867	hypothetical prote	667	29	52.7	319	2	I50519	sox 19 protein - z
595	29	52.7	153	2	C91023	hypothetical prote	668	29	52.7	320	2	I51030	ubiquinol-cytochro
596	29	52.7	153	2	A64998	Protein elaa - Bsc	669	29	52.7	322	2	B57407	3alpha-hydroxyster
597	29	52.7	153	2	S49998	hypothetical prote	670	29	52.7	323	2	I73674	chlorocone reduct
598	29	52.7	157	2	S22361	hypothetical prote	671	29	52.7	324	1	JC4280	carbonyl reductase
599	29	52.7	160	2	S00714	phycocyanin 1 alph	672	29	52.7	324	2	F72049	peptide ABC transp
600	29	52.7	162	1	CFKKA	C-phycocyanin alph	673	29	52.7	324	2	G86575	ABC ATFase dipepti
601	29	52.7	162	1	CFYCAA	C-phycocyanin alph	674	29	52.7	326	1	S15835	3-oxo-beta-sterol
602	29	52.7	162	2	T11978	phycocyanin alpha	675	29	52.7	326	1	S41120	cholestenone 5beta
603	29	52.7	163	1	CFYCA	C-phycocyanin alph	676	29	52.7	326	2	AB0142	molybdenum cofacto
604	29	52.7	163	2	B35126	phycocyanin alpha	677	29	52.7	327	2	T31149	sopB protein homol
605	29	52.7	167	2	AD2507	hypothetical prote	678	29	52.7	330	2	AS3742	calponin, acidic -
606	29	52.7	172	1	NKVGDD	core protein p19 -	679	29	52.7	332	2	JC1336	phosphoribulokinase
607	29	52.7	182	2	A72240	conserved hypothet	680	29	52.7	333	2	H89015	protein B0213.7 [1
608	29	52.7	183	2	JC4568	ribosomal protein	681	29	52.7	334	2	D83164	conserved hypothet
609	29	52.7	184	2	T38216	hypothetical prote	682	29	52.7	337	2	AC1211	glycosyltransferase
610	29	52.7	188	2	B49773	ecdysone-dependent	683	29	52.7	343	2	D86198	cysteine proteinase
611	29	52.7	197	2	E70349	anthranilate synth	684	29	52.7	343	2	B85074	probable transposo
612	29	52.7	201	2	AC0363	conserved hypothet	685	29	52.7	344	2	S42383	hypothetical prote
613	29	52.7	204	2	A82673	guanylate kinase X	686	29	52.7	348	2	S13323	glucan endo-1,3-be

687	29	52.7	350	2	AG0879	A/G-specific adeni	760	29	52.7	468	2	T32586	hypothetical prote
688	29	52.7	350	2	A40647	methylat-ion-indepe	761	29	52.7	474	2	F97264	6-Phospho-Beta-D-G
689	29	52.7	363	2	H83893	hypothetical prote	762	29	52.7	484	2	T39200	zinc finger protei
690	29	52.7	364	2	G89015	protein B0213.8 li	763	29	52.7	485	2	A84043	chromosome replica
691	29	52.7	365	2	B83710	hypothetical prote	764	29	52.7	491	2	S58330	probable membrane
692	29	52.7	366	2	J39888	mannitol-1-phospha	765	29	52.7	493	2	T18789	hypothetical prote
693	29	52.7	366	2	JC7690	Gfi-1-like protein	766	29	52.7	505	2	T07900	probable 3-oxoacyl
694	29	52.7	368	2	UN0718	cysteine proteinas	767	29	52.7	506	2	T07934	probable 3-oxoacyl
695	29	52.7	370	2	A27098	larvicidal toxin 4	768	29	52.7	507	2	G89908	Catalase imported
696	29	52.7	370	2	S07712	larvicidal toxin 4	769	29	52.7	509	1	S04346	steroid 17alpha-mo
697	29	52.7	370	2	D82111	larvicidal toxin 4	770	29	52.7	510	1	S64059	stearoyl-CoA 9-des
698	29	52.7	373	2	D71428	cysteine proteinas	771	29	52.7	518	1	N1BCBT	nitrogenase (EC 1.
699	29	52.7	373	2	S52766	secY protein - Str	772	29	52.7	521	2	S27475	nitrogenase (EC 1.
700	29	52.7	383	2	T04641	homeobox protein 1	773	29	52.7	528	2	E71886	type I restriction
701	29	52.7	384	2	D70517	hypothetical prote	774	29	52.7	530	2	H72864	AcOrf-119 protein
702	29	52.7	384	2	S17778	strH protein - Str	775	29	52.7	530	2	H82801	conserved hypothet
703	29	52.7	386	2	T35438	probable secreted	776	29	52.7	534	1	VCWVSF	env polyprotein -
704	29	52.7	386	2	T09019	phosphoprotein pho	777	29	52.7	538	2	A85075	probable transposo
705	29	52.7	387	2	T33413	hypothetical prote	778	29	52.7	544	2	T24913	hypothetical prote
706	29	52.7	388	2	C85323	protein phosphatas	779	29	52.7	545	2	T02279	hypothetical prote
707	29	52.7	390	1	E48563	I6 protein - fowlp	780	29	52.7	546	2	T06415	canexin - soybean
708	29	52.7	391	1	S02192	cellular tumor ant	781	29	52.7	554	2	H82446	isocitrate lyase (
709	29	52.7	399	2	S70634	translation elonga	782	29	52.7	551	2	S26858	isocitrate lyase (
710	29	52.7	403	2	T20070	hypothetical prote	783	29	52.7	552	2	T32581	hypothetical prote
711	29	52.7	403	2	F81201	conserved hypothet	784	29	52.7	553	2	G71639	hypothetical prote
712	29	52.7	403	2	B46165	envelope surface g	785	29	52.7	554	2	H82446	conserved hypothet
713	29	52.7	404	2	T02294	hypothetical prote	786	29	52.7	557	2	T07632	isocitrate lyase (
714	29	52.7	405	2	F81778	conserved hypothet	787	29	52.7	558	2	T07631	isocitrate lyase (
715	29	52.7	407	2	I39152	zinc finger protei	788	29	52.7	562	2	T32581	hypothetical prote
716	29	52.7	408	2	C46165	envelope surface g	789	29	52.7	579	2	T24536	hypothetical prote
717	29	52.7	408	2	T30587	hypothetical prote	790	29	52.7	580	2	A37107	spermatogenesis pr
718	29	52.7	416	2	G81296	adenylosuccinate s	791	29	52.7	582	2	S08686	finger protein 2FP
719	29	52.7	419	2	T39266	hypothetical prote	792	29	52.7	582	2	C90165	conserved hypothet
720	29	52.7	420	2	S06579	HOMEOBOX PROTEIN K	793	29	52.7	584	2	A49596	genome polyprotein
721	29	52.7	421	1	EFHST	finger protein (cl	794	29	52.7	585	2	B49596	homothallic switch
722	29	52.7	421	1	T09379	translation elonga	795	29	52.7	586	2	S59301	homothallic switch
723	29	52.7	421	2	F84414	probable translati	796	29	52.7	586	2	JC2407	cell pattern forma
724	29	52.7	422	2	S93319	hypothetical prote	797	29	52.7	590	2	A44068	hypothetical prote
725	29	52.7	426	2	A49892	probable membrane	798	29	52.7	592	2	E89772	hypothetical prote
726	29	52.7	426	2	A49892	L-ornithine N5-ox	799	29	52.7	592	2	T22885	hypothetical prote
727	29	52.7	427	2	T04318	homeobox protein L	800	29	52.7	603	2	B86608	probable phosphohy
728	29	52.7	427	2	T17010	knotted-like home	801	29	52.7	603	2	F72017	protein F3F9.10 li
729	29	52.7	428	2	A36945	4 animobutyrate am	802	29	52.7	605	2	T05243	transketolase NMB1
730	29	52.7	430	2	F83027	adenylosuccinate s	803	29	52.7	615	2	A72627	hypothetical prote
731	29	52.7	430	2	C96346	FlcP4.3 protein -	804	29	52.7	619	2	T28958	hypothetical prote
732	29	52.7	431	2	F97318	acyl-CoA thioester	805	29	52.7	642	1	VCWVFG	env polyprotein -
733	29	52.7	432	1	AJECDS	adenylosuccinate s	806	29	52.7	642	1	VCWVS2	env polyprotein pr
734	29	52.7	432	2	A86114	adenylosuccinate s	807	29	52.7	642	2	T10533	env polyprotein pr
735	29	52.7	432	2	A71049	adenylosuccinate s	808	29	52.7	652	2	H96924	probable phosphohy
736	29	52.7	432	2	G97653	adenylosuccinate s	809	29	52.7	657	2	E96812	protein F3F9.10 li
737	29	52.7	432	2	A82877	adenylosuccinate s	810	29	52.7	659	2	B81082	transketolase NMB1
738	29	52.7	432	2	A82877	adenylosuccinate s	811	29	52.7	659	2	A81862	transketolase (EC
739	29	52.7	432	2	F82055	adenylosuccinate s	812	29	52.7	660	2	T22794	hypothetical prote
740	29	52.7	432	2	G64133	adenylosuccinate s	813	29	52.7	662	1	VCWVUB	env polyprotein -
741	29	52.7	432	2	A80047	adenylosuccinate s	814	29	52.7	662	1	VCWVGF	env polyprotein -
742	29	52.7	433	2	H84995	adenylosuccinate s	815	29	52.7	662	2	A25982	env polyprotein -
743	29	52.7	434	2	A10337	tetrahydrofolylpol	816	29	52.7	664	2	AG0113	transketolase (EC
744	29	52.7	436	2	E72292	glycerol-3-phospha	817	29	52.7	664	2	A11237	transketolase homo
745	29	52.7	438	2	A71026	probable aminotran	818	29	52.7	664	2	AF1600	transketolase PA05
746	29	52.7	439	2	T09214	choline monooxygen	819	29	52.7	665	2	B83577	hypothetical prote
747	29	52.7	440	2	AG1367	nitrilotriacetate	820	29	52.7	666	2	T35864	conserved hypothet
748	29	52.7	440	2	AH1736	nitrilotriacetate	821	29	52.7	672	2	C69120	hypothetical prote
749	29	52.7	440	2	B82803	adenylosuccinate s	822	29	52.7	689	2	T19959	DNA helicase recG
750	29	52.7	441	2	B71816	hypothetical prote	823	29	52.7	693	1	E64139	zinc finger protei
751	29	52.7	443	2	D83346	L-ornithine N5-ox	824	29	52.7	693	2	I37570	probable membrane
752	29	52.7	443	2	C85074	hypothetical prote	825	29	52.7	693	2	S64904	organic solvent to
753	29	52.7	443	2	C85074	serine/threonine-s	826	29	52.7	713	2	H97827	beta-galactosidase
754	29	52.7	443	2	S38327	probable mitochond	827	29	52.7	716	2	JU0275	glycerol-3-phospha
755	29	52.7	447	2	T00435	hemolysin - Helico	828	29	52.7	722	2	T20362	probable transcrip
756	29	52.7	449	1	B64706	Na+-transporting A	829	29	52.7	728	2	A48830	hypothetical prote
757	29	52.7	449	2	H69862	transcription fact	830	29	52.7	728	2	H64346	GRF pyrophosphokin
758	29	52.7	466	1	TWFF	probable 4-aminobu	831	29	52.7	729	2	A89946	conserved hypothet
759	29	52.7	466	2	H71234		832	29	52.7	729	2	D72079	

833	29	52.7	729	2	H86544	CT283 hypothetical	906	29	52.7	3165	2	S15010	hypothetical prote
834	29	52.7	730	2	G64062	primosomal replica	907	29	52.7	3844	2	T18402	asparagine/asparta
835	29	52.7	732	2	AF0938	primosomal protein	908	29	52.7	4725	1	A44357	dyslin heavy chain
836	29	52.7	732	2	F91236	primosomal protein	909	29	52.7	5170	2	T15348	glycine/proline-ri
837	29	52.7	732	2	AD0014	primosomal protein	910	28.5	51.8	173	2	T51469	myb-related protei
838	29	52.7	732	2	F86083	primosomal protein	911	28.5	51.8	280	2	T00737	3beta-hydroxy-Delt
839	29	52.7	732	2	A35505	primosomal replica	912	28.5	51.8	280	2	T51667	A-alpha X protein
840	29	52.7	736	1	M4XR3D	structural protein	913	28.5	51.8	373	1	DEBOHS	hypothetical prote
841	29	52.7	736	2	S23654	Mu2 protein - reov	914	28.5	51.8	384	2	B70675	hypothetical prote
842	29	52.7	738	2	T40035	hypothetical prote	915	28.5	51.8	532	2	S62748	hypothetical prote
843	29	52.7	743	2	S52146	amsF protein - Erw	916	28.5	51.8	538	2	H70379	hypothetical prote
844	29	52.7	751	2	AG1999	(p)ppGpp 3-pyropho	917	28.5	51.8	557	2	T19686	hypothetical prote
845	29	52.7	759	2	AE2429	hypothetical prote	918	28.5	51.8	572	2	T20764	hypothetical prote
846	29	52.7	779	1	S61571	suppressor protein	919	28.5	51.8	782	2	T22134	hypothetical prote
847	29	52.7	781	2	G96991	secreted protease	920	28.5	51.8	1643	2	T14274	versican precursor
848	29	52.7	803	1	OKFPFS	protein-tyrosine k	921	28.5	51.8	3381	2	T42389	highly acidic prot
849	29	52.7	809	2	E90016	hyaluronate lyase	922	28	50.9	51	2	B81443	hemSTUV operon pro
850	29	52.7	816	2	T08978	serine proteinase	923	28	50.9	70	2	S54439	sok protein - Bsch
851	29	52.7	827	2	T39608	zinc finger transc	924	28	50.9	74	2	S00302	hypothetical prote
852	29	52.7	838	2	G81444	molybdopterin-cont	925	28	50.9	74	2	T22504	hypothetical prote
853	29	52.7	840	2	I48968	major fibrous shea	926	28	50.9	84	2	S18426	hypothetical prote
854	29	52.7	849	2	I49060	major 80,000 Mr fi	927	28	50.9	87	2	S07959	cytochrome b5, mic
855	29	52.7	854	1	WMBP12	gene 12 protein -	928	28	50.9	88	2	T17785	hypothetical prote
856	29	52.7	854	1	WMBP22	gene 12 protein -	929	28	50.9	89	2	F64756	probable membrane
857	29	52.7	854	2	T23837	hypothetical prote	930	28	50.9	96	2	A44971	hypothetical prote
858	29	52.7	856	2	C85023	hypothetical prote	931	28	50.9	98	1	CBHU5E	cytochrome b5, ery
859	29	52.7	860	2	E85074	hypothetical prote	932	28	50.9	98	1	JC5783	cytochrome b5, ery
860	29	52.7	868	2	D69297	transmembrane olig	933	28	50.9	98	1	UN0316	cytochrome b5, ery
861	29	52.7	870	2	T30110	hypothetical prote	934	28	50.9	98	2	PH1083	Ig light chain V r
862	29	52.7	884	2	S55651	DNA helicase-prima	935	28	50.9	98	2	AE2219	hypothetical prote
863	29	52.7	888	2	E71608	ATP-dept. acyl-CoA	936	28	50.9	100	2	JC5596	cytochrome b5, bra
864	29	52.7	920	2	F86420	probable receptor-	937	28	50.9	100	2	T05364	auxin-induced prot
865	29	52.7	937	1	DJVVZM	DNA-directed DNA p	938	28	50.9	101	2	C72540	hypothetical prote
866	29	52.7	937	2	A24878	DNA-directed DNA p	939	28	50.9	103	2	PH1528	Ig H chain V regio
867	29	52.7	943	2	G84402	dipeptide ABC tran	940	28	50.9	106	2	PL0262	Ig kappa chain V r
868	29	52.7	961	2	G90053	hypothetical prote	941	28	50.9	106	2	T44366	hypothetical prote
869	29	52.7	993	2	C82687	glycine decarboxyl	942	28	50.9	107	4	S57707	hypothetical prote
870	29	52.7	1006	2	DJVV241	DNA-directed DNA p	943	28	50.9	110	1	KVMS10	Ig kappa chain V r
871	29	52.7	1006	2	T30802	DNA-directed DNA p	944	28	50.9	116	2	G89050	Ig kappa chain V r
872	29	52.7	1025	2	B81751	exodeoxyribonuclea	945	28	50.9	120	2	A34871	Ig kappa chain (an
873	29	52.7	1058	2	H98015	carbamoyl-phosphat	946	28	50.9	121	2	B56700	hypothetical prote
874	29	52.7	1074	2	T01884	hypothetical prote	947	28	50.9	121	2	C71480	hypothetical prote
875	29	52.7	1074	2	S05614	regulatory protein	948	28	50.9	122	2	D72462	conserved hypotet
876	29	52.7	1125	1	F70177	transcription-repa	949	28	50.9	128	2	H70429	hypothetical prote
877	29	52.7	1125	2	G71274	hypothetical prote	950	28	50.9	130	2	H84133	hypothetical prote
878	29	52.7	1133	2	S54496	probable membrane	951	28	50.9	130	2	H69155	hypothetical prote
879	29	52.7	1160	2	A36256	DNA-binding protei	952	28	50.9	133	1	CBHO5	cytochrome b5, mic
880	29	52.7	1164	2	T06144	disease resistance	953	28	50.9	133	2	S70967	bfpG protein - Esc
881	29	52.7	1172	2	S32689	parasporel crystal	954	28	50.9	133	2	AG1963	photosystem II l1
882	29	52.7	1191	2	S76414	beta transducin-li	955	28	50.9	133	2	B30242	stem cell protein
883	29	52.7	1205	2	A55015	bumetanide-sensiti	956	28	50.9	134	1	CBHU5	cytochrome b5, mic
884	29	52.7	1205	2	T13809	probable disintegr	957	28	50.9	134	1	CBPG5	cytochrome b5, mic
885	29	52.7	1239	2	H82926	conserved hypotet	958	28	50.9	134	1	CBRT5	cytochrome b5, mic
886	29	52.7	1272	2	DVH91C	multidrug resistanc	959	28	50.9	134	1	CBRT5	hypothetical prote
887	29	52.7	1276	1	T49316	trfA protein - sli	960	28	50.9	136	2	JQ2266	hypothetical prote
888	29	52.7	1386	2	T14004	MAP kinase kinase	961	28	50.9	136	2	A72585	hypothetical prote
889	29	52.7	1390	2	T39225	adenylate cyclase	962	28	50.9	137	2	B83475	hypothetical prote
890	29	52.7	1401	2	B42239	hypothetical prote	963	28	50.9	137	2	T30143	hypothetical prote
891	29	52.7	1416	2	T20823	hypothetical prote	964	28	50.9	137	2	S06571	finger protein (cl
892	29	52.7	1421	2	T49500	hypothetical prote	965	28	50.9	138	2	S06571	hypothetical prote
893	29	52.7	1478	2	S20117	protein kinase BCK	966	28	50.9	139	2	T34244	hypothetical prote
894	29	52.7	1478	2	T03277	pol protein - yeas	967	28	50.9	141	2	T10195	hypothetical prote
895	29	52.7	1576	2	G86467	hypothetical prote	968	28	50.9	142	2	A83093	50S ribosomal prot
896	29	52.7	1587	2	E90704	Rhs core protein w	969	28	50.9	143	2	H83935	hypothetical prote
897	29	52.7	1616	2	H85554	hypothetical prote	970	28	50.9	144	2	S23660	superoxide dismuta
898	29	52.7	1645	2	T21982	protein kinase GCN	971	28	50.9	144	2	C97281	ribosomal protein
899	29	52.7	1659	1	OKBYN2	hypothetical prote	972	28	50.9	145	2	S60456	cysteine proteinase
900	29	52.7	1661	2	T21993	hypothetical prote	973	28	50.9	145	2	AB1399	ribosomal protein
901	29	52.7	1663	2	T21993	hypothetical prote	974	28	50.9	145	2	AB1775	ribosomal protein
902	29	52.7	1737	2	T17101	probable voltage-a	975	28	50.9	147	2	I54245	lanolin M - rat (f
903	29	52.7	1761	2	T13675	hypothetical prote	976	28	50.9	149	2	D50226	hypothetical prote
904	29	52.7	2150	2	T51629	sensory transducti	977	28	50.9	152	2	S57427	cysteine proteinase
905	29	52.7	2352	2	T43431	alpha-glucan synth	978	28	50.9	152	2	AC0286	conserved hypotet

979 28 50.9 155 2 S57426 cysteine proteinase
 980 28 50.9 155 2 H95015 hypothetical prote
 981 28 50.9 156 2 JCS752 iron-uptake regula
 982 28 50.9 157 2 F81383 ferric uptake regu
 983 28 50.9 157 2 S44239 fur protein - Camp
 984 28 50.9 159 2 C71192 probable molybdenu
 985 28 50.9 161 2 A31901 lincomycin resist
 986 28 50.9 161 2 A25633 lincomycin resist
 987 28 50.9 163 2 I40858 superoxide dismut
 988 28 50.9 168 2 S08557 finger protein (cl
 989 28 50.9 170 2 I39892 hypothetical prote
 990 28 50.9 170 2 B71864 hypothetical prote
 991 28 50.9 172 2 T26906 HD family hydrola
 992 28 50.9 173 2 F97105 hypothetical prote
 993 28 50.9 177 2 T19612 hypothetical prote
 994 28 50.9 182 2 F64569 hypothetical prote
 995 28 50.9 183 2 A54731 alpha-1 acid glyco
 996 28 50.9 186 2 G86864 hypothetical prote
 997 28 50.9 187 2 AG1388 conserved hypothet
 998 28 50.9 187 2 A11763 conserved hypothet
 999 28 50.9 190 2 D72515 hypothetical prote
 1000 28 50.9 197 2 A54842 COP9 protein - Ara

ALIGNMENTS

RESULT 1
 S59870
 fork head domain protein crocodile - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004
 C:Accession: S59870; A46178
 R:Haacker, U.; Kaufmann, E.; Hartmann, C.; Juergens, G.; Knoechel, W.; Jaekle, H.
 EMBO J. 14, 5306-5317, 1995
 A:Title: The Drosophila fork head domain protein crocodile is required for the establish
 A:Reference number: S59870; MUID:96080166; PMID:7489720
 A:Accession: S59870
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-508 <HAE>
 A:Cross-references: UNIPROT:P32027; UNIPARC:UPI0000001B0F
 R:Haacker, U.; Grossniklaus, U.; Gehring, W.J.; Jaekle, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8754-8758, 1992
 A:Title: Developmentally regulated Drosophila gene family encoding the fork head domain.
 A:Reference number: A46178; MUID:92409595; PMID:1356269
 A:Accession: A46178
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 55-182 <HAC>
 A:Cross-references: UNIPARC:UPI000016BBEC; GB:M96440; NID:q157425; PIDN:AAF02177.1; PID:
 A:Note: sequence extracted from NCBI backbone (NCBI:P114222)
 C:Genetics:
 A:Gene: croc
 A:Cross-references: FlyBase:FBgn0014143
 F:70-161/Domain: fork head DNA-binding domain homology <FHD>

Query Match 76.4%; Score 42; DB 2; Length 508;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
 |||||
 Db 273 IHHSAYPY 280

RESULT 2
 PH1065
 Ig kappa chain V region (clone 163.47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: PH1065
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1065
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-98 <TIL>
 A:Cross-references: UNIPROT:Q9RIAS; UNIPARC:UPI0000176AB5
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 74.5%; Score 41; DB 2; Length 98;
 Best Local Similarity 66.7%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 9
 |||||
 Db 89 LHYDEFPY 97

RESULT 3
 T31344
 GP80 precursor - southern cattle tick (fragment)
 C:Species: Boophilus microplus (southern cattle tick)
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31344
 R:Irving, D.; Smith, D.R.; Sharp, P.; Riding, G.; Briscoe, S.; Tellam, R.L.
 submitted to the EMBL Data Library, February 1996
 A:Description: cDNA and deduced amino acid sequences of GP80, a glycoprotein from Boophi
 A:Reference number: Z21009
 A:Accession: T31344
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1289 <HRV>
 A:Cross-references: UNIPROT:Q17174; UNIPARC:UPI00000754B9; EMBL:U49934; NID:gi224122; PI

Query Match 74.5%; Score 41; DB 2; Length 1289;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHEYPYPT 9
 |||||
 Db 1275 HHEYPYPT 1282

RESULT 4
 H90165
 hypothetical protein purA [imported] - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: H90165
 R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
 arrett, R.A.; Ragan, M.A.; Sensesen, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: H90165
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-335 <KUR>
 A:Cross-references: UNIPROT:Q980P5; UNIPARC:UPI00000641D7; GB:AE006641; NID:gi13813381; P1
 C:Genetics:
 A:Gene: purA

Query Match 72.7%; Score 40; DB 2; Length 335;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
 |||||
 Db 180 LYHGEYPY 187

```

RESULT 5
PL0275
Ig kappa chain V region (anti-DNA, GNVK and 6QVK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0275
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0275
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
A:Cross-references: UNIPARC:UPI0000176B09
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
: | |||||
DB 94 MQHLEYPYT 102

RESULT 6
E26317
Ig kappa chain V region (H37-311) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: E26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: E26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A10
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
: | |||||
DB 94 MQHLEYPYT 102

RESULT 7
A26317
Ig kappa chain V region (H37-80) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: A26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

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EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: A26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A16
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
: | |||||
DB 94 MQHLEYPYT 102

RESULT 8
PL0274
Ig kappa chain V region (anti-DNA, S10GVK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0274
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0274
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
A:Cross-references: UNIPARC:UPI0000176B0A
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
: | |||||
DB 94 MQHLEYPYT 102

RESULT 9
F26317
Ig kappa chain V regions (H35-C6, H220-25) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: F26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: F26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A1A
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene

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C;Comment: These identical chains, derived from different mice, were isolated from hybridoma cell lines.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 94 MQHLEYPYT 102

RESULT 10
G26317
Ig kappa chain V region (H37-40) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: G26317
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a hybridoma protein
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: G26317
A;Molecule type: DNA
A;Residues: 1-112 <CAT>
A;Cross-references: UNIPARC:UPI0000176A11
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus hemagglutinin
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 94 MQHLEYPYT 102

RESULT 11
B26317
Ig kappa chain V region (H37-43) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: B26317
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a hybridoma protein
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: B26317
A;Molecule type: DNA
A;Residues: 1-112 <CAT>
A;Cross-references: UNIPARC:UPI0000176A12
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus hemagglutinin
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 94 MQHLEYPYT 102

RESULT 12

S29593
Ig kappa chain (MM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S29593
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29593
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-197 <SEV>
A;Cross-references: UNIPARC:UPI0000115F08; EMBL:X57856; NID:952588; PIDN:CAA40991.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 70.9%; Score 39; DB 2; Length 197;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 109 MQHLEYPYT 117

RESULT 13

C87409
hypothetical protein CC1290 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87409
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87409
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <STO>
A;Cross-references: UNIPROT:Q9A8R1; UNIPARC:UPI00000C732D; GB:AE005673; NID:g13422625; P
C;Genetics:
A;Gene: CC1290

Query Match 70.9%; Score 39; DB 2; Length 240;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 230 VHHSSLEPYT 238

RESULT 14

D82491
hypothetical protein VCA0181 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82491
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <HEI>
A;Cross-references: UNIPROT:Q9KMY5; UNIPARC:UPI00000C3462; GB:AE004358; GB:AE003853; NID

A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C:Genetics:
A:Gene: VCA0181
A:Map position: 2

Query Match 70.9%; Score 39; DB 2; Length 291;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
||| :|||
Db 142 LHHGQYNYT 150

RESULT 15
A53186
flUG protein - Emericella nidulans
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53186
R:Lee, B.N.; Adams, T.H.
Genes Dev. 8, 641-651, 1994

A:Title: The Aspergillus nidulans flUG gene is required for production of an extracellular
A:Reference number: A53186; MUID:95011568; PMID:7926755
A:Accession: A53186
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-865 <LEE>
A:CROSS-references: UNIPROT:P38094; UNIPARC:UPI000012AA48; GB:L27817; NID:g450257; PID:g450257
C:Genetics:
A:Gene: flUG
A:Introns: 375/3; 790/1

Query Match 70.9%; Score 39; DB 2; Length 865;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
||| :|||
Db 296 LLHSSYPYT 304

RESULT 16
T43162
vitellogenin - gypsy moth
C:Species: Lymantria dispar (gypsy moth)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43162; T43268
R:Hiremath, S.T.; Lehtoma, K.
submitted to the EMBL Data Library, June 1996
A:Description: Gypsy moth vitellogenin mRNA.
A:Reference number: Z22321

A:Accession: T43162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1747 <HIR>
A:CROSS-references: UNIPROT:Q25269; UNIPARC:UPI000007E826; EMBL:U60186; NID:g13999940; PID:g13999940
R:Hiremath, S.; Lehtoma, K.
Arch. Insect Biochem. Physiol. 36, 151-164, 1997
A:Title: Structure of the gypsy moth vitellogenin gene.
A:Reference number: Z22378; MUID:97468497; PMID:9327584
C:Accession: T43268
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-819, 'Q', 821-1747 <HI2>
A:CROSS-references: UNIPARC:UPI0000084020; EMBL:U90756; NID:g2894826; PID:g2894827; PIDN:g2894827
C:Genetics:
A:Introns: 11/1; 725/2; 796/3; 1120/1; 1410/1; 1477/2
C:Superfamily: boll weevil vitellogenin

Query Match 70.9%; Score 39; DB 2; Length 1747;
Best Local Similarity 66.7%; Pred. No. 16+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
||| :|||
Db 1012 LHHSWPYS 1020

RESULT 17
D38601
Ig kappa chain V region (6A7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: D38601
R:Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: D38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <GOS>
A:CROSS-references: UNIPARC:UPI0000115178; GB:M57981; NID:g196408; PIDN:AAAG3362.1; PID:g196408
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 99;
Best Local Similarity 75.0%; Pred. No. 7, 6;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HHSSEYPYT 9
||| :|||
Db 81 HRSSEYPYT 88

RESULT 18
B23986
Ig kappa chain precursor V region (IR2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
C:Accession: B23986
R:Hellman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.
Gene 40, 107-114, 1985
A:Title: Structure and expression of kappa-chain genes in two IgE-producing rat immunocyte
A:Reference number: A91541; MUID:86137406; PMID:3005117
A:Accession: B23986
A:Molecule type: mRNA
A:Residues: 1-129 <HEL>
A:CROSS-references: UNIPARC:UPI000017679F
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
||| :|||
Db 111 LQYSEYPYT 119

RESULT 19
H90889
hypothetical protein ECs2088 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C:Accession: H90889
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinsagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90889

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <HAV>
A;Cross-references: UNIPROT:Q8XAT9; UNIPARC:UPI00000D0682; GB:BA000007; PIDN:BA035511.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2088

Query Match 69.1%; Score 38; DB 2; Length 328;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
:||:||||
Db 245 IHHPRHPT 253

RESULT 20
G64901
ABC-type transport protein bl484 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: G64901
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64901
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-328 <BLAT>
A;Cross-references: UNIPROT:P77268; UNIPARC:UPI000013A941; GB:AE000245; GB:U000096; NID:9
A;Experimental source: strain K-12, substrain MGL655
C;Keywords: ATP; nucleotide binding; P-loop
F;25-233/Domain: ATP-binding cassette homology <ABC>
F;42-49/Region: nucleotide-binding motif A (P-loop)

Query Match 69.1%; Score 38; DB 2; Length 328;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
:||:||||
Db 245 IHHPRHPT 253

RESULT 21
A85728
hypothetical protein Z2226 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: A85728
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <STO>
A;Cross-references: UNIPROT:Q8XAT9; UNIPARC:UPI00000D0682; GB:AE005174; NID:g12515197; F
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2226

Query Match 69.1%; Score 38; DB 2; Length 328;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
:||:||||

Db 245 IHHPRHPT 253

RESULT 22
T19115
hypothetical protein C08H9.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19115
R;Lloyd, C.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z19074
A;Accession: T19115
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-399 <WIL>
A;Cross-references: UNIPROT:Q17840; UNIPARC:UPI00000822DF; EMBL:Z54342; PIDN:CAA91153.1;
A;Experimental source: clone C08H9
C;Genetics:
A;Gene: CESP:C08H9.14
A;Map position: 2
A;Introns: 39/1; 134/2

Query Match 69.1%; Score 38; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
:|||||
Db 203 HSEYPY 208

RESULT 23
C82483
hypothetical protein VCA0237 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82483
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82483
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HEI>
A;Cross-references: UNIPROT:Q9KWT3; UNIPARC:UPI00000C348F; GB:AE004364; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0237
A;Map position: 2

Query Match 67.3%; Score 37; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
:|||||
Db 179 LHHSLFPY 186

RESULT 24
A99240
anthranilate synthase component II (trpGD) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C;Accession: A99240
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139
A:Accession: A99240
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <KUR>
A:Cross-references: UNIPROT:Q06129; UNIPARC:UPI0000137630; GB:AE006641; NID:gl3814072; P
C:Genetics:
A:Gene: trpGD
C:Superfamily: GMP synthase/anthranilate synthase; trpG homology

Query Match 67.3%; Score 37; DB 2; Length 195;

Best Local Similarity 71.4%; Pred. No. 23;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYP 7

|||||

DB 162 IHHEYP 168

RESULT 25

B40635

anthranilate synthase (EC 4.1.3.27) component II [validated] - Sulfolobus solfataricus

N:Alternate names: anthranilate synthase beta chain; glutamine amidotransferase

C:Species: Sulfolobus solfataricus

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004

C:Accession: B40635

R:Tutino, M.L.; Scarano, G.; Marino, G.; Sannia, G.; Cubellis, M.V.

J. Bacteriol. 175, 299-302, 1993

A:Title: Tryptophan biosynthesis genes trpEGC in the thermoacidophilic archaeobacterium S

A:Reference number: A40635; MUID:93106970; PMID:8416906

A:Accession: B40635

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-195 <TUT>

A:Cross-references: UNIPROT:Q06129; UNIPARC:UPI0000112A5A; GB:M98048; NID:gl52936; PIDN:

A:Experimental source: MT-4

A:Note: sequence extracted from NCBI backbone (NCBIN:121234, NCBI:P:121236)

C:Genetics:

A:Gene: trpG

C:Complex: heterotetramer; two component I chains (PIR:JCS323), two component II chains

C:Function: <ANT>

A:Description: EC 4.1.3.27 [validated, MUID:97168965]

A:Pathway: tryptophan biosynthesis

A:Note: first step

C:Function: <COM2>

A:Description: EC 2.6.-.- [validated, MUID:99380543]; glutamine amidotransferase; compon

r channel to a synthase active site

A:Note: belongs to the family of "triad" glutamine amidotransferases

C:Superfamily: GMP synthase/anthranilate synthase; trpG homology

C:Keywords: carbon-carbon lyase; oxo-acid-lyase; tryptophan biosynthesis

F:4-192/Domain: trpG homology <TRG>

F:84/Active site: Cys #status predicted

Query Match 67.3%; Score 37; DB 2; Length 195;

Best Local Similarity 71.4%; Pred. No. 23;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYP 7

|||||

DB 162 IHHEYP 168

RESULT 26

D84719

hypothetical protein At2g31330 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84719

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84719

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-326 <STO>

A:Cross-references: UNIPROT:Q9SID5; UNIPARC:UPI00000A608D; GB:AE002093; NID:g4589967; P

C:Genetics:

A:Gene: At2g31330

A:Map position: 2

Query Match 67.3%; Score 37; DB 2; Length 326;

Best Local Similarity 62.5%; Pred. No. 40;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HHSEYPYT 9

|||||

DB 66 HHQSYPT 73

RESULT 27

T52184

zinc transporter ZIP2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52184

R:Grotz, N.; Fox, T.; Connolly, E.; Park, W.; Guerinot, M.L.; Eide, D.

Proc. Natl. Acad. Sci. U.S.A. 95, 7220-4, 1998

A:Title: Identification of a family of zinc transporter genes from Arabidopsis that res

A:Reference number: Z55114; MUID:9618566; PMID:9618566

A:Accession: T52184

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-353 <GRO>

A:Cross-references: UNIPROT:Q9LTH9; UNIPARC:UPI00000A7A9F; EMBL:AF033536; PIDN:AAC24198

A:Experimental source: strain Landsberg erecta

C:Genetics:

A:Gene: ZIP2

C:Function:

A:Description: involved in zinc uptake

Query Match 67.3%; Score 37; DB 2; Length 353;

Best Local Similarity 75.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8

|||||

DB 122 LKHSEYPY 129

RESULT 28

D69974

formate dehydrogenase homolog yrhE - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004

C:Accession: D69974

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoz

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chr

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.P

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, P.; Kurita, K.; Lapidus, A.; Lardinols,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellr

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seroi

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestre, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: D69974

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-980 <KUN>
A:Cross-references: UNIPROT:O05397; UNIPARC:UPI0000060805; GB:Z99117; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yrhE
C:Superfamily: NAD-dependent formate dehydrogenase, alpha subunit; ferredoxin 2 [4Fe-4S]
F:146-213/Domain: ferredoxin 2 [4Fe-4S] homology <FER>

Query Match 67.3%; Score 37; DB 2; Length 980;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: || : |||
Db 122 IEHQKYPYT 130

RESULT 29
S57451
cysteine proteinase (EC 3.4.22.-) 3 - Tritrichomonas foetus (fragment)
C:Species: Tritrichomonas foetus
A:Variety: strain F2
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C:Accession: S57451
R:Mallinson, D.J.; Livingstone, J.; Appleton, K.M.; Lees, S.; Coombs, G.H.; North, M.J.
submitted to the EMBL Data Library, June 1995
A:Description: Multiple cysteine proteinases of the pathogenic protozoan tritrichomonas f
A:Reference number: S57421
A:Accession: S57451
A:Molecule type: DNA
A:Residues: 1-157 <MAL>
A:Cross-references: UNIPROT:Q26987; UNIPARC:UPI00000800CFD; EMBL:X87776; NID:9871554; PID
A:Experimental source: strain F2
C:Genetics:
A:Gene: TFCP3
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase

Query Match 65.5%; Score 36; DB 2; Length 157;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
: || : |||
Db 60 HEDYPYT 66

RESULT 30
E75151
molybdenum cofactor biosynthesis protein (moac) PAB2103 - Pyrococcus abyssi (strain Orsa
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: E75151
R:anonymous; Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75151
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-159 <KAW>
A:Cross-references: UNIPROT:Q9VLQ7; UNIPARC:UPI00000346A5; GB:AJ248284; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2103
C:Superfamily: molybdenum cofactor precursor Z biosynthesis protein MoaC

Query Match 65.5%; Score 36; DB 2; Length 159;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
: || : |||
Db 136 HGQYPYT 142

RESULT 31
F83898
spore germination protein BH1990 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83898
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83898
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <STO>
A:Cross-references: UNIPROT:Q9KBD8; UNIPARC:UPI000000C3D74; GB:AP001513; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1990
C:Superfamily: spore germination protein III

Query Match 65.5%; Score 36; DB 2; Length 178;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
: || : |||
Db 132 IKHSDYPY 139

RESULT 32
A99949
hypothetical protein opp-1D [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A99949
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A99949
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <KUR>
A:Cross-references: UNIPROT:Q99RG9; UNIPARC:UPI000000CAC99; GB:BA0000018; PID:gl3702414; P
A:Experimental source: strain N315
C:Genetics:
A:Gene: opp-1D

Query Match 65.5%; Score 36; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: || : |||
Db 239 LHHPEHYVT 247

RESULT 33
B82212
hypothetical protein VC1330 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82212
R:Heideberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.B.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82212
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <HEI>
A:CROSS-references: UNIPROT:Q9KSC8; UNIPARC:UPI00000C2F5B; GB:AE004213; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1330
A:Map position: 1

Query Match 65.5%; Score 36; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8
:||||: ||
Db 85 VHHSDLUPY 92

RESULT 34
G90032
hypothetical protein SA2123 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Accession: G90032
A:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89759; MUID:21311952; PMID:11418146
A:Accession: G90032
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <KUR>
A:CROSS-references: UNIPROT:Q99RUI; UNIPARC:UPI0000054A06; GB:BA000018; PID:gl3702132; F
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2123

Query Match 65.5%; Score 36; DB 2; Length 294;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHSEYP 7
:||||:
Db 112 HHSDYP 117

RESULT 35
T15375
hypothetical protein C02B8.6 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
A:Accession: T15375
R:Johnson, D.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of *C. elegans* cosmid C02B8.
A:Reference number: S69012
A:Accession: T15375
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-347 <JOH>
A:CROSS-references: UNIPARC:UPI000017B716; EMBL:U40421; NID:gi065521; PID:gi065524; PIDN
C:Genetics:
A:Gene: CESP-C02B8.6
A:Introns: 69/1; 92/1; 117/1; 195/1

Query Match 65.5%; Score 36; DB 2; Length 347;
Best Local Similarity 71.4%; Pred. No. 64;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
:||||:
Db 145 HSDFFPT 151

RESULT 36
C96620
protein T30B16.23 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: C96620
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huiziar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marfiali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96620
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1076 <STO>
A:CROSS-references: UNIPROT:Q9LQ50; UNIPARC:UPI000009E2B8; GB:AE005173; NID:g8778749; P
C:Genetics:
A:Gene: T30B16.23
A:Map position: 1

Query Match 65.5%; Score 36; DB 2; Length 1076;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHSEY 6
:||||:
Db 921 LHHSEY 926

RESULT 37
A88554
protein C38C10.5a [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A:Accession: A88554
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Accession: A88554
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1385 <STO>
A:CROSS-references: UNIPROT:Q03570; UNIPARC:UPI000002B707; GB:chr_III; PIDN:CAA79551.1;
C:Genetics:
A:Gene: C38C10.5a
A:Map position: 3
C:Superfamily: *Caenorhabditis elegans* hypothetical protein C38C10.5

Query Match 65.5%; Score 36; DB 2; Length 1385;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYP 7
:||||:
Db 1377 LHHQOYP 1383

```
RESULT 38
B88554
Protein C38C10.5b [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B88554
R;anonymouse, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: B88554
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Molecule type: DNA
A;Residues: 1-1391 <STO>
A;Cross-references: UNIPROT:Q03570; UNIPARC:UPI000013B807; GB:chr_III; PIDN:CAA82365.1;
A;Note: cDNA EST EMBL:Cl1839 comes from this gene
C;Genetics:
A;Gene: C38C10.5b
A;Map position: 3
C;Superfamily: Caenorhabditis elegans hypothetical protein C38C10.5

Query Match      65.5%; Score 36; DB 2; Length 1391;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYP 7
    ||| :||
Db 1383 LHHQOYP 1389

RESULT 39
A55535
versican precursor - mouse
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
versican
N;Contains: glial hyaluronate-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55535
R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate
A;Reference number: A55535; MUID:9512551; PMID:7822336
A;Accession: A55535
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2397 <RES>
A;Cross-references: UNIPARC:UPI000002717E; GB:D16263; NID:g862460; PIDN:BAA03796.1; PID:
F;1-20/Domain: versican; C-type lectin homology; complement factor H repeat homology; EG
F;21-1654/Domain: signal sequence #status predicted <SIG>
F;167-244/Domain: versican #status predicted <MAR>
F;265-346/Domain: link protein repeat homology <LNK1>
F;2095-2126/Domain: link protein repeat homology <LNK2>
F;2133-2164/Domain: EGF homology <EG1>
F;2133-2164/Domain: EGF homology <EG2>
F;2171-2291/Domain: C-type lectin homology <LCH>
F;2298-2354/Domain: complement factor H repeat homology <PHD>

Query Match      65.5%; Score 36; DB 1; Length 2397;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEY 6
    |||||
Db 1505 LHHSEY 1510

RESULT 40
H69859
hypothetical protein ykoL - Bacillus subtilis
C;Species: Bacillus subtilis
```

```
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69859
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69859
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-60 <KUN>
A;Cross-references: UNIPROT:O34763; UNIPARC:UPI00000602C4; GB:Z99110; GB:Z99111; GB:AL00
A;Experimental source: strain 168
C;Genetics:
A;Gene: ykoL

Query Match      63.6%; Score 35; DB 2; Length 60;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHSEYPYT 9
    :|||
Db 52 NHHKYPYT 59

RESULT 41
C84218
hypothetical protein Vng0599c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84218
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84218
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-93 <STO>
A;Cross-references: UNIPROT:Q9HRP7; UNIPARC:UPI000006369A; GB:AE004437; NID:g10580195; P
C;Genetics:
A;Gene: VNG0599C

Query Match      63.6%; Score 35; DB 2; Length 93;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
    :|||
Db 86 HARYPYT 92

RESULT 42
D26317
Ig kappa chain V region (H37-84) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1998 #sequence_revision 15-Dec-1998 #text_change 21-Jan-2000
C;Accession: D26317
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
```

EMBO J. 5, 1577-1587, 1986
A>Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: D26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A18
A:Experimental source: strain Balb/c
A>Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 63.6%; Score 35; DB 2; Length 112;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHSEYPT 9
: | |||:
94 MQHLEPT 102

Db

RESULT 43
I26317
Ig kappa chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: I26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A>Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: I26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A0D
A:Experimental source: strain Balb/c
A>Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 63.6%; Score 35; DB 2; Length 112;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHSEYPT 9
: | |||:
94 MQHLEPT 102

Db

RESULT 44
S04574
Ig kappa chain precursor V region (MRL-RP24L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04574
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A>Title: Molecular analysis of the murine lupus-associated anti-self response: involveme
A:Reference number: S04573; MUID:87133856; PMID:3102255
A:Accession: S04574
A:Molecule type: mRNA
A:Residues: 1-127 <KOF>
A:Cross-references: UNIPARC:UPI0000115DFF; EMBL:X14621; NID:952404; PIDN:CAA32774.1; PID
A>Note: The authors translated the codon TAT for residue 30 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 63.6%; Score 35; DB 2; Length 127;
Best Local Similarity 71.4%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 9
: | |||:
111 HNEYPWT 117

Db

RESULT 45
A69835
hypothetical protein yhjR - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A:Accession: A69835
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertel
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrast, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, A
A:Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69835
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-145 <KUN>
A:Cross-references: UNIPROT:O07572; UNIPARC:UPI00000601B8; GB:Z99109; GB:AL009126; NID:
A:Experimental source: strain 168
C:Genetics:
A:Gene: yhjR

Query Match 63.6%; Score 35; DB 2; Length 145;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSEYPT 8
: | |||:
1 MHYSYPT 8

Db

RESULT 46
H95210
type IV prepilin peptidase, probable [imported] - Streptococcus pneumoniae (strain TIGR4
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
A:Accession: H95210
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, P.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KUR>
A:Cross-references: UNIPROT:Q97P36; UNIPARC:UPI00000519C7; GB:AE005672; PIDN:AAK75881.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI808

Query Match 63.6%; Score 35; DB 2; Length 219;

Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYP 7
Db 111 HHQYYP 116

RESULT 47
T22282
hypothetical protein F46B3.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22282
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19541
A;Accession: T22282
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-304 <WLT>
A;Cross-references: UNIPROT:Q9XV13; UNIPARC:UPI000007D4D9; EMBL:Z81540; PIDN:CAB04407.1;
A;Experimental source: clone F46B3
C;Genetics:
A;Gene: CESP:F46B3.11
A;Map position: 5
A;Introns: 51/3; 67/2; 163/3; 217/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K02H11.4

Query Match 63.6%; Score 35; DB 2; Length 304;
Best Local Similarity 71.4%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYPY 8
Db 7 HHQIYPY 13

RESULT 48
T52299
squamosa promoter binding protein-homolog 3 [imported] - garden snapdragon
C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52299
R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.
Gene 237, 91-104, 1999
A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Reference number: Z25236; MUID:99453765; PMID:10524240
A;Accession: T52299
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-305 <CAR>
A;Cross-references: UNIPROT:Q9SNV5; UNIPARC:UPI00000AB0F0; EMBL:AJ011621; PIDN:CAB56568.
C;Genetics:
A;Gene: sbph3

Query Match 63.6%; Score 35; DB 2; Length 305;
Best Local Similarity 57.1%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYPY 8
Db 60 HHQIYPY 66

RESULT 49
S07916
RF4 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1
C;Species: Kluyveromyces marxianus var. lactis, Candida spbaerica
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S07916; S22787; S32600
R;Stark, M.J.R.; Mileham, A.J.; Romanos, M.A.; Boyd, A.
Nucleic Acids Res. 12, 6011-6030, 1984

A;Title: Nucleotide sequence and transcription analysis of a linear DNA plasmid associat
A;Reference number: S07353; MUID:84297209; PMID:6473099
A;Accession: S07916
A;Molecule type: DNA
A;Residues: 1-428 <STA>
A;Cross-references: UNIPROT:P09806; UNIPARC:UPI0000133797; EMBL:X00762; NID:G2842; PIDN:
R;Hishinuma, F.; Nakamura, K.; Hirai, K.; Nishizawa, R.; Gunge, N.; Maeda, T.
Nucleic Acids Res. 12, 7581-7597, 1984
A;Title: Cloning and nucleotide sequences of the linear DNA killer plasmids from yeast.
A;Reference number: S07358; MUID:85037931; PMID:6387625
A;Accession: S22787
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-428 <HTS>
A;Cross-references: UNIPARC:UPI0000133797; EMBL:X01095; NID:G2847; PIDN:CAA25570.1; PID:
R;Sor, F.; Fukuhara, H.
Curr. Genet. 9, 147-155, 1995
A;Title: Structure of a linear plasmid of the yeast Kluyveromyces lactis; compact organi
A;Reference number: S32598
A;Accession: S32600
A;Molecule type: DNA
A;Residues: 1-428 <SOR>
A;Cross-references: UNIPARC:UPI0000133797; EMBL:X07127; NID:G2827; PIDN:CAA30138.1; PID:
C;Genetics:
A;Genome: plasmid

Query Match 63.6%; Score 35; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYP 7
Db 276 HHKEYP 281

RESULT 50
T32301
hypothetical protein M151.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32301
R;Gattung, S.; Gosla, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid M151.
A;Reference number: Z21148
A;Accession: T32301
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-494 <GAT>
A;Cross-references: UNIPROT:O17121; UNIPARC:UPI000017BAD5; EMBL:AF024502; PIDN:AAB70378.
A;Experimental source: strain Bristol N2; clone M151
C;Genetics:
A;Gene: CESP:M151.1
A;Map position: 2
A;Introns: 42/2; 57/3; 91/1; 161/1; 206/1; 263/1; 309/1; 327/1; 352/1; 366/1; 390/1; 410

Query Match 63.6%; Score 35; DB 2; Length 494;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HHSEYPYT 9
Db 97 HHADHPHT 104

Search completed: May 11, 2006, 16:38:14
Job time : 24.2787 secs

GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:16:20 ; Search time 83.2131 Seconds
(without alignments)
76.307 Million cell updates/sec

Title: US-10-808-538-6
Perfect score: 55
Sequence: 1 LHSEYPYT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	81.8	337	2	Q4JAU1 SULAC
2	44	80.0	266	2	Q5ZD00 VIBF1
3	43	78.2	407	2	Q6HA07 BRALA
4	43	78.2	704	2	Q4V464 DROME
5	43	78.2	2159	2	Q7KVD8 DROSOPHILA
6	43	78.2	2649	2	Q9W0T2 DROSOPHILA
7	43	78.2	2669	2	Q95VB8 DROSOPHILA
8	43	78.2	2669	2	Q9W0T1 DROSOPHILA
9	42	76.4	186	2	Q6LXU6 METMP
10	42	76.4	293	2	Q7Q6E2 ANOGA
11	42	76.4	387	2	Q6TYQ4 PAPHA
12	42	76.4	390	2	Q6TYQ6 MACMU
13	42	76.4	508	1	CROC DROME
14	42	76.4	508	2	Q53YH1 DROSOPHILA
15	42	76.4	677	2	Q7V4W3 PROCHLORO
16	42	76.4	2705	2	Q9W6V6 CHICK
17	41	74.5	315	2	Q623S5 CAENORHABDI
18	41	74.5	943	2	Q7JKS4 9VIRU
19	41	74.5	1289	2	Q17174 BOOMI
20	40	72.7	335	2	Q980P5 SULSO
21	40	72.7	335	2	Q975Y7 SULTO
22	40	72.7	378	2	Q9AJU2 SACTO
23	40	72.7	587	2	Q86JT5 DICDI
24	40	72.7	873	1	HEPA HCMVA
25	40	72.7	873	2	Q6RXD5 HCMV
26	40	72.7	873	2	Q6SW42 HCMV
27	40	72.7	1828	2	Q80TD2 MOUSE
28	40	72.7	2346	2	Q9ULCI MOUSE
29	40	72.7	2715	2	Q9WTS6 MOUSE
30	39	70.9	111	2	Q8EJW8 SHEON
31	39	70.9	112	2	Q6LEW8 MOUSE

32	39	70.9	202	2	Q746U6 GBOSL
33	39	70.9	234	2	Q5XKG4 MOUSE
34	39	70.9	240	2	Q9A8R1 CAUCR
35	39	70.9	281	2	Q8DSU2 VIBVU
36	39	70.9	281	2	Q7MCM0 VIBVU
37	39	70.9	289	2	Q87G78 VIBPA
38	39	70.9	291	2	Q9KMY5 VIBCH
39	39	70.9	755	2	Q7S199 NEUCR
40	39	70.9	860	2	Q4WU9 ASPFU
41	39	70.9	865	1	FLUG EMENI
42	39	70.9	865	2	Q51PK8 MAGGR
43	39	70.9	865	2	Q5B3R1 EMENI
44	39	70.9	877	2	Q5PZ35 AJECA
45	39	70.9	1747	2	Q25265 LYMDI
46	39	70.9	1747	2	Q25269 LYMDI
47	39	70.9	2725	2	Q9UKZ4 HUMAN
48	39	70.9	2725	2	Q5JZ17 HUMAN
49	39	70.9	2731	2	Q9WTS4 MOUSE
50	38	69.1	235	2	Q8XYZ8 RALSO
51	38	69.1	276	2	Q72U85 LEPIC
52	38	69.1	276	2	Q8F0V1 LEPIN
53	38	69.1	328	1	YDDP ECOLI
54	38	69.1	328	2	Q8XAT9 ECO57
55	38	69.1	328	2	Q83KV6 SHIFL
56	38	69.1	336	2	Q9DDQ8 XENLA
57	38	69.1	393	2	Q6N9F1 RHOPA
58	38	69.1	398	2	Q9NRU0 HUMAN
59	38	69.1	399	2	Q17840 CABEL
60	38	69.1	454	2	Q76XF2 9CAUD
61	38	69.1	496	2	Q4V7X9 XENLA
62	38	69.1	734	2	Q75DPI ASHGO
63	38	69.1	959	2	Q9NXU8 HUMAN
64	38	69.1	959	2	Q4W5P9 HUMAN
65	38	69.1	972	2	Q9FLH9 ARATH
66	38	69.1	2916	2	Q8V1P9 HUMAN
67	37	67.3	158	2	Q4PKF6 9BACT
68	37	67.3	169	2	Q870Y2 NEUCR
69	37	67.3	189	2	Q9KMT3 VIBCH
70	37	67.3	195	1	TRPG SULSO
71	37	67.3	262	1	WOX3A MAIZE
72	37	67.3	267	2	Q52PG6 BACST
73	37	67.3	290	2	Q8BFV6 PARTE
74	37	67.3	302	2	Q65QP8 MANSM
75	37	67.3	326	2	Q9SID5 ARATH
76	37	67.3	333	2	Q5KQ37 CRYNE
77	37	67.3	342	2	Q91F03 GVCP
78	37	67.3	353	1	ZIP2 ARATH
79	37	67.3	354	2	Q59K30 CANAL
80	37	67.3	367	2	Q5WKJ7 BACSK
81	37	67.3	395	2	Q6TYO7 MIOA
82	37	67.3	396	2	Q89IC1 BRAJA
83	37	67.3	422	2	Q7XPC8 OYSA
84	37	67.3	434	2	Q7V8L0 PROMM
85	37	67.3	456	2	Q4J9X8 SULAC
86	37	67.3	493	2	Q9LRA5 ARATH
87	37	67.3	539	2	Q9BS20 HUMAN
88	37	67.3	545	2	Q8S9K1 ARATH
89	37	67.3	549	1	ZNF34 HUMAN
90	37	67.3	552	2	Q74721 KUULA
91	37	67.3	554	2	Q6CRL8 KUULA
92	37	67.3	577	2	Q5WBZ1 BACSK
93	37	67.3	603	2	Q5WK8 LRGPL
94	37	67.3	606	2	Q561D6 CRYNE
95	37	67.3	622	2	Q5BED4 EMENI
96	37	67.3	663	2	Q9UVU1 PICME
97	37	67.3	800	2	Q7X9G6 9NAGN
98	37	67.3	945	2	Q7TP79 RAT
99	37	67.3	980	2	Q795Y4 BACSU
100	37	67.3	982	2	Q05397 BACSU
101	37	67.3	1197	2	Q7R1R4 GIALA
102	37	67.3	1343	2	Q91FW9 IRV6
103	36.5	66.4	733	2	Q926C7 RHIME
104	36	65.5	67	2	Q6TUI6 ASCSU

Q746u6	geobacter s
Q5xkg4	mus musculus
Q9a8r1	caulobacter
Q8dsu2	vibrio vuln
Q7mcw0	vibrio vuln
Q87g78	vibrio para
Q9kmy5	vibrio chol
Q7s199	neurospora
Q4wu9	aspergillus
P38094	emericaella
Q51pk8	magnaporthe
Q5b3r1	aspergillus
Q5p235	ajellomyces
Q25265	lymantria d
Q25269	lymantria d
Q9ukz4	homo sapien
Q5jz17	homo sapien
Q9wts4	mus musculus
Q8xyz8	raletonia s
Q72u85	leptosira
Q8f0v1	leptosira
P77268	escherichia
Q8xat9	escherichia
Q83kv6	shigella fl
Q9ddq8	xenopus lae
Q6n9f1	rhodopseudo
Q9nr00	homo sapien
Q17840	caenorhabdi
Q76xf2	enterobacte
Q4v7x9	xenopus lae
Q75dpl	ashbya goss
Q9nxu8	homo sapien
Q4w5p9	homo sapien
Q9flh9	arabidopsis
Q6v1p9	homo sapien
Q4pkf6	uncultured
Q870y2	neurospora
Q9kmt3	vibrio chol
Q06129	sulfolobus
Q70u1	zea mays (m
Q52pg6	bacillus st
Q6bfv6	paramecium
Q65qp8	mannheimia
Q9sid5	arabidopsis
Q5kq37	cryptococcu
Q91f03	cydia pomon
Q91th9	arabidopsis
Q5wkj7	candida alb
Q6tyo7	miopithecu
Q89ic1	bradyrhizob
Q7xpc8	oryza sativ
Q7v8l0	prochloroco
Q4j9x8	sulfolobus
Q9lra5	arabidopsis
Q9bs20	homo sapien
Q8s9k1	arabidopsis
Q81z26	homo sapien
Q74721	kluyveromy
Q6crl8	kluyveromy
Q5wbz1	bacillus cl
Q5wk8	legionella
Q561d6	cryptococcu
Q5bed4	aspergillus
Q9uvu1	pichia mech
Q7x9g6	delphinium
Q7tp79	rattus norv
Q795y4	bacillus su
Q05397	bacillus su
Q7r1r4	giardia lam
Q91fw9	chilo iride
Q926c7	rhizobium m
Q6tui6	ascaris suu

105	36	65.5	129	2	Q4Y952	PLASMODIUM
106	36	65.5	146	2	Q4MLK0	BACILLUS CE
107	36	65.5	146	2	Q6HH29	BACILLUS TH
108	36	65.5	146	2	Q7J506	BACILLUS CE
109	36	65.5	146	2	Q81BV3	BACILLUS AN
110	36	65.5	146	2	Q81NV9	BACILLUS AN
111	36	65.5	146	2	Q639P8	BACILLUS CE
112	36	65.5	157	2	Q26987	TRITICOMO
113	36	65.5	159	1	MOAC_PYRAB	
114	36	65.5	167	2	Q5AYC9	EMENI
115	36	65.5	169	2	Q65YW0	9VIRU
116	36	65.5	178	2	Q9KBD8	BACILLUS HA
117	36	65.5	213	2	Q929Q3	BACILLUS HA
118	36	65.5	252	1	MED20	DROME
119	36	65.5	260	2	Q90WX2	BRACHYDANIO
120	36	65.5	271	2	Q9ZGN9	STAPHYLOCOCC
121	36	65.5	271	2	Q99RG9	STAPHYLOCOCC
122	36	65.5	271	2	Q8NUX3	STAPHYLOCOCC
123	36	65.5	271	2	Q7A3N3	STAPHYLOCOCC
124	36	65.5	271	2	Q6GDY1	STAPHYLOCOCC
125	36	65.5	271	2	Q6G6K6	STAPHYLOCOCC
126	36	65.5	271	2	Q9HDB7	STAPHYLOCOCC
127	36	65.5	275	2	Q9KSC8	VIBRIO CHOL
128	36	65.5	294	2	Q5HDM5	STAPHYLOCOCC
129	36	65.5	294	2	Q6G6V8	STAPHYLOCOCC
130	36	65.5	294	2	Q6GEA3	STAPHYLOCOCC
131	36	65.5	294	2	Q8NV64	STAPHYLOCOCC
132	36	65.5	294	2	Q931G0	STAPHYLOCOCC
133	36	65.5	294	2	Q99RU1	STAPHYLOCOCC
134	36	65.5	309	2	Q4ZVG6	PSEUDOMONAS
135	36	65.5	335	2	Q5AV98	EMENI
136	36	65.5	347	1	YVZ6	CABEL
137	36	65.5	383	2	Q6TYQ5	CERAE
138	36	65.5	393	2	Q96635	TRYCR
139	36	65.5	441	2	Q5RDT6	PONPY
140	36	65.5	448	2	Q5DCC8	SCHJA
141	36	65.5	452	2	Q59U75	CANAL
142	36	65.5	457	2	Q750A7	ASHGO
143	36	65.5	481	2	Q4YX4	DICDI
144	36	65.5	524	2	Q4P217	USTMA
145	36	65.5	555	2	Q7R985	PLAYO
146	36	65.5	559	2	Q6D978	ERWCT
147	36	65.5	574	2	Q5B2T8	EMENI
148	36	65.5	642	2	Q7XX97	ORYSA
149	36	65.5	646	2	Q6FXI4	CANGA
150	36	65.5	664	2	Q5S059	9SACH
151	36	65.5	664	2	Q5UVU2	PICME
152	36	65.5	684	2	Q5CWA6	CRYPV
153	36	65.5	701	2	Q97357	TRYCR
154	36	65.5	977	2	Q9LQ50	ARATH
155	36	65.5	1076	2	Q9W614	ORYZIAS LAT
156	36	65.5	1100	2	Q9W614	ORYZIAS LAT
157	36	65.5	1134	2	Q87342	ORYZIAS LAT
158	36	65.5	1374	1	RGR1	CABEL
159	36	65.5	1596	2	Q8T307	TRYBB
160	36	65.5	1888	2	Q4QID1	LEIMA
161	36	65.5	2575	2	Q5ZDC4	MAGR
162	36	65.5	3358	1	Q5PG2	MOUSE
163	36	65.5	3848	2	Q8IDR0	PLAF7
164	35	64.5	1661	2	Q7QX84	GIALA
165	35	63.6	60	1	YKOL	BACSU
166	35	63.6	93	1	RNP4	HALSA
167	35	63.6	96	2	Q9W512	DROME
168	35	63.6	119	2	Q59X20	CANAL
169	35	63.6	140	2	Q6C9B9	YARLI
170	35	63.6	145	2	O07572	BACSU
171	35	63.6	153	1	MYELA	XENLA
172	35	63.6	167	2	Q4N1I9	THEPA
173	35	63.6	176	2	Q6AC33	LEIXX
174	35	63.6	191	2	Q4UB03	THEAN
175	35	63.6	204	2	Q4WY89	ASPERGILLUS
176	35	63.6	206	2	Q4SSN9	TETNG
177	35	63.6	211	2	Q561J0	CRYNE

178	35	63.6	211	2	Q5KQ93	CRYNE
179	35	63.6	212	2	Q6PDR8	MOUSE
180	35	63.6	219	2	Q97P36	STRPN
181	35	63.6	229	2	Q6SSG6	9CNID
182	35	63.6	240	2	Q4RHL6	TETNG
183	35	63.6	250	2	Q9MD46	SCHMA
184	35	63.6	261	2	Q5B0Z6	EMENI
185	35	63.6	261	2	Q4WNG6	ASPERGILLUS
186	35	63.6	265	1	WOX3B	MAIZE
187	35	63.6	276	2	Q4RX60	TETNG
188	35	63.6	283	2	Q94UX7	SCHJA
189	35	63.6	283	2	Q94NU5	SCHJA
190	35	63.6	284	2	Q94UX4	SCHJA
191	35	63.6	289	2	Q9H692	HUMAN
192	35	63.6	297	2	Q5B1S4	EMENI
193	35	63.6	302	2	Q621Q0	CABER
194	35	63.6	305	2	Q9SNV5	ANTMA
195	35	63.6	306	2	Q4N040	THEPA
196	35	63.6	313	2	Q5B9S1	EMENI
197	35	63.6	313	2	Q82HH8	STRAW
198	35	63.6	313	2	Q4V790	XENTR
199	35	63.6	316	2	Q6AMT8	DESFS
200	35	63.6	326	2	Q9XV13	CABEL
201	35	63.6	329	2	Q4P9Z5	USTMA
202	35	63.6	329	2	Q7MZJ5	PHOLL
203	35	63.6	333	2	Q8SYD6	DROME
204	35	63.6	334	2	Q5HK08	STAEQ
205	35	63.6	334	2	Q8CQK3	STAEQ
206	35	63.6	339	2	Q811C7	DROPS
207	35	63.6	350	2	Q65GN5	BACILD
208	35	63.6	351	2	Q66JQ2	MOUSE
209	35	63.6	359	2	Q5ATZ3	EMENI
210	35	63.6	364	2	Q9B8X3	SCHMA
211	35	63.6	371	2	Q9B900	SCHJA
212	35	63.6	372	2	Q9B8V1	9TREM
213	35	63.6	372	2	Q9B898	9TREM
214	35	63.6	392	2	Q4T4W4	TETNG
215	35	63.6	401	2	Q6JHM9	9PSEU
216	35	63.6	428	1	RP4	KLULA
217	35	63.6	431	2	Q9V635	DROME
218	35	63.6	447	2	Q14913	HUMAN
219	35	63.6	447	2	Q8BX23	MOUSE
220	35	63.6	471	2	Q4R732	MACFA
221	35	63.6	505	2	Q6PC79	BRARE
222	35	63.6	523	1	TRPE	VIBCH
223	35	63.6	548	2	Q4S2T7	TETNG
224	35	63.6	555	2	Q6LGN4	PHOPR
225	35	63.6	587	2	Q9IAA1	CARAU
226	35	63.6	604	2	Q819K7	9TRYP
227	35	63.6	611	2	Q6CVT5	ERWCT
228	35	63.6	685	2	Q7R1Q9	GIALA
229	35	63.6	693	2	Q88PD6	PSEPK
230	35	63.6	702	2	Q96JL8	HUMAN
231	35	63.6	716	2	Q5QYB1	IDILO
232	35	63.6	729	2	Q8A916	BACTN
233	35	63.6	743	2	Q4UAS1	THEAN
234	35	63.6	766	1	FGD4	MOUSE
235	35	63.6	766	1	FGD4	RAT
236	35	63.6	809	2	Q6XZC4	ASTMI
237	35	63.6	826	1	LOZEN	DROME
238	35	63.6	830	2	Q6ZSL7	HUMAN
239	35	63.6	842	2	Q61B81	HUMAN
240	35	63.6	845	2	Q6XZF4	ASTMI
241	35	63.6	849	2	Q9XSR4	SOVIN
242	35	63.6	848	2	Q87TF2	VIBPA
243	35	63.6	880	2	Q54W38	DICDI
244	35	63.6	977	2	Q51QV3	MAGGR
245	35	63.6	985	2	Q4XQ36	PLACH
246	35	63.6	993	2	Q48915	MICAE
247	35	63.6	1173	2	Q9VHC2	DROME
248	35	63.6	1271	2	Q7QT29	GIALA
249	35	63.6	1413	2	Q9VJJ8	DROME
250	35	63.6	1485	2	Q52D73	MAGGR

Q5KQ93	CRYPTOCOCCU
Q6PDR8	MUS MUSCULU
Q97P36	STREPTOCOCC
Q6SSG6	NEMATOSTELL
Q4RHL6	TETRAODON N
Q9MD46	SCHISTOSOMA
Q5B0Z6	ASPERGILLUS
Q4WNG6	ASPERGILLUS
Q6313	ZEAE MAYS (M
Q4RX60	TETRAODON N
Q94UX7	SCHISTOSOMA
Q94NU5	SCHISTOSOMA
Q94UX4	SCHISTOSOMA
Q9H692	HOMO SAPIEN
Q5B1S4	ASPERGILLUS
Q621Q0	CAENORHABDI
Q9SNV5	ANTIRRHINUM
Q4N040	THEILERIA P
Q5B9S1	ASPERGILLUS
Q82HH8	STREPTOMYCE
Q4V790	XENOPUS TRO
Q6AMT8	DESULFOTALE
Q9XV13	CAENORHABDI
Q4P9Z5	USTILAGO MA
Q7MZJ5	PHOTORHABDU
Q8SYD6	DROSOPHILA
Q5HK08	STAPHYLOCOCC
Q8CQK3	STAPHYLOCOCC
Q811C7	DROSOPHILA
Q65GN5	BACILLUS LI
Q66JQ2	MUS MUSCULU
Q5ATZ3	ASPERGILLUS
Q9B8X3	SCHISTOSOMA
Q9B900	SCHISTOSOMA
Q9B8V1	SCHISTOSOMA
Q9B898	SCHISTOSOMA
Q4T4W4	TETRAODON N
Q6JHM9	SACCHAROPOL
RP4	KLUYVEROMYCE
Q9V635	DROSOPHILA
Q14913	HOMO SAPIEN
Q8BX23	MUS MUSCULU
Q4R732	MACACA FASC
Q6PC79	BRACHYDANIO
Q9KST2	VIBRIO CHOL
Q4S2T7	TETRAODON N
Q6LGN4	PHOTOBACTER
Q9IAA1	CARASSIUS A
Q819K7	TRYPAELOSOMA
Q6CVT5	ERWINIA CAR
Q7R1Q9	GIARDIA LAM
Q88PD6	PSEUDOMONAS
Q96JL8	HOMO SAPIEN
Q5QYB1	IDIOGRAMMA
Q8A916	BACTERIOIDES
Q4UAS1	THEILERIA A
Q91ZT5	MUS MUSCULU
Q88387	RATTUS NORV
Q6XZC4	ASTERINA MI
Q9W349	DROSOPHILA
Q6ZSL7	HOMO SAPIEN
Q61B81	HOMO SAPIEN
Q6XZF4	ASTERINA MI
Q9XSR4	BOS TAURUS
Q87TF2	VIBRIO PARA
Q54W38	DICTYOSTELI
Q51QV3	MAGNAPORTHE
Q4XQ36	PLASMODIUM
Q48915	MICROCYSTIS
Q9VHC2	DROSOPHILA
Q7QT29	GIARDIA LAM
Q9VJJ8	DROSOPHILA
Q52D73	MAGNAPORTHE

251	35	63.6	1652	2	Q7SHK6_NEUCR	Q7shk6 neurospora	324	34	61.8	267	2	Q62W67_BACLD	Q62w67 bacillus li
252	35	63.6	1700	2	Q9VUJ9_DROME	Q9vj9 drosophila	325	34	61.8	270	2	Q832I7_ENTFA	Q832i7 enterococcu
253	35	63.6	1821	2	Q64EZ1_TENMO	Q64ez1 tenebrio mo	326	34	61.8	280	2	Q9MA71_ARATH	Q9ma71 arabidopsis
254	35	63.6	1872	2	Q17083_9HME	Q17083 athalia ros	328	34	61.8	284	2	Q5LQGA_ARATH	Q5lqga arabidopsis
255	35	63.6	1879	2	Q9WJ11_9VIRU	Q9wj11 venezuelan	328	34	61.8	286	2	Q5LML9_SILPO	Q5lml9 silicibacte
256	35	63.6	1907	2	Q9U5D8_9HEMI	Q9u5d8 plautia sta	329	34	61.8	292	2	Q8ZBG4_YERPE	Q8zbg4 yersinia pe
257	35	63.6	2086	2	Q484Q3_TETNG	Q484q3 tetraodon n	330	34	61.8	292	2	Q86F19_YERPS	Q86f19 yersinia ps
258	35	63.6	2114	2	Q8RTG4_MICAE	Q8rtg4 microcystis	331	34	61.8	294	2	Q960H8_DROME	Q960h8 drosophila
259	35	63.6	2126	2	Q93LR1_MICAE	Q93lr1 microcystis	332	34	61.8	296	2	Q72VC5_LBPIC	Q72vc5 leptospira
260	35	63.6	2126	2	Q93LR2_MICAE	Q93lr2 microcystis	333	34	61.8	296	2	Q8F8X0_LBPIN	Q8f8x0 leptospira
261	35	63.6	2126	2	Q9RNB0_MICAE	Q9rnb0 microcystis	334	34	61.8	297	2	Q18068_CAEEL	Q18068 caenorhabdi
262	35	63.6	2126	2	Q9S1A8_MICAE	Q9s1a8 microcystis	334	34	61.8	302	2	Q8D1C2_YERPE	Q8d1c2 yersinia pe
263	35	63.6	2411	2	Q6CKV6_KLULA	Q6ckv6 kluyveromyc	336	34	61.8	309	2	Q7V0M6_PROMP	Q7v0m6 prochloroco
264	35	63.6	2485	1	POLN_BEVW3	P36327 venezuelan	337	34	61.8	312	2	Q65KS1_BACLD	Q65ks1 bacillus li
265	35	63.6	2485	2	Q1TCG5_9VIRU	Q1tcg5 venezuelan	338	34	61.8	313	2	Q9KBQ6_BACHD	Q9kbq6 bacillus ha
266	35	63.6	2485	2	Q9IR88_9VIRU	Q9ir88 venezuelan	339	34	61.8	315	2	Q87XF0_PRESM	Q87xf0 pseudomonas
267	35	63.6	2485	2	Q9JPT5_9VIRU	Q9jpt5 venezuelan	340	34	61.8	318	2	Q97206_LEIMA	Q97206 leishmania
268	35	63.6	2485	2	Q9WTD5_9VIRU	Q9wtd5 venezuelan	341	34	61.8	323	2	Q7Q5Q7_ANOGA	Q7q5q7 anopheles g
269	35	63.6	2492	1	POLN_BEVWP	P27282 venezuelan	342	34	61.8	324	2	Q9V6A7_DROME	Q9v6a7 drosophila
270	35	63.6	2492	1	POLN_BEVVT	P27288 venezuelan	343	34	61.8	326	2	Q87PW8_VIBPA	Q87pw8 vibrio para
271	35	63.6	2493	2	Q8BJT2_9VIRU	Q8bjt2 venezuelan	344	34	61.8	328	2	Q6GAT4_STAAS	Q6gat4 staphylococ
272	35	63.6	2493	2	Q8UYL4_9VIRU	Q8uyt4 venezuelan	345	34	61.8	328	2	Q6G195_STAAR	Q6g195 staphylococ
273	35	63.6	2493	2	Q91KW9_9VIRU	Q91kw9 venezuelan	346	34	61.8	328	2	Q7A6F0_STAAN	Q7a6f0 staphylococ
274	35	63.6	2493	2	Q5XQC5_9VIRU	Q5xqc5 venezuelan	347	34	61.8	328	2	Q8NXD5_STAAN	Q8nxd5 staphylococ
275	35	63.6	2493	2	Q5QWQ0_9VIRU	Q5qwm0 venezuelan	348	34	61.8	328	2	Q9V9V8_STAAM	Q9v9v8 staphylococ
276	35	63.6	2493	2	Q90163_9VIRU	Q90163 venezuelan	349	34	61.8	328	2	Q5HH92_STAAC	Q5hh92 staphylococ
277	35	63.6	2493	2	Q66592_9VIRU	Q66592 venezuelan	350	34	61.8	328	2	Q8BP53_OCEIH	Q8bp53 oceanobacil
278	35	63.6	2493	2	Q66594_9VIRU	Q66594 venezuelan	351	34	61.8	328	2	Q82568_9NFA	Q82568 influenza a
279	35	63.6	3574	2	Q8IDA8_PLAF7	Q8ida8 plasmodium	352	34	61.8	328	2	Q82576_9NFA	Q82576 influenza a
280	35	63.6	6680	2	Q5CKT7_CRYPV	Q5ckt7 cryptospori	353	34	61.8	328	2	Q82577_9NFA	Q82577 influenza a
281	34.5	62.7	223	2	Q7SBG2_NEUCR	Q50172 mycobacteri	354	34	61.8	329	2	Q82580_9NFA	Q82580 influenza a
282	34	61.8	36	2	Q50172_MYCLE	Q50172 mycobacteri	355	34	61.8	329	2	Q40648_9NFA	Q40648 influenza a
283	34	61.8	43	2	Q4YN78_PLABE	Q4yn78 plasmodium	356	34	61.8	329	2	Q40652_9NFA	Q40652 influenza a
284	34	61.8	70	2	Q6P7U3_MOUSE	Q6p7u3 mus musculu	357	34	61.8	329	2	Q40653_9NFA	Q40653 influenza a
285	34	61.8	80	2	Q9LXU0_ARATH	Q9lxu0 arabidopsis	358	34	61.8	329	2	Q40654_9NFA	Q40654 influenza a
286	34	61.8	96	2	Q9CBY7_MYCLE	Q9cby7 mycobacteri	359	34	61.8	329	2	Q40655_9NFA	Q40655 influenza a
287	34	61.8	114	1	YBGS_YEAST	P38188 saccharomyc	360	34	61.8	329	2	Q40656_9NFA	Q40656 influenza a
288	34	61.8	133	2	Q9SD43_ARATH	P69433 escherichia	361	34	61.8	329	2	Q40661_9NFA	Q40661 influenza a
289	34	61.8	137	1	PGAD_ECO57	P69433 escherichia	362	34	61.8	329	2	Q40663_9NFA	Q40663 influenza a
290	34	61.8	137	1	PGAD_ECOLI	P8fj32 escherichia	363	34	61.8	329	2	Q40665_9NFA	Q40665 influenza a
291	34	61.8	137	2	Q8FJ32_ECOL6	P8fj32 escherichia	364	34	61.8	329	2	Q40673_9NFA	Q40673 influenza a
292	34	61.8	137	2	Q8C9P8_MOUSE	Q8c9p9 mus musculu	365	34	61.8	329	2	Q40674_9NFA	Q40674 influenza a
293	34	61.8	141	2	Q8TP14_METAC	Q8tp14 methanosarc	366	34	61.8	329	2	Q40675_9NFA	Q40675 influenza a
294	34	61.8	145	2	Q6PAR6_MOUSE	Q6par6 mus musculu	367	34	61.8	329	2	Q40676_IAB53	Q40676 influenza a
295	34	61.8	149	2	Q72UA0_LBPIC	Q72ua0 leptospira	368	34	61.8	329	2	Q40680_9NFA	Q40680 influenza a
296	34	61.8	149	2	Q8FOT2_LBPIN	Q8fot2 leptospira	369	34	61.8	329	2	Q40683_9NFA	Q40683 influenza a
297	34	61.8	152	2	Q5N8Y7_ORYSA	Q5n8y7 oryza sativ	370	34	61.8	329	2	Q40684_9NFA	Q40684 influenza a
298	34	61.8	154	1	NUSB_BORER	Q7wnt2 bordetella	371	34	61.8	329	2	Q40685_9NFA	Q40685 influenza a
299	34	61.8	154	1	NUSB_BORPA	Q7w142 bordetella	372	34	61.8	329	2	Q40686_9NFA	Q40686 influenza a
300	34	61.8	154	1	NUSB_BORPE	Q7vtn3 bordetella	373	34	61.8	329	2	Q40688_9NFA	Q40688 influenza a
301	34	61.8	197	2	Q9PBQ4_XYLFA	Q9pbq4 xyella fas	374	34	61.8	329	2	Q40689_9NFA	Q40689 influenza a
302	34	61.8	202	2	Q5XHD9_XENLA	Q5xhd9 xenopus lae	375	34	61.8	329	2	Q40690_9NFA	Q40690 influenza a
303	34	61.8	202	2	Q8P4M9_XENTR	Q8p4m9 xenopus tro	376	34	61.8	329	2	Q40691_9NFA	Q40691 influenza a
304	34	61.8	208	2	Q8IP43_DROME	Q8ip43 drosophila	377	34	61.8	329	2	Q40692_9NFA	Q40692 influenza a
305	34	61.8	211	2	Q52KY9_CHICK	Q52ky9 gallus gall	378	34	61.8	329	2	Q40693_9NFA	Q40693 influenza a
306	34	61.8	211	2	Q6NTV8_XENLA	Q6ntv8 xenopus lae	379	34	61.8	329	2	Q40694_9NFA	Q40694 influenza a
307	34	61.8	212	1	USP49_HUMAN	Q9b944 homo sapien	380	34	61.8	329	2	Q40695_9NFA	Q40695 influenza a
308	34	61.8	212	1	USP49_MOUSE	Q9r0x0 mus musculu	381	34	61.8	329	2	Q40696_9NFA	Q40696 influenza a
309	34	61.8	212	2	Q5T8J1_HUMAN	Q5t8j4 homo sapien	382	34	61.8	329	2	Q40698_9NFA	Q40698 influenza a
310	34	61.8	212	2	Q4R4S8_MACFA	Q4r4s8 macaca fasc	383	34	61.8	329	2	Q40870_9NFA	Q40870 influenza a
311	34	61.8	212	2	Q5XIE9_RAT	Q5xie9 rattus norv	384	34	61.8	329	2	Q40871_9NFA	Q40871 influenza a
312	34	61.8	221	2	Q6MR13_BDEBA	Q6mr13 bdellovibri	385	34	61.8	329	2	Q40872_9NFA	Q40872 influenza a
313	34	61.8	224	2	Q4J0K6_AZOVI	Q4j0k6 azotobacter	386	34	61.8	329	2	Q40873_9NFA	Q40873 influenza a
314	34	61.8	237	2	Q721R2_LISMF	Q721r2 listeria mo	387	34	61.8	329	2	Q40874_9NFA	Q40874 influenza a
315	34	61.8	237	2	Q8Y8J3_LISMO	Q8y8j9 listeria mo	388	34	61.8	329	2	Q40877_9NFA	Q40877 influenza a
316	34	61.8	237	2	Q92DB4_LISIN	Q92db4 listeria in	389	34	61.8	329	2	Q40878_9NFA	Q40878 influenza a
317	34	61.8	238	2	P94157_SYNP6	P94157 synchococc	390	34	61.8	329	2	Q40879_9NFA	Q40879 influenza a
318	34	61.8	239	2	Q976P2_SULTO	Q976p2 sulfolobus	391	34	61.8	329	2	Q40880_9NFA	Q40880 influenza a
319	34	61.8	241	2	Q8UF00_AGR5	Q8uf00 agrobacteri	392	34	61.8	329	2	Q57029_9NFA	Q57029 influenza a
320	34	61.8	248	1	LUMQ_PHOLE	Q51872 photobacter	393	34	61.8	329	2	Q67056_9NFA	Q67056 influenza a
321	34	61.8	249	1	Q5NIS7_SYNP6	Q5nis7 synchococc	394	34	61.8	329	2	Q82560_9NFA	Q82560 influenza a
322	34	61.8	256	2	Q8CUQ6_OCEIH	Q8cuq6 oceanobacil	395	34	61.8	329	2	Q82560_9NFA	Q82560 influenza a
323	34	61.8	264	2	Q5KWI3_GEOKA	Q5kwi3 geobacillus	396	34	61.8	329	2	Q82560_9NFA	Q82560 influenza a

337	34	61.8	329	2	Q82830_9INFA	Q82830	influenza a
338	34	61.8	329	2	Q82831_9INFA	Q82831	influenza a
339	34	61.8	329	2	Q91IM1_9INFA	Q91im1	influenza a
400	34	61.8	329	2	Q91IM2_9INFA	Q91im2	influenza a
401	34	61.8	329	2	Q91IM3_9INFA	Q91im3	influenza a
402	34	61.8	329	2	Q91IM4_9INFA	Q91im4	influenza a
403	34	61.8	329	2	Q91IM5_9INFA	Q91im5	influenza a
404	34	61.8	329	2	Q91IM6_9INFA	Q91im6	influenza a
405	34	61.8	329	2	Q91IM7_9INFA	Q91im7	influenza a
406	34	61.8	329	2	Q91LX9_9INFA	Q91lx9	influenza a
407	34	61.8	330	2	Q7LZY0_9INFA	Q7lzy0	influenza a
408	34	61.8	332	1	SIASH2_BRARE	Q7sly3	brachydanio
409	34	61.8	332	2	Q70D57_XENLA	Q70d57	xenopus lae
410	34	61.8	332	2	Q70D56_XENTR	Q70d56	xenopus tro
411	34	61.8	333	2	Q8ZY36_PVRAB	Q8zy26	pyrobaculum
412	34	61.8	337	1	NAC94_ARATH	Q9fiw5	arabidopsis
413	34	61.8	337	2	P87690_9INFA	P87690	influenza a
414	34	61.8	339	2	Q5E7R0_VIBF1	P876r0	vibrio fisc
415	34	61.8	339	2	P87687_9INFA	P87687	influenza a
416	34	61.8	345	2	Q9JFU0_9INFA	Q9jfu0	influenza a
417	34	61.8	346	2	Q6C821_YARLI	Q6c8z1	yarrowia li
418	34	61.8	346	2	Q9Q4Q1_9INFA	Q9q4q1	influenza a
419	34	61.8	347	2	Q82773_9INFA	Q82773	influenza a
420	34	61.8	347	2	Q82775_9INFA	Q82775	influenza a
421	34	61.8	347	2	Q82821_9INFA	Q82821	influenza a
422	34	61.8	349	2	Q8ST50_ENCCU	O8sts0	encephalito
423	34	61.8	351	2	Q510K1_ENTHI	Q510k1	entamoeba h
424	34	61.8	352	2	Q9KF48_BACHD	Q9kf48	bacillus ha
425	34	61.8	356	2	Q4ZU36_PSESY	Q4zu36	pseudomonas
426	34	61.8	358	2	Q49599_METKA	Q49599	methanopyru
427	34	61.8	358	2	Q8TYK7_METKA	O8tyk7	methanopyru
428	34	61.8	360	2	Q45344_CAEEL	Q45344	caenorhabdi
429	34	61.8	360	2	Q39839_9INFA	Q39839	influenza a
430	34	61.8	362	2	Q84174_9INFA	Q84174	influenza a
431	34	61.8	362	2	Q4SPR1_TETNG	Q4sept1	tetraodon n
432	34	61.8	363	2	Q6DM62_9INFA	Q6dm62	influenza a
433	34	61.8	363	2	Q6DM66_9INFA	Q6dm66	influenza a
434	34	61.8	363	2	Q6DM69_9INFA	Q6dm69	influenza a
435	34	61.8	363	2	Q6DM70_9INFA	Q6dm70	influenza a
436	34	61.8	363	2	Q6DM75_9INFA	Q6dm75	influenza a
437	34	61.8	363	2	Q6DM77_9INFA	Q6dm77	influenza a
438	34	61.8	363	2	Q6DM78_9INFA	Q6dm78	influenza a
439	34	61.8	363	2	Q6DM80_9INFA	Q6dm80	influenza a
440	34	61.8	363	2	Q6DM92_9INFA	Q6dm92	influenza a
441	34	61.8	363	2	Q6DM94_9INFA	Q6dm94	influenza a
442	34	61.8	363	2	Q6DM95_9INFA	Q6dm95	influenza a
443	34	61.8	363	2	Q6DM96_9INFA	Q6dm96	influenza a
444	34	61.8	363	2	Q6DM97_9INFA	Q6dm97	influenza a
445	34	61.8	363	2	Q6DM98_9INFA	Q6dm98	influenza a
446	34	61.8	363	2	Q6DM99_9INFA	Q6dm99	influenza a
447	34	61.8	363	2	Q6DMB5_9INFA	Q6dmb5	influenza a
448	34	61.8	363	2	Q6DMB6_9INFA	Q6dmb6	influenza a
449	34	61.8	363	2	Q6DMB7_9INFA	Q6dmb7	influenza a
450	34	61.8	363	2	Q6DMB9_9INFA	Q6dmb9	influenza a
451	34	61.8	363	2	Q6DMC4_9INFA	Q6dmc4	influenza a
452	34	61.8	363	2	Q6DMD2_9INFA	Q6dmd2	influenza a
453	34	61.8	363	2	Q6DMD3_9INFA	Q6dmd3	influenza a
454	34	61.8	363	2	Q6DMD4_9INFA	Q6dmd4	influenza a
455	34	61.8	363	2	Q6DMD6_9INFA	Q6dmd6	influenza a
456	34	61.8	363	2	Q6DMD7_9INFA	Q6dmd7	influenza a
457	34	61.8	363	2	Q6DMD8_9INFA	Q6dme0	influenza a
458	34	61.8	363	2	Q6DME1_9INFA	Q6dme1	influenza a
459	34	61.8	363	2	Q6DME2_9INFA	Q6dme2	influenza a
460	34	61.8	363	2	Q6DME3_9INFA	Q6dme3	influenza a
461	34	61.8	363	2	Q6DME5_9INFA	Q6dme5	influenza a
462	34	61.8	363	2	Q6DMB8_9INFA	Q6dme8	influenza a
463	34	61.8	363	2	Q6DMB9_9INFA	Q6dme9	influenza a
464	34	61.8	363	2	Q6DMF0_9INFA	Q6dmf0	influenza a
465	34	61.8	363	2	Q6DMF1_9INFA	Q6dmf1	influenza a
466	34	61.8	363	2	Q6DMF2_9INFA	Q6dmf2	influenza a
467	34	61.8	363	2	Q6DMF4_9INFA	Q6dmf4	influenza a
468	34	61.8	363	2	Q6DMF5_9INFA	Q6dmf5	influenza a
469	34	61.8	367	2	Q82ZS2_ENTFA	Q82zs2	enterococcus

470	34	61.8	368	2	Q837J9_ENTFA	Q837j9	enterococu
471	34	61.8	371	2	P87685_TAB52	P87685	influenza a
472	34	61.8	377	2	Q97VA4_SULSO	Q97va4	sulfolobus
473	34	61.8	380	2	Q58M92_9CAUD	Q58m92	cyanophage
474	34	61.8	392	2	Q5LAL2_BACFN	Q5lal2	bacteroides
475	34	61.8	392	2	Q8A6X9_BACTN	Q8a6x9	bacteroides
476	34	61.8	392	2	Q64R07_BACFR	Q64r07	bacteroides
477	34	61.8	404	2	Q4G137_HUMAN	Q4g137	homo sapien
478	34	61.8	418	2	Q8EHG3_SHEON	Q8ehg3	shewanella
479	34	61.8	420	1	PEA2_YEAST	P40091	saccharomyc
480	34	61.8	423	1	ZN557_HUMAN	Q8n988	homo sapien
481	34	61.8	424	2	Q5JPC5_HUMAN	Q5jpc5	homo sapien
482	34	61.8	427	2	Q50V98_ENTHI	Q50v98	entamoeba h
483	34	61.8	427	2	Q6XX20_ANTIMA	Q6xx20	antirrhinum
484	34	61.8	436	2	Q50LT3_ENTHI	Q50lt3	entamoeba h
485	34	61.8	444	2	Q9APH9_LEGLO	Q9aph9	legionella
486	34	61.8	452	2	Q749H3_GEOSL	Q749h3	geobacter s
487	34	61.8	452	2	Q4SW70_TETNG	Q4sw70	tetraodon n
488	34	61.8	453	2	Q97P27_STRPN	Q97p27	streptococc
489	34	61.8	456	2	Q5QLT6_ORYSA	Q5qlt6	oryza sativ
490	34	61.8	463	2	Q8VJG6_MYCTU	O8vjg6	mycobacteri
491	34	61.8	463	2	P95024_MYCTU	P95024	mycobacteri
492	34	61.8	463	2	Q7TYD3_MYCBO	Q7tyd3	mycobacteri
493	34	61.8	471	2	Q8NB16_HUMAN	Q8nb16	homo sapien
494	34	61.8	474	2	Q6DIT5_XENTR	Q6dit5	xenopus tro
495	34	61.8	475	2	Q9L9K9_PASMU	Q9l9k9	pasteurella
496	34	61.8	477	2	Q62CD8_BURMA	Q62cd8	burkholderi
497	34	61.8	487	2	Q8DNM5_STRRK	Q8dnm5	streptococc
498	34	61.8	497	2	Q9P736_NEUCR	Q9p736	neurospora
499	34	61.8	497	2	Q63KP3_BURPS	Q63kp3	burkholderi
500	34	61.8	501	1	ZNFC63_MOUSE	Q9z1d7	mus musculu
501	34	61.8	501	2	Q8C6D3_MOUSE	Q8c6d3	mus musculu
502	34	61.8	501	2	Q8R0D8_MOUSE	Q8r0d8	mus musculu
503	34	61.8	508	2	Q6ZQB8_MOUSE	Q6zqb8	mus musculu
504	34	61.8	532	2	Q7QG89_ANOGA	Q7qg89	anopheles g
505	34	61.8	539	2	Q6BQ75_DEBHA	Q6bq75	debaromyce
506	34	61.8	544	2	Q6UEI7_MESCR	Q6uei7	meserymyce
507	34	61.8	562	2	Q6DMD9_9INFA	Q6dm9	influenza a
508	34	61.8	562	2	Q6DMB6_TAB53	Q6dmb6	influenza a
509	34	61.8	562	2	Q6DMF3_9INFA	Q6dmf3	influenza a
510	34	61.8	562	2	Q6DMF6_9INFA	Q6dmf6	influenza a
511	34	61.8	562	2	Q6DMF7_9INFA	Q6dmf7	influenza a
512	34	61.8	562	2	Q6DMF8_9INFA	Q6dmf8	influenza a
513	34	61.8	566	2	O11283_TAB53	O11283	influenza a
514	34	61.8	566	2	Q8UXB4_9INFA	Q8uxr4	influenza a
515	34	61.8	570	2	Q4I1B5_GIBZE	Q4i1b5	gibberella
516	34	61.8	585	2	Q4IK02_GIBZE	Q4ik02	gibberella
517	34	61.8	621	2	Q6H415_ORYSA	Q6h415	oryza sativ
518	34	61.8	664	2	Q5S060_9SACH	Q5s060	pichia sp.
519	34	61.8	669	2	Q8G4J2_BIFLO	Q8g4j2	bifidobacte
520	34	61.8	685	2	Q9NL46_CIOIN	Q9nl46	ciona intes
521	34	61.8	685	2	Q4JF68_CIOIN	Q4jff68	gibberella
522	34	61.8	707	2	Q4JF68_GIBZE	Q4jff68	gibberella
523	34	61.8	709	2	Q6CIH8_KULUA	Q6cih8	kluyveromyc
524	34	61.8	713	2	Q9V4N4_DROME	Q9v4n4	drosophiila
525	34	61.8	720	2	Q89WB3_BRAJA	Q89wb3	bradyrhizob
526	34	61.8	722	2	Q6NCN8_RHOPA	Q6ncn8	rhodospseudo
527	34	61.8	725	2	Q9HDP5_PODAN	Q9hdp5	podospora a
528	34	61.8	731	1	YB88_YEAST	P38330	saccharomyc
529	34	61.8	739	1	THIED_COREF	Q8fth8	c multific
530	34	61.8	745	2	Q54GA8_DICDI	Q54ga8	dictyosteli
531	34	61.8	753	2	Q6AWB4_DROME	Q6awe4	drosophiila
532	34	61.8	759	2	O31626_BACSU	O31626	bacillus su
533	34	61.8	764	2	Q5ZD68_ORYSA	Q5zd68	oryza sativ
534	34	61.8	767	2	Q9YTK6_SHERP	Q9ytk6	acteline her
535	34	61.8	769	2	Q95TYJ0_DROME	Q95tj0	drosophiila
536	34	61.8	773	2	O8IG87_DROME	Q8ig87	drosophiila
537	34	61.8	810	2	O8IJN1_PLAF7	O8ijn1	plasmodium
538	34	61.8	857	2	Q5V524_HALMA	Q5v524	haloarmula
539	34	61.8	880	2	O8IJZ3_PLAF7	O8ijz3	plasmodium
540	34	61.8	884	2	Q3TUF1_ANOGA	Q3tuf1	anopheles g
541	34	61.8	892	2	Q7PRJ9_ANOGA	Q7prj9	anopheles g
542	34	61.8	914	2	Q72PR7_LEPIC	Q72pr7	leptospira

543	34	61.8	914	2	Q8P6I1_LEPIN	Q8f6i1 leptospira	616	33	60.0	230	2	Q8SS32_ENCCU	Q8se32 encephalito
544	34	61.8	919	2	Q5LH5_ENTHI	Q5lhb5 entamoeba h	617	33	60.0	235	2	Q76647_CABEL	Q76647 caenothabdi
545	34	61.8	943	1	AR52_DROME	Q9v9k7 drosophila	618	33	60.0	236	2	Q7UGT4_RHOBA	Q7ugt4 rhodopirell
546	34	61.8	943	2	Q53XG1_DROME	Q53xg1 drosophila	619	33	60.0	237	2	Q6CW75_KLULA	Q6cw75 kryptococcu
547	34	61.8	980	2	Q52GD2_MAGGR	Q52gd2 magnaporthe	620	33	60.0	238	2	Q55WT4_CRYNE	Q55wt4 kryptococcu
548	34	61.8	1085	2	Q59NV7_CANAL	Q59nv7 candida alb	621	33	60.0	238	2	Q5KJG3_CRYNE	Q5kjg3 kryptococcu
549	34	61.8	1111	2	Q7SAB0_NEUCR	Q7sab0 neurospora	622	33	60.0	241	2	Q4YIWC_TABSO	Q4yiw6 taenia soli
550	34	61.8	1198	2	Q4S5Z4_TETNG	Q4s5z4 tetradon n	623	33	60.0	241	2	Q84617_CHVPI	Q84617 paramecium
551	34	61.8	1218	2	Q7TIP4_HAJUR	Q7tip4 raja erinac	624	33	60.0	242	2	Q9V9W2_DROME	Q9v9w2 drosophila
552	34	61.8	1262	2	Q84KC6_HORVU	Q84kc6 hordeum vul	625	33	60.0	247	2	Q53RD5_HUMAN	Q53rd5 homo sapien
553	34	61.8	1359	2	Q4WVT4_ASPFU	Q4wvt4 aspergillus	626	33	60.0	252	1	ZG28_XENLA	P18716 xenopus lae
554	34	61.8	1380	2	Q5KE38_CRYNE	Q5ke38 kryptococcu	627	33	60.0	255	1	BIOH_VIBCH	Q9kn14 vibrio chol
555	34	61.8	1398	2	Q5SPB8_CRYNE	Q5spb8 kryptococcu	628	33	60.0	255	2	Q93HG2_STRAW	Q93hg2 streptomyc
556	34	61.8	1487	2	Q8LHX5_PLAP7	Q8lhx5 plasmodium	629	33	60.0	262	2	Q9V9W3_DROME	Q9v9w3 drosophila
557	34	61.8	1557	2	Q9X577_BACSU	Q9x577 bacillus su	630	33	60.0	268	2	Q5BVY5_SCHJA	Q5bv55 schistosoma
558	34	61.8	1639	2	Q4P8V0_USTMA	Q4p8v0 ustilago ma	631	33	60.0	269	2	Q6A893_PROAC	Q6a893 propionibac
559	34	61.8	1658	2	Q9H0J4_HUMAN	Q9h0j4 homo sapien	632	33	60.0	271	1	AACC3_PSAE	P29808 pseudomonas
560	34	61.8	1663	2	Q6LPA6_PLAP7	Q6lpa6 plasmodium	633	33	60.0	281	2	Q4FNVE_9RICK	Q4fnv5 candidatus
561	34	61.8	1680	2	Q410X9_GIBBEZ	Q410x9 gibberella	634	33	60.0	281	2	Q7TWI8_MYCBO	Q7twi8 mycobacteri
562	34	61.8	1707	2	Q9VE54_DROSOPH	Q9ve54 drosophila	635	33	60.0	281	2	Q06248_MYCTU	Q06248 mycobacteri
563	34	61.8	1784	2	Q86HD9_DICDI	Q86hd9 dictyosteli	636	33	60.0	283	2	Q7Q991_ANOGA	Q7q991 anopheles g
564	34	61.8	1829	2	Q551P7_DICDI	Q551p7 dictyosteli	637	33	60.0	284	2	Q5AU98_EMENI	Q5au98 aspergillus
565	34	61.8	1867	2	Q81DT8_PLAP7	Q81dt8 plasmodium	638	33	60.0	284	2	Q5LT68_SILPO	Q5lt68 silicibacte
566	34	61.8	1936	2	Q9U5F3_9HEMI	Q9u5f3 graptopsalt	639	33	60.0	287	2	Q87TJ1_SMYTH	Q87tj1 symbiobacte
567	34	61.8	1987	2	Q813V5_PLAP7	Q813v5 plasmodium	640	33	60.0	292	2	Q80W53_MOUSE	Q80w53 mus musculu
568	34	61.8	2133	2	Q6CN46_KLULA	Q6cn46 kluyveromyc	641	33	60.0	297	2	Q54YR6_DICDI	Q54yr6 dictyosteli
569	34	61.8	2214	1	PYR1_YEAST	P07259 saccharomyc	642	33	60.0	301	2	Q72BZ6_DRSVH	Q72b26 desulfovibr
570	34	61.8	2228	2	Q6CN46_KLULA	Q6cn46 kluyveromyc	643	33	60.0	308	1	OPPF_STRWU	P72499 streptococc
571	34	61.8	2410	2	Q5A249_EMENI	Q5a249 aspergillus	644	33	60.0	309	1	S39A2_HUMAN	Q9np94 homo sapien
572	34	61.8	2410	2	Q45675_BACSU	Q45675 bacillus su	645	33	60.0	309	2	Q9UD20_HUMAN	Q9ud20 homo sapien
573	34	61.8	3583	2	Q70KJ7_BACAM	Q70kj7 bacillus am	646	33	60.0	309	2	Q4QQJ1_HUMAN	Q4qqj1 homo sapien
574	34	61.8	3587	1	SRAFAB_BACSU	Q40747 bacillus su	647	33	60.0	309	2	Q4V9S4_HUMAN	Q4v9s4 homo sapien
575	34	61.8	3588	1	SRAFAB_BACSU	P27206 bacillus su	648	33	60.0	309	2	Q4R9D0_MACFA	Q4r9d0 macaca fasc
576	34	61.8	4780	2	Q1E54_PLAP7	Q1e54 plasmodium	649	33	60.0	314	2	Q72LTO_LBPCIC	Q72lto leptospira
577	34	61.8	9506	2	Q59D28_DROME	Q59d28 drosophila	650	33	60.0	314	2	Q8EY89_LESPIN	Q8ey89 leptospira
578	33	60.0	54	2	Q6B8F7_9ACAR	Q6b8f7 ixodes paci	651	33	60.0	318	2	Q8YNV3_ANASP	Q8ynv3 anabaena sp
579	33	60.0	54	2	Q4PN51_IXOSC	Q4pn51 ixodes scap	652	33	60.0	319	2	Q50UT4_ENTHI	Q5out4 entamoeba h
580	33	60.0	80	2	Q8X2Q5_ECO57	Q8x2q5 escherichia	653	33	60.0	321	2	Q7RZU5_NEUCR	Q7rzu5 trimeresoru
581	33	60.0	81	2	Q86HB7_DICDI	Q86hb7 dictyosteli	654	33	60.0	323	1	SVMP_TRIFL	P29695 trimeresoru
582	33	60.0	89	2	Q8X6F6_ECO57	Q8x6f6 escherichia	655	33	60.0	324	2	Q5KQ53_AKGHB	Q5kq53 agkistrodon
583	33	60.0	90	2	Q9H365_HUMAN	Q9h365 homo sapien	656	33	60.0	328	2	Q82567_9INFA	Q82567 influenza a
584	33	60.0	90	2	Q4R9Y9_TETNG	Q4r9y9 tetradon n	657	33	60.0	328	2	Q82575_9INFA	Q82575 influenza a
585	33	60.0	101	2	Q9NIG2_DROME	Q9ni92 drosophila	658	33	60.0	328	2	Q82578_9INFA	Q82578 influenza a
586	33	60.0	103	2	Q4GZC1_9TRYP	Q4gzcl trypanosoma	659	33	60.0	329	2	Q40649_9INFA	Q40649 influenza a
587	33	60.0	109	2	Q9YDL4_AERPE	Q9ydl4 aeropyrum p	660	33	60.0	329	2	Q40651_9INFA	Q40651 influenza a
588	33	60.0	124	2	Q54WQ7_DICDI	Q54wq7 dictyosteli	661	33	60.0	329	2	Q40662_9INFA	Q40662 influenza a
589	33	60.0	125	2	Q9BXZ2_HUMAN	Q9bxz2 homo sapien	662	33	60.0	329	2	Q40664_9INFA	Q40664 influenza a
590	33	60.0	161	2	Q910Q1_LSDV	Q910q1 lumpy skin	663	33	60.0	329	2	Q40677_9INFA	Q40677 influenza a
591	33	60.0	164	2	Q7YR90_BOVIN	Q7yr90 bos taurus	664	33	60.0	329	2	Q40678_IAS06	Q40678 influenza a
592	33	60.0	166	2	Q5DGK3_SCHJA	Q5dgk3 schistosoma	665	33	60.0	329	2	Q40679_9INFA	Q40679 influenza a
593	33	60.0	169	2	Q5WB23_BACSK	Q5wb23 bacillus cl	666	33	60.0	329	2	Q40681_9INFA	Q40681 influenza a
594	33	60.0	170	2	Q5TPC4_ANOGA	Q5tpc4 anopheles g	667	33	60.0	329	2	Q40682_9INFA	Q40682 influenza a
595	33	60.0	176	2	Q8TA55_CABEL	Q8ta55 caenothabdi	668	33	60.0	329	2	Q40802_9INFA	Q40802 influenza a
596	33	60.0	185	2	Q8EJ46_SHEON	Q8ej46 shewanella	669	33	60.0	329	2	Q40803_9INFA	Q40803 influenza a
597	33	60.0	186	2	Q6NZ23_BRARE	Q6nzz3 brachydanio	670	33	60.0	329	2	Q40804_9INFA	Q40804 influenza a
598	33	60.0	187	2	Q5F8F0_NEIGI	Q5f8f0 neisseria g	671	33	60.0	329	2	Q40805_9INFA	Q40805 influenza a
599	33	60.0	187	2	Q9JUF3_NEIMA	Q9juf3 neisseria m	672	33	60.0	329	2	Q40806_9INFA	Q40806 influenza a
600	33	60.0	189	2	Q4X0P1_ASPFU	Q4x0p1 aspergillus	673	33	60.0	329	2	Q40807_9INFA	Q40807 influenza a
601	33	60.0	194	2	Q677A5_9ASPA	Q677a6 hyacinthus	674	33	60.0	329	2	Q40808_9INFA	Q40808 influenza a
602	33	60.0	201	2	Q5B3H1_EMENI	Q5b3hl aspergillus	675	33	60.0	329	2	Q40809_9INFA	Q40809 influenza a
603	33	60.0	204	2	Q9P820_CANAL	Q9p820 candida alb	676	33	60.0	329	2	Q40815_IAXIT	Q40815 influenza a
604	33	60.0	205	2	Q8YT18_ANASP	Q8yt18 anabaena sp	677	33	60.0	329	2	Q40869_9INFA	Q40869 influenza a
605	33	60.0	210	2	Q5KLP3_CRYNE	Q5klp3 kryptococcu	678	33	60.0	329	2	Q40875_9INFA	Q40875 influenza a
606	33	60.0	210	2	Q55Y95_CRYNE	Q55y95 kryptococcu	679	33	60.0	329	2	Q40876_9INFA	Q40876 influenza a
607	33	60.0	214	2	Q7VC23_PROMA	Q7vc23 prochloroco	680	33	60.0	329	2	Q70682_9INFA	Q70682 influenza a
608	33	60.0	216	2	Q93P81_9SPHI	Q93p81 microscilla	681	33	60.0	329	2	Q70684_9INFA	Q70684 influenza a
609	33	60.0	217	2	Q4TE83_TETNG	Q4te83 tetradon n	682	33	60.0	329	2	Q70685_9INFA	Q70685 influenza a
610	33	60.0	218	2	Q9JRY5_NEIMB	Q9jry5 neisseria m	683	33	60.0	329	2	Q70686_9INFA	Q70686 influenza a
611	33	60.0	222	2	Q4MND4_BACCE	Q4mnd4 bacillus ce	684	33	60.0	329	2	Q70687_9INFA	Q70687 influenza a
612	33	60.0	225	1	CSSR_BACSU	Q32192 bacillus su	685	33	60.0	329	2	Q70688_9INFA	Q70688 influenza a
613	33	60.0	226	2	Q72YP4_BACCI	Q72yp4 bacillus ce	686	33	60.0	329	2	Q70689_9INFA	Q70689 influenza a
614	33	60.0	226	2	Q81KCS_BACAN	Q81kcs bacillus an	687	33	60.0	329	2	Q70690_9INFA	Q70690 influenza a
615	33	60.0	226	2	Q632M1_BACCC	Q632m1 bacillus ce	688	33	60.0	329	2	Q93088_9INFA	Q93088 influenza a

689	33	329	2	Q67014_9INFA	Q67014 influenza a	762	33	60.0	378	2	Q4G0U8_HUMAN	Q4g0u8 homo sapien
690	33	329	2	Q67015_9INFA	Q67015 influenza a	763	33	60.0	378	2	Q7PX98_ANOGA	Q7px98 anopheles g
691	33	329	2	Q67028_9INFA	Q67028 influenza a	764	33	60.0	378	2	Q811Y0_PLAF7	Q811y0 plasmodium
692	33	329	2	Q67033_9INFA	Q67033 influenza a	764	33	60.0	379	2	Q702S3_CIOIN	Q702s3 ciona intes
693	33	329	2	Q67035_9INFA	Q67035 influenza a	766	33	60.0	379	2	Q7U4A1_SYNFX	Q7u4a1 synechococc
694	33	329	2	Q67133_9INFA	Q67133 influenza a	767	33	60.0	380	2	Q5ND66_ORYLA	Q5nd66 oryzias lat
695	33	329	2	Q67141_9INFA	Q67141 influenza a	768	33	60.0	380	2	Q6IM18_HUMAN	Q6im18 homo sapien
696	33	329	2	Q67330_9INFA	Q67330 influenza a	769	33	60.0	384	2	Q82QO1_STRAW	Q82qq1 streptomyce
697	33	329	2	Q9Q8E8_9INFA	Q9Q8E8 influenza a	770	33	60.0	387	2	Q5LPH8_SILPO	Q5lph8 silicibacte
698	33	330	2	Q931D9_RHIME	Q931d9 rhizobium m	771	33	60.0	388	2	Q90XH2_BRARE	Q90xh2 brachydanio
699	33	331	2	Q6KB56_TETNG	Q6kb56 tetraodon n	772	33	60.0	389	2	Q5TKN2_ORYSA	Q5tkn2 oryza sativ
700	33	332	2	Q5BJB1_BRARE	Q5bjb1 brachydanio	773	33	60.0	390	1	MEIS1_HUMAN	Q00470 homo sapien
701	33	334	2	Q4RF25_TETNG	Q4rf25 tetraodon n	774	33	60.0	390	1	MEIS1_MOUSE	Q60954 mus musculu
702	33	339	2	P87683_9INFA	P87683 influenza a	775	33	60.0	390	2	Q5SVC8_MOUSE	Q5svc8 mus musculu
703	33	340	2	P87684_9INFA	P87684 influenza a	776	33	60.0	394	2	Q57G86_SALCH	Q57g86 salmonella
704	33	340	2	Q6DM87_9INFA	Q6dm87 influenza a	777	33	60.0	394	2	Q5PIF9_SALPA	Q5pif9 salmonella
705	33	340	2	Q5OJ70_BRARE	Q5oj70 brachydanio	778	33	60.0	394	2	Q82XK3_SALTI	Q82xk3 salmonella
706	33	341	2	Q5OPV9_ENTHI	Q5opv9 entamoeba h	779	33	60.0	394	2	Q8ZJZ6_SALTY	Q8zjz6 salmonella
707	33	342	2	Q5MAR2_ENTHI	Q5mar2 entamoeba h	780	33	60.0	397	2	Q7Q3M6_ANOGA	Q7q3m6 anopheles g
708	33	342	2	Q98TC1_TRIFL	Q98tcl trimeresu	781	33	60.0	397	2	Q7R1Z3_GIALA	Q7r1z3 giardia lam
709	33	345	2	Q875D2_PODAN	Q875d2 podospora a	782	33	60.0	400	2	Q9FFS9_ARATH	Q9ffs9 arabidopsis
710	33	347	2	Q82772_9INFA	Q82772 influenza a	783	33	60.0	402	2	Q6U7Q0_HUMAN	Q6u7q0 homo sapien
711	33	347	2	Q82789_9INFA	Q82789 influenza a	784	33	60.0	403	2	Q9FTF0_ARATH	Q9fft0 arabidopsis
712	33	347	2	Q82791_9INFA	Q82791 influenza a	785	33	60.0	406	2	Q5CZS4_BRARE	Q5czs4 brachydanio
713	33	349	2	Q8BSA0_MOUSE	Q8bsa0 mus musculu	786	33	60.0	416	2	Q4WDY3_ASPFU	Q4wdy3 aspergillus
714	33	349	2	Q5ZJ30_CHICK	Q5zj30 gallus gall	787	33	60.0	417	2	Q7UIZ0_RHOBA	Q7uiz0 rhodopirell
715	33	349	2	Q70DS8_CHICK	Q70ds8 gallus gall	788	33	60.0	424	2	Q599S5_SYNY3	Q599s5 synechocyst
716	33	350	1	SIA4B_HUMAN	Q16842 h cmp-n-ace	789	33	60.0	430	2	Q4JTH6_CORJK	Q4jth6 corynebacte
717	33	350	1	SIA4B_MOUSE	Q11204 m cmp-n-ace	790	33	60.0	433	2	Q4RWT4_TETNG	Q4rwt4 tetraodon n
718	33	350	1	SIA4B_PANTR	Q6kb58 p cmp-n-ace	791	33	60.0	436	2	Q7S185_NEUCR	Q7s185 neurospora
719	33	350	1	SIA4B_RAT	Q11205 r cmp-n-ace	792	33	60.0	437	2	Q4UGG3_THEAN	Q4ugg3 theileria a
720	33	350	2	Q6H8M9_BOVIN	Q6h8m9 bos taurus	793	33	60.0	438	2	Q4ULF8_RICPE	Q4ulf8 rickettsia
721	33	350	2	Q8BP10_MOUSE	Q8bp10 mus musculu	794	33	60.0	438	2	Q88XP1_LACPL	Q88xp1 lactobacill
722	33	350	2	Q91WH6_MOUSE	Q91wh6 mus musculu	795	33	60.0	439	2	Q9ZD23_RICPR	Q9zdd3 rickettsia
723	33	350	2	Q5OJ63_FUGRU	Q5oj63 fugu rubrip	796	33	60.0	440	2	Q7P8M2_RICSI	Q7p8m2 rickettsia
724	33	351	2	Q5TIN7_TETNG	Q5tin7 tetraodon n	797	33	60.0	440	2	Q6BWK9_RICTY	Q6bwk9 rickettsia
725	33	351	2	Q6NUA1_XENLA	Q6nu41 xenopus lae	798	33	60.0	440	2	Q92HL1_RICCN	Q92hl1 rickettsia
726	33	351	2	Q702S1_FUGRU	Q702s1 fugu rubrip	799	33	60.0	446	2	Q5FP15_GLUOX	Q5fp15 gluconobact
727	33	355	2	Q955Y2_TAESA	Q955y2 taenia sagi	800	33	60.0	447	2	Q7M6X2_MOUSE	Q7m6x2 mus musculu
728	33	355	2	Q955Y9_TAESO	Q955y9 taenia soli	801	33	60.0	453	2	Q8FWL8_BRUSU	Q8fwl8 brucella su
729	33	355	2	Q958U8_ECHGR	Q958u8 echinococcu	802	33	60.0	453	2	Q937R6_BRUME	Q937r6 brucella me
730	33	355	2	Q955Z0_TAESO	Q955z0 taenia soli	803	33	60.0	455	2	Q876G1_SACBA	Q876g1 saccharomyc
731	33	355	2	Q955Y4_TAESO	Q955y4 taenia soli	804	33	60.0	458	2	Q5T3V6_HUMAN	Q5t3v6 homo sapien
732	33	355	2	Q955Y6_TAESO	Q955y6 taenia soli	805	33	60.0	462	2	Q6JHM3_9PSEU	Q6jhm3 saccharopol
733	33	355	2	Q955Y6_TAESO	Q955y6 taenia soli	806	33	60.0	465	2	Q5SVC9_MOUSE	Q5svc9 mus musculu
734	33	355	2	Q9TE80_ECHMU	Q9te80 echinococcu	807	33	60.0	466	2	Q9V586_DROME	Q9v586 drosophila
735	33	355	2	Q955Y7_TAESO	Q955y7 taenia soli	808	33	60.0	467	2	Q17233_BOMMO	Q17233 bombyx mori
736	33	355	2	Q953N0_ECHGR	Q953n0 echinococcu	809	33	60.0	474	1	2N256_HUMAN	Q9y2p7 homo sapien
737	33	355	2	Q955Y8_TAESO	Q955y8 taenia soli	810	33	60.0	474	2	Q53Y85_HUMAN	Q53y85 homo sapien
738	33	355	2	Q94PH7_TAESO	Q94ph7 taenia soli	811	33	60.0	478	1	NOE3_HUMAN	Q96pb7 homo sapien
739	33	355	2	Q955Y5_TAESO	Q955y5 taenia soli	812	33	60.0	478	1	NOE3_MOUSE	P63056 mus musculu
740	33	355	2	Q955Y5_TAESO	Q955y5 taenia soli	813	33	60.0	478	1	NOE3_RAT	P63057 rattus norv
741	33	355	2	Q955Y3_CEST	Q955y3 taenia asia	814	33	60.0	478	2	Q6BUC3_DEBHA	Q6buc3 debaryomyce
742	33	357	2	Q955Y3_CEST	Q955y3 taenia asia	815	33	60.0	478	2	Q6IMJ0_HUMAN	Q6imj0 homo sapien
743	33	357	2	Q9B8W9_CEST	Q9b8w9 taenia cras	816	33	60.0	482	2	Q06032_YEAST	Q06032 saccharomyc
744	33	359	2	Q39835_9INFA	Q39835 influenza a	817	33	60.0	482	2	Q6ESZ9_ORYSA	Q6esz9 oryza sativ
745	33	360	2	Q9WA91_9INFA	Q9wa91 influenza a	818	33	60.0	485	2	Q51GC2_ENTHE	Q51gc2 entamoeba h
746	33	363	2	Q6DM79_9INFA	Q6dm79 influenza a	819	33	60.0	487	2	Q61L00_CAEBR	Q61l00 caenorhabdi
747	33	363	2	Q6DM81_9INFA	Q6dm81 influenza a	820	33	60.0	492	2	Q5HZS9_XENLA	Q5hzs9 xenopus lae
748	33	363	2	Q6DM82_9INFA	Q6dm82 influenza a	821	33	60.0	498	2	Q4XXZ2_PLACH	Q4xxz2 plasmodium
749	33	363	2	Q6DM84_9INFA	Q6dm84 influenza a	822	33	60.0	519	1	2NF35_HUMAN	P13682 homo sapien
750	33	363	2	Q6DM87_9INFA	Q6dm87 influenza a	823	33	60.0	519	2	Q53Y54_HUMAN	Q53y54 homo sapien
751	33	365	2	Q9T0U9_DROME	Q9t0u9 drosophila	824	33	60.0	520	2	Q4SSK9_TETNG	Q4ssk9 tetraodon n
752	33	365	2	Q95818_HYMDI	Q95818 hymenolepis	825	33	60.0	523	1	RPN3_YEAST	P40016 saccharomyc
753	33	370	2	Q4YCQ7_PLABE	Q4ycq7 plasmodium	826	33	60.0	525	2	Q9VN56_DROME	Q9vn56 drosophila
754	33	370	2	Q9C1L0_MOUSE	Q9c1l0 mus musculu	827	33	60.0	530	2	Q7U6V5_SYNFX	Q7u6v5 synechococc
755	33	372	2	Q9HG90_SCHPO	Q9hgp0 schizosacch	828	33	60.0	531	2	Q8A8B9_BACTN	Q8a8b9 bacteroides
756	33	374	2	Q9H7K3_HUMAN	Q9h7k3 homo sapien	829	33	60.0	565	2	Q81QF1_DROME	Q81qf1 drosophila
757	33	374	2	Q702S4_CIOSA	Q702s4 ciona savig	830	33	60.0	566	2	Q825Z5_9INFA	Q825z5 influenza a
758	33	374	2	Q6EV31_BRARE	Q6ev31 brachydanio	831	33	60.0	566	2	Q9EA37_9INFA	Q9ea37 influenza a
759	33	374	2	Q5ND65_ORYLA	Q5nd65 oryzias lat	832	33	60.0	583	1	DRTS_PLACH	P20712 plasmodium
760	33	375	2	Q80642_ARATH	Q80642 arabidopsis	833	33	60.0	587	2	Q6MF24_PAROW	Q6mf24 paracantham
761	33	376	2	Q9FP66_ARATH	Q9fp66 arabidopsis	834	33	60.0	603	2	Q4MK67_BACCE	Q4mk67 bacillus ce

835	33	60.0	603	2	Q6HL93_BACHK	Q6Ll93 bacillus th	908	33	60.0	1625	2	Q52GA8_MAGGR	Q52ga8 magnaporthe
836	33	60.0	603	2	Q73B33_BACC1	Q73b33 bacillus ce	909	33	60.0	1767	2	Q6VZM2_CNPV	Q6vzm2 canarypox v
837	33	60.0	603	2	Q81T10_BACAN	Q81t10 bacillus ce	910	33	60.0	1854	2	Q5KGM7_CRYNE	Q5kgm7 cryptococc
838	33	60.0	604	2	Q63DS0_BACCZ	Q63ds0 bacillus ce	911	33	60.0	1873	2	Q4S162_TBING	Q4s162 tetroadon n
839	33	60.0	604	2	Q13801_SCHPO	Q13801 schizosacch	912	33	60.0	1953	2	Q5BI67_DROME	Q5bi67 drosophila
840	33	60.0	608	2	Q4HAY5_9BEO	Q4hay5 deinococcus	913	33	60.0	2144	2	Q8G982_OSCAG	Q8g982 oscillatori
841	33	60.0	624	2	Q6QW81_AZOB	Q6qw81 azospirillum	914	33	60.0	2254	2	Q5S875_CRYNE	Q5s875 cryptococc
842	33	60.0	626	2	Q4Q6L1_LEIMA	Q4q6l1 leishmania	915	33	60.0	2473	2	Q55JH8_DICDI	Q55jh8 dictyosteli
843	33	60.0	628	2	Q7KVK6_DROME	Q7kvk6 drosophila	916	33	60.0	2528	2	Q9VYL3_DROME	Q9vyl3 drosophila
844	33	60.0	640	2	Q4MOK5_9BURK	Q4mok5 burkholderi	917	33	60.0	2591	2	Q54959_STRPR	Q54959 streptomyce
845	33	60.0	647	2	Q610E5_CAEBR	Q610e5 caenorhabdi	918	33	60.0	2617	2	Q7R000_GIALA	Q7r000 giardia lam
846	33	60.0	650	2	Q73220_SYNY3	Q73220 synectocyst	919	33	60.0	3182	2	Q7QV55_GIALA	Q7qv55 giardia lam
847	33	60.0	651	2	Q5EAZ7_BRARE	Q5eaz7 brachydanio	920	33	60.0	4540	2	Q5SEG2_DICDI	Q5seg2 dictyosteli
848	33	60.0	655	2	Q51QY6_MAGGR	Q51qy6 magnaporthe	921	32.5	59.1	150	1	DUT_METH	Q27642 methanobact
849	33	60.0	655	2	Q4WYT1_ASPFU	Q4wyt1 aspergillus	922	32.5	59.1	261	2	Q6PY59_9VIRU	Q6py59 hyposoter f
850	33	60.0	660	2	Q5SCL6_DICDI	Q5scl6 dictyosteli	923	32.5	59.1	305	1	META_BACTN	Q8a531 bacteroides
851	33	60.0	660	2	Q00885_DICDI	Q00885 dictyosteli	924	32.5	59.1	394	2	Q8NC33_HUMAN	Q8nce33 homo sapien
852	33	60.0	662	2	Q7S9B5_NEUCR	Q7s9b5 neurospora	925	32.5	59.1	394	2	Q9H6N0_HUMAN	Q9h6n0 homo sapien
853	33	60.0	671	2	Q8A9Y2_BACTN	Q8a9y2 bacteroides	926	32.5	59.1	394	2	Q8RR47_STRSU	Q8rr47 streptococc
854	33	60.0	695	2	Q9UTM2_SCHPO	Q9utm2 schizosacch	927	32.5	59.1	403	2	Q93HW5_STRSU	Q93hw5 streptococc
855	33	60.0	713	2	Q7NVB0_CHRVO	Q7nvb0 chromobacte	928	32.5	59.1	484	2	Q5L759_CHLAB	Q5l759 chlamydophi
856	33	60.0	717	2	Q5A315_CANAL	Q5a315 candida alb	929	32.5	59.1	500	2	Q8KU92_ENTFA	Q8ku92 enterococc
857	33	60.0	719	2	Q8DYD5_STRAS	Q8dyd5 streptococc	930	32.5	59.1	503	2	Q61P80_HUMAN	Q61pe80 homo sapien
858	33	60.0	732	2	Q8B3Z8_STRAS	Q8b3z8 streptococc	931	32.5	59.1	536	2	Q5DZ80_VIBF1	Q5dze0 vibrio fisc
859	33	60.0	739	2	Q9C0Y0_SCHPO	Q9c0y0 schizosacch	932	32.5	59.1	545	2	Q7IMF7_HUMAN	Q7imf7 homo sapien
860	33	60.0	750	2	Q01348_DROME	Q01348 drosophila	933	32.5	59.1	644	2	Q9NT61_HUMAN	Q9nt61 homo sapien
861	33	60.0	759	2	Q62WL9_BACLD	Q62wl9 bacillus li	934	32.5	59.1	653	2	Q7TOV1_XENLA	Q7tov1 xenopus lae
862	33	60.0	760	2	Q65L81_BACLD	Q65l81 bacillus li	935	32.5	59.1	688	2	Q74HS9_LACJO	Q74hs9 lactobacill
863	33	60.0	768	2	Q4UHW9_THEAN	Q4uhw9 theileria a	936	32.5	59.1	800	2	Q8BK85_MOUSE	Q8bkb5 mus musculu
864	33	60.0	780	2	Q6NNZ8_DROME	Q6nnz8 drosophila	937	32.5	59.1	857	2	Q6GLS2_XENTR	Q6gl52 xenopus tro
865	33	60.0	803	2	Q9VTD3_DROME	Q9vtd3 drosophila	938	32.5	59.1	865	2	Q4R8S8_PONFY	Q4r8s8 macaca faec
866	33	60.0	803	2	Q5BIH1_DROME	Q5bih1 drosophila	939	32.5	59.1	882	2	Q5R4P8_PONFY	Q5r4p8 pongo pygma
867	33	60.0	837	2	Q4SGD9_TETNG	Q4sgd9 tetraodon n	940	32.5	59.1	896	2	Q7L525_HUMAN	Q7l525 homo sapien
868	33	60.0	858	1	P0E6C_HUMAN	P51160 homo sapien	941	32.5	59.1	896	2	Q6ZN10_HUMAN	Q6zn10 homo sapien
869	33	60.0	858	2	Q5VY23_HUMAN	Q5vy29 homo sapien	942	32.5	59.1	898	2	Q5O417_RAT	Q5o417 rattus norv
870	33	60.0	866	2	Q6BKY5_DEBHA	Q6bky5 debaryomyce	943	32.5	59.1	900	2	Q8BY46_MOUSE	Q8by46 mus musculu
871	33	60.0	866	2	Q4WR40_ASPFU	Q4wr40 aspergillus	944	32.5	59.1	906	2	Q5A0V5_CANAL	Q5a0v5 candida alb
872	33	60.0	867	2	Q70FJ3_ASPFU	Q70fj3 aspergillus	945	32.5	59.1	986	2	Q6ZN55_HUMAN	Q6zn55 homo sapien
873	33	60.0	881	1	YJ78_YEAST	P39535 saccharomyc	946	32	58.2	55	2	P89495_YEAST	P89495 saccharomyc
874	33	60.0	889	2	Q4H2G6_CJOIN	Q4h2g6 ciona intes	947	32	58.2	83	2	Q7ONL9_ANOGA	Q7onl9 anopheles g
875	33	60.0	937	2	Q9VZM8_DROME	Q9vzm9 drosophila	948	32	58.2	84	2	Q8TJA0_METAC	Q8tja0 methanosarc
876	33	60.0	967	2	Q63HK3_HUMAN	Q63hk3 homo sapien	949	32	58.2	84	2	Q9JXY3_NEIME	Q9jxy3 neisseria m
877	33	60.0	970	2	Q4RNE3_TETNG	Q4rne3 tetraodon n	950	32	58.2	87	2	Q8T4M2_HYDAT	Q8t4m2 hydra atten
878	33	60.0	973	2	Q5RAQ4_PONFY	Q5raq4 pongo pygma	951	32	58.2	87	2	Q8T6S3_HYDAT	Q8t6s3 hydra atten
879	33	60.0	983	2	Q7RAH2_PLAYO	Q7rah2 plasmodium	952	32	58.2	87	2	Q8T6S4_HYDAT	Q8t6s4 hydra atten
880	33	60.0	997	2	Q5AYB5_DICDI	Q5ayb5 dictyosteli	953	32	58.2	88	2	Q9VFG8_DROME	Q9vfg8 drosophila
881	33	60.0	998	2	Q7RLZ5_PLAYO	Q7rlz5 plasmodium	954	32	58.2	88	2	Q4N8J9_THERA	Q4n8j9 theileria p
882	33	60.0	1006	2	Q8QS12_PONGINE	Q8qs12 pongine her	955	32	58.2	91	2	Q891W6_ORISA	Q891w6 oryza sativ
883	33	60.0	1007	2	Q6BMX1_DEBHA	Q6bmx1 debaryomyce	956	32	58.2	91	2	Q6ZEG3_SYNY3	Q6zeg3 synectocyst
884	33	60.0	1011	2	Q52G72_MAGGR	Q52g72 magnaporthe	957	32	58.2	102	2	Q73SN3_MYCPA	Q73sn3 mycobacteri
885	33	60.0	1030	2	Q9ERP4_MOUSE	Q9erp4 mus musculu	958	32	58.2	108	1	KV1L_HUMAN	P01604 homo sapien
886	33	60.0	1048	2	Q5BDU7_EMENI	Q5bdut aspergillus	959	32	58.2	108	1	KV5Q_MOUSE	P01650 mus musculu
887	33	60.0	1049	2	Q4LQX3_9BURK	Q4lqx3 burkholderi	960	32	58.2	108	1	KV5R_MOUSE	P01651 mus musculu
888	33	60.0	1068	2	Q5JG97_PYRKO	Q5jg97 pyrococcus	961	32	58.2	108	1	KV5S_MOUSE	P01652 mus musculu
889	33	60.0	1069	2	Q4WTC1_ASPFU	Q4wtc1 aspergillus	962	32	58.2	108	2	Q7N1F1_PHOLL	Q7n1p1 photorhabdu
890	33	60.0	1085	2	Q4FXK2_LEIMA	Q4fxk2 leishmania	963	32	58.2	112	2	Q9SL45_ARATH	Q9sl45 arabidopsis
891	33	60.0	1090	2	Q54Y43_DICDI	Q54y43 dictyosteli	964	32	58.2	113	1	KV2F_MOUSE	P01630 mus musculu
892	33	60.0	1098	2	Q7R8R5_PLAYO	Q7r8r5 plasmodium	965	32	58.2	113	1	Q4L9V4_STAHL	Q4l9v4 staphylococ
893	33	60.0	1099	2	Q4KPF6_DICDI	Q4kpf6 dictyosteli	966	32	58.2	129	2	Q08559_YEAST	Q08559 saccharomyc
894	33	60.0	1160	2	Q4WXM4_ASPFU	Q4wxm4 aspergillus	967	32	58.2	130	2	Q9FK01_ARATH	Q9fk01 arabidopsis
895	33	60.0	1179	2	Q752B4_ASHGO	Q752b4 ashbya gos	968	32	58.2	142	2	Q07094_ERWCH	Q07094 erwinia chr
896	33	60.0	1218	2	Q6OY57_CAEBR	Q6oy57 caenorhabdi	969	32	58.2	142	2	Q83AX8_COXBU	Q83ax8 coxiella bu
897	33	60.0	1226	2	Q20362_CAEEL	Q20362 caenorhabdi	970	32	58.2	146	2	Q8ET11_OCEIH	Q8et11 oceanobacil
898	33	60.0	1227	1	B3A3_MOUSE	P15283 mus musculu	971	32	58.2	147	1	NDD_BPR70	P42268 bacterioph
899	33	60.0	1227	1	B3A3_RAT	P23348 rattus norv	972	32	58.2	149	2	Q9XVU7_CAEEL	Q9xvu7 caenorhabdi
900	33	60.0	1227	1	Q9ERP5_MOUSE	Q9erp5 mus musculu	973	32	58.2	151	1	NDD_BPT4	P45556 bacterioph
901	33	60.0	1232	1	B3A3_HUMAN	P48751 homo sapien	974	32	58.2	151	1	NDD_BPT6	P42265 bacterioph
902	33	60.0	1232	1	Q5RB85_PONFY	Q5rb85 pongo pygma	975	32	58.2	152	1	NDD_BPK3	P69191 bacterioph
903	33	60.0	1233	1	B3A3_RABIT	Q18917 oryctolagus	976	32	58.2	152	1	NDD_BPR32	P69190 bacterioph
904	33	60.0	1239	2	Q68EG4_MOUSE	Q68eg4 mus musculu	977	32	58.2	152	1	NDD_BPR69	P42267 bacterioph
905	33	60.0	1259	2	Q6YIQ9_HUMAN	Q6yiq9 homo sapien	978	32	58.2	152	1	NDD_BPT2	P69189 bacterioph
906	33	60.0	1273	2	Q51HY5_MAGGR	Q51hy5 magnaporthe	979	32	58.2	166	2	Q8LIS6_9BACT	Q8lis6 uncultured
907	33	60.0	1444	2	Q7S2W3_NEUCR	Q7s2w3 neurospora	980	32	58.2	173	2	Q6GPT2_XENLA	Q6gpt2 xenopus lae

981 32 58.2 174 2 Q4UH23 THEAN Q4uh23 theileria a
 982 32 58.2 175 2 Q5CY80 MOUSE Q5cy80 mus musculus
 983 32 58.2 177 2 Q57255_9POXV Q57255 vaccinia vi
 984 32 58.2 179 2 Q8WQ06_0STOS Q8wq06 ostertagia
 985 32 58.2 182 1 V807_VACCV P68445 vaccinia vi
 986 32 58.2 182 1 V807_VACCV P68444 vaccinia vi
 987 32 58.2 182 2 Q6RZC2_9POXV Q6rzc2 rabbitpox v
 988 32 58.2 182 2 Q76ZL6_9POXV Q76zl6 vaccinia vi
 989 32 58.2 182 2 Q77TF8_VACCT Q77tf8 vaccinia vi
 990 32 58.2 182 2 Q8WGA1_9POXV Q8wga1 vaccinia vi
 991 32 58.2 182 2 Q72743_COWPX Q72743 cowpox viru
 992 32 58.2 182 2 Q5IXK8_MONPV Q5ixk8 monkeypox v
 993 32 58.2 186 2 Q744F4_MYCPA Q744f4 mycobacteri
 994 32 58.2 188 2 Q24865_ENTIV Q24865 entamoeba i
 995 32 58.2 191 2 Q59NL6_CANAL Q59nl6 candida alb
 996 32 58.2 191 2 Q32Q07_MYCPA Q32q07 mycobacteri
 997 32 58.2 199 2 Q5WZG4_LEGPL Q5wz94 legionella
 998 32 58.2 201 2 Q50TK6_ENTHI Q50tk6 entamoeba h
 999 32 58.2 202 2 Q5Z9Y3_ORYSA Q5z9y3 oryza sativ
 1000 32 58.2 203 2 Q5TT81_ANOGA Q5tt81 anopheles g

ALIGNMENTS

RESULT 1
 Q4JAU1_SULAC
 ID Q4JAU1_SULAC PRELIMINARY; PRT; 337 AA.
 AC Q4JAU1;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Adenylosuccinate synthase (EC 6.3.4.4).
 GN OrderedLocusNames=Saci_0709;
 OS Sulfolobus acidocaldarius.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2285;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
 RX PubMed=15995215; DOI=10.1128/JB.187.14.4992-4999.2005;
 RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
 RA Grev B., Aways M., Zibat A., Klenk H.-P., Garrett R.A.;
 RT "The genome of Sulfolobus acidocaldarius, a model organism of the
 RT Crenarchaeota";
 RL J. Bacteriol. 187:4992-4999(2005).
 DR EMBL; CP000077; AAY80088.1; -; Genomic_DNA.
 KW Complete proteome; Ligase.
 SQ SEQUENCE 337 AA; 37211 MW; B2CF40D4CE555073 CRC64;

Query Match 81.8%; Score 45; DB 2; Length 337;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LHHSEYPT 9
 | : | | | | |
 Db 180 LYHGEYPT 188

RESULT 2
 Q5D200_VIBF1
 ID Q5D200_VIBF1 PRELIMINARY; PRT; 266 AA.
 AC Q5D200;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical membrane associated protein.
 GN OrderedLocusNames=VPA0926;
 OS Vibrio fischeri (strain ATCC 700601 / E5114).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=312309;

[1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP PubMed=15703294; DOI=10.1073/pnas.0409900102;
 RX Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
 RA Lostron P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
 RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
 RT "Complete genome sequence of *Vibrio fischeri*: a symbiotic bacterium
 RT with pathogenic congeners";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
 DR EMBL; CP000021; AAW87996.1; -; Genomic_DNA.
 DR InterPro; IPR006685; MscS_channel.
 DR Pfam; PF00924; MS_channel; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 266 AA; 30755 MW; 9AAFOB1E039B7D78 CRC64;
 Query Match 80.0%; Score 44; DB 2; Length 266;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LHHSEYPT 9
 | | | | | | |
 Db 127 LHSQDYPT 135

RESULT 3
 Q6HA07_BRALA
 ID Q6HA07_BRALA PRELIMINARY; PRT; 407 AA.
 AC Q6HA07;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Serine protease inhibitor precursor.
 GN Names=sp1;
 OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 OX NCBI_TaxID=7740;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Toedtman U., Krueger O., Regg H.;
 RT "Amphioxus serpins.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -|- SIMILARITY: Belongs to the serpin family.
 DR EMBL; AJ548509; CAD68157.1; -; mRNA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000886; ER_target_S.
 DR InterPro; IPR000295; Prot_inh_Lserp2.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin_1.
 DR PRINTS; PR00780; LEUSERPINII.
 DR SMART; SMO0093; SERPIN; 1.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Protease; Serpin; Signal.
 FT SIGNAL 1
 22 Potential.
 SQ SEQUENCE 407 AA; 46111 MW; AB246F7E087B63AA CRC64;

Query Match 78.2%; Score 43; DB 2; Length 407;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
 | | | | | | |
 Db 103 LHSQDYPT 111

RESULT 4
 Q4V464_DROME
 ID Q4V464_DROME PRELIMINARY; PRT; 704 AA.
 AC Q4V464;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IP08936p (IP08936p) (fragment).
GN Name=E(bxb);
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Celniker S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT023142; AAY55558.1; -; mRNA.
FT NON TER 704 704
SQ SEQUENCE 704 AA; 80815 MW; 005E28D23CC92A6D CRC64;
Query Match 78.2%; Score 43; DB 2; Length 704;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LHHSEVPYPT 9
DB 296 LSHTBYPYPT 304
RESULT 5
Q7KV08 DROME
ID Q7KV08_DROME PRELIMINARY; PRT; 2159 AA.
AC Q7KV08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG32346-PC isoform C.
GN Name=E(bxb); ORFNames=CG32346;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003467; AAS64922.1; -; Genomic DNA.
DR Ensembl; CG32346; Drosophila melanogaster.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000637; A+T hook.
DR InterPro; IPR004022; DPT.
DR InterPro; IPR001965; Znf PHD.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF06628; PHD; 1.
DR SMART; SM00571; DDT; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS50827; DDT; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
SQ SEQUENCE 2159 AA; 241632 MW; 318BDE0E966A5CF8 CRC64;

Query Match

78.2%; Score 43; DB 2; Length 2159;

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Db	296 LSHTSEYPYT 304		
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ID	Q9W0T2 DROME PRELIMINARY;	PRT; 2649 AA.	
AC	Q9W0T2;		
DT	01-MAY-2000 (TRENBLrel. 13, Created)		
DT	01-OCT-2002 (TRENBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TRENBLrel. 26, Last annotation update)		
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GN	Name=E(bx); ORFNames=CG32346;		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_taxID=7227;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;		
RA	Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.P.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
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RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
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RA	Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,		
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RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
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RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebb J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RT	"The genome sequence of Drosophila melanogaster."		
RL	Science 287:2185-2195(2000).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=22426065; PubMed=12537568;		
RA	Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,		
RA	Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,		
RA	George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,		
RA	Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,		
RA	Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,		
RA	Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,		
RT	"Finishing a whole-genome shotgun: release 3 of the Drosophila		
	melanogaster euchromatic genome sequence."		
	Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).		
	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=22426070; PubMed=12537573;		
RA	Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,		
RA	Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,		
RA	Ashburner M., Celniker S.E.,		
RT	"The transposable elements of the Drosophila melanogaster euchromatic		
RT	a genomics perspective."		
RL	Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=22426069; PubMed=12537572;		
RA	Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,		
RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,		
RA	Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,		
RA	Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,		
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,		
RA	Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,		
RA	Lewis S.E.,		
RT	"Annotation of the Drosophila melanogaster euchromatic genome: a		
RT	systematic review."		
RL	Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).		
RN	[5]		
RP	NUCLEOTIDE SEQUENCE.		
RG	Berkeley Drosophila Genome Project;		
RA	Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,		
RA	Hoskins R., Stapleton M., Paclebb J., Park S., Svirskas R., Smith E.,		
RA	Yu C., Rubin G.,		
RT	"Drosophila melanogaster release 4 sequence."		
RT	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	NUCLEOTIDE SEQUENCE.		
RG	FlyBase;		
RL	Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AE003467; AAF47361.2; -; Genomic_DNA.		
DR	HSP; Q03330; I861.		
DR	Ensembl; CG32346; Drosophila melanogaster.		
DR	FlyBase; FBgn0000541; CG32346.		
DR	FlyBase; FBgn0000541; E(bx).		
DR	GO; GO:0016589; C:NURF complex; IDA.		
DR	GO; GO:0006338; P:chromatin remodeling; IMP.		
DR	GO; GO:0030097; P:hemopoiesis; IMP.		
DR	GO; GO:0042766; P:nucleosome mobilization; IDA.		
DR	GO; GO:0006350; P:transcription; IDA.		
DR	InterPro; IPR00637; A+T hook.		
DR	InterPro; IPR001487; Bromodomain.		
DR	InterPro; IPR004022; DDT.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR001965; Znf_PHD.		
DR	Pfam; PF02178; At_hook; 1.		
DR	Pfam; PF00439; Bromodomain; 1.		
DR	Pfam; PF02791; DDT; 1.		
DR	Pfam; PF00628; PHD; 3.		
DR	PRINTS; PR00503; BROMODOMAIN.		
DR	SMART; SM00384; AT_hook; 2.		
DR	SMART; SM00297; BROMO; 1.		
DR	SMART; SM00571; DDT; 1.		
DR	SMART; SM00249; PHD; 3.		
DR	PROSITE; PS00633; BROMODOMAIN_1; 1.		
DR	PROSITE; PS50014; BROMODOMAIN_2; 1.		
DR	PROSITE; PS50827; DDT; 1.		
DR	PROSITE; PS01186; EGF_2; UNKNOWN_2.		
DR	PROSITE; PS01359; ZF_PHD_1; 1.		
DR	PROSITE; PS50016; ZF_PHD_2; 2.		
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	Best Local Similarity 77.8%; Pred. No. 2.5e+02;		
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Db          296 LSHTSEPYT 304
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AC Q95VB8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nucleosome remodeling factor large subunit NURF301.
CN Name=E(bx); Synonyms=Nurf301; ORFNames=CG32346;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21468388; PubMed=11583616; DOI=10.1016/S1097-2765(01)00345-8;
RA Xiao H., Sandaltzopoulos R., Wang H., Hamiche A., Ranallo R., Lee K.,
RA Fu D., Wu C.;
RT "Dual functions of largest NURF subunit NURF301 in nucleosome sliding
RT and transcription factor interactions.";
RL Mol. Cell 8:531-543(2001).
DR EMBL; AF417921; AAL16644.1; -; mRNA.
DR HSSP; Q03330; 1B61.
DR Ensembl; CG32346; Drosophila melanogaster.
DR FlyBase; FBgn0000541; CG32346.
DR FlyBase; FBgn0000541; E(bx).
DR GO; GO:0016589; C:NURF complex; IDA.
DR GO; GO:0006338; P:chromatin remodeling; IMP.
DR GO; GO:0030097; P:hemoiesis; IMP.
DR GO; GO:0042766; P:nucleosome mobilization; IDA.
DR GO; GO:0006350; P:transcription; IDA.
DR InterPro; IPR000637; A+T hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001965; ZnF PHD.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF00439; Bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF00628; PHD; 3.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT hook; 2.
DR SMART; SM00297; BRMO; 1.
DR SMART; SM00571; DDT; 1.
DR SMART; SM00249; PHD; 3.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS00014; BROMODOMAIN_2; 1.
DR PROSITE; PS00827; DDT; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00016; ZF_PHD_2; 2.
SQ SEQUENCE 2669 AA; 300686 MW; 6B4925AFFFA489D6F CRC64;

Query Match 78.2%; Score 43; DB 2; Length 2669;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LHSEPYT 9
Db 296 LSHTSEPYT 304
RESULT 8
Q9W0T1 DROME
ID Q9W0T1_DROME PRELIMINARY; PRT; 2669 AA.
AC Q9W0T1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG32346-PA, isoform A.
CN Name=E(bx); ORFNames=CG32346;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;

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RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003467; AAN1431.1; -; Genomic_DNA.
DR HSSP; Q03330; 1861.
DR Ensembl; CG32346; Drosophila melanogaster.
DR FlyBase; FBgn0000541; CG32346.
DR FlyBase; FBgn0000541; E(bx).
DR GO; GO:0016589; C:NURF complex; IDA.
DR GO; GO:0006338; P:chromatin remodeling; IMP.
DR GO; GO:0030097; P:hemoicosis; IMP.
DR GO; GO:0042766; P:nucleosome mobilization; IDA.
DR GO; GO:0006350; P:transcription; IDA.
DR InterPro; IPR006637; A-T hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF02178; AT hook; 1.
DR Pfam; PF00433; Bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF00628; PHD; 3.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT hook; 2.
DR SMART; SM00297; BRGMO; 1.
DR SMART; SM00571; DDT; 1.
DR SMART; SM00249; PHD; 3.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS0014; BROMODOMAIN_2; 1.
DR PROSITE; PS00827; DDT; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00016; ZF_PHD_2; 2.
SQ SEQUENCE 2669 AA; 300684 MW; 261FF7B7CEEF781B CRC64;
Query Match 78.2%; Score 43; DB 2; Length 2669;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LHSSEYPT 9
| | | | |
Db 296 LSHTSEYPT 304
RESULT 9
Q6LXU6 METMP
ID Q6LXU6 METMP PRELIMINARY; PRT; 186 AA.
AC Q6LXU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=MMPI251;
OS Methanococcus maripaludis.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S2 / LL;
RX PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,
RA Hackett M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogenotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6956-6969(2004).
DR EMBL; BX957222; CAF30807.1; -; Genomic_DNA.
DR InterPro; IPR000644; CBS.
DR Pfam; PF00571; CBS; 1.
DR SMART; SM00116; CBS; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 186 AA; 20246 MW; 23AD5B4B5A7DC8D5 CRC64;
Query Match 76.4%; Score 42; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LHSSEYPT 9
| | | | |
Db 139 IHNSEYPT 147
RESULT 10
Q7Q6E2 ANOGA
ID Q7Q6E2 ANOGA PRELIMINARY; PRT; 293 AA.
AC Q7Q6E2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000013521 (Fragment).
GN ORFNames=ENSANGG0000011032;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008960; EAA11069.2; -; Genomic_DNA.
DR SMR; Q7Q6E2; 58-150.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.

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FT NON_TER 293 293
SQ SEQUENCE 293 AA; 33527 MW; 83DC1B9CC174D800 CRC64;

Query Match 76.4%; Score 42; DB 2; Length 293;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSEYPY 8
DB 259 LHSEYPY 266

RESULT 11
Q6TYQ4 PAFPA PRELIMINARY; PRT; 387 AA.
AC Q6TYQ4;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Sperm ion channel (Fragment).
GN Name=CATSPERI;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22922087; PubMed=14523237; DOI=10.1073/pnas.2033555100;
RA Podlaha O., Zhang J.;
RT "Positive selection on protein-length in the evolution of a primate
spem ion channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:12241-12246(2003).
DR EMBL; AY382302; AAQ95779.1; -; Genomic_DNA.
FT NON_TER 387 387
SQ SEQUENCE 387 AA; 44024 MW; 410986D88E56361A CRC64;

Query Match 76.4%; Score 42; DB 2; Length 387;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHSEYPY 9
DB 259 HHSEYPY 266

RESULT 12
Q6TYQ6 MACMU PRELIMINARY; PRT; 390 AA.
AC Q6TYQ6;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Sperm ion channel (Fragment).
GN Name=CATSPERI;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22922087; PubMed=14523237; DOI=10.1073/pnas.2033555100;
RA Podlaha O., Zhang J.;
RT "Positive selection on protein-length in the evolution of a primate
spem ion channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:12241-12246(2003).
DR EMBL; AY382300; AAQ95779.1; -; Genomic_DNA.
FT NON_TER 390 390
SQ SEQUENCE 390 AA; 44371 MW; 74D9EACDA43B2666 CRC64;

Query Match 76.4%; Score 42; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 48;

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Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHSEYPY 9
DB 259 HHSEYPY 266

RESULT 13
ID CROC DROME STANDARD; PRT; 508 AA.
AC P32027; Q9VP32;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Fork head domain protein crocodile (FKH protein FDI).
GN Name=croc; Synonyms=FDI, FD78E; ORFNames=CG5069;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Canton-S;
RX MEDLINE=96080166; PubMed=7489720;
RA Haecker U., Kaufmann E., Hartmann C., Juergens G., Knoechel W.,
RA Jaekle H.;
RT "The Drosophila fork head domain protein crocodile is required for the
establishment of head structures.";
RL EMBL J. 14:5306-5317(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikkos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [3]

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OX NCBI_TaxID=74547;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer P.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Shah M.,
RA Johnson Z.L., Land M.B., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinner E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572100; CAE21999.1; -; Genomic_DNA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008258; LT catalytic.
DR InterPro; IPR000189; Transglyc_AS.
DR Pfam; PF01464; SLT; 1.
DR PROSITE; PS00922; TRANSGLYCOSYLASE; 1.
DR Complete proteome; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 26 Potential.
SQ SEQUENCE 677 AA; 75412 MW; 3FA1D88B41B90D7D CRC64;

Query Match 76.4%; Score 42; DB 2; Length 677;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8
DB 516 LHHSQHPY 523
J. Cell Sci. 112:2019-2032(1999).

RESULT 16
Q9W6V6 CHICK
ID Q9W6V6_CHICK PRELIMINARY; PRT; 2705 AA.
AC Q9W6V6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Teneurin-1.
GN Name=tene-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=99276595; PubMed=10341219;
RA Minet A.D., Rubin B.P., Tucker R.P., Baumgartner S.,
RA Chiquet-Ehrismann R.;
RA "Teneurin-1, a vertebrate homologue of the Drosophila pair-rule gene
RT ten-m, is a neuronal protein with a novel type of heparin-binding
RT domain.";
RL J. Cell Sci. 112:2019-2032(1999).
DR EMBL; AJ238613; CAB43098.1; -; mRNA.
DR HSP; P01135; 1MOX.
DR Ensembl; ENSGALG00000008442; Gallus gallus.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR009471; Ten_N.
DR InterPro; IPR006530; YD.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF01436; NHL; 5.
DR Pfam; PF05593; RHS repeat; 6.
DR Pfam; PF06484; Ten_N; 1.
DR SMART; SM00181; EGF; 6.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR PROSITE; PS00022; EGF 1; 8.
DR PROSITE; PS01186; EGF_2; 7.

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DR PROSITE; PS00026; EGF 3; 4.
SQ SEQUENCE 2705 AA; 302386 MW; 230F03D1999037D2 CRC64;

Query Match 76.4%; Score 42; DB 2; Length 2705;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
DB 882 LHHDEYGYT 890
III|II|

RESULT 17
Q623S5 CAEBR
ID Q623S5 CAEBR PRELIMINARY; PRT; 315 AA.
AC Q623S5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG01743.
GN Name=CBG01743;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100009; CAB58577.1; -; Genomic_DNA.
SQ SEQUENCE 315 AA; 35483 MW; FC88A4C9C56B4E35 CRC64;

Query Match 74.5%; Score 41; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8
DB 289 LHHAAYPY 296
III|II|

RESULT 18
Q8UKS4 9VIRU
ID Q8UKS4_9VIRU PRELIMINARY; PRT; 943 AA.
AC Q8UKS4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative methyl transferase.
GN Name=orf37;
OS Heliothis zea virus 1.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.
OX NCBI_TaxID=29250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22174892; PubMed=12186886;
RX DOI=10.1128/JVI.76.18.9024-9034.2002;
RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
RA Chen H.H.;
RT "Analysis of the complete genome sequence of the Hs-1 virus suggests
RT that it is related to members of the Baculoviridae.";
RL J. Virol. 76:9024-9034(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Chao Y.;

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RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Chen H.H., Yeh W.B., Tso D.J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF451898; AAN04332.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR002877; RnmJftsJ_mtfase.
DR Pfam; PF01728; FtsJ; 1.
KW Transferase.
SQ SEQUENCE 943 AA; 104698 MW; 96B2009F4ADDEEA4 CRC64;

Query Match 74.5%; Score 41; DB 2; Length 943;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHSEYPYT 9

Db 550 HHNQPYPS 557
||:||||:

RESULT 19

ID Q17174_BOOMI PRELIMINARY; PRT; 1289 AA.
AC Q17174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GP80 (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=yeerongpilly;
RX MEDLINE=21625935; PubMed=11751009; DOI=10.1016/S0304-4017(01)00573-8;
RA Tellam R.L., Kemp D., Ridding G., Briscoe S., Smith D., Sharp P.,
RA Irving D., Willadsen P.;
RT "Reduced oviposition of Boophilus microplus feeding on sheep
ET vaccinated with vitellin".
RL Vet. Parasitol. 103:141-156(2002).
DR EMBL; U49934; AAA92143.1; -; mRNA.
DR PIR; T31344; T31344.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00216; VWD; 1.
FT NON_TER 1 1

SQ SEQUENCE 1289 AA; 147185 MW; 29A01B3E393DB644 CRC64;
Query Match 74.5%; Score 41; DB 2; Length 1289;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HHSEYPYT 9

Db 1275 HHPEPYT 1282
||:||||:

RESULT 20

ID Q980P5_SULSO
AC Q980P5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adenylosuccinate synthase (IMP--aspartate ligase) (PurA)
DE (EC 6.3.4.4).
GN Name=PurA; OrderedLocusNames=SSO0242;

OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.14122098;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Regan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -1- SIMILARITY: Belongs to the adenylosuccinate synthetase family.
DR EMBL; AE006661; AAK40583.1; -; Genomic DNA.
DR PIR; H90165; H90165.
DR HSRP; P12283; IADE.
DR GO; GO:0004019; F:adenylosuccinate synthase activity; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0016874; P:ligase activity; IEA.
DR GO; GO:0006164; P:purine nucleotide biosynthesis; IEA.
DR InterPro; IPR001114; Asucc synthase.
DR InterPro; IPR000897; SRP54_GTP_bd.
DR Pfam; PF00709; Adenylosucc_synth; 1.
DR PRODOM; PD001188; Asucc synthase; 1.
DR PROSITE; PS01266; ADENYLOSUCIN SYN_1; 1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
KW Complete proteome; GTP-binding; Ligase; Magnesium; Metal-binding;
KW Nucleotide-binding; Purine biosynthesis.
SQ SEQUENCE 335 AA; 37440 MW; C01E75900BEF1918 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 335;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSEYPY 8

Db 180 LYHGEYPY 187
|:|||||

RESULT 21

ID Q975Y7_SULTO PRELIMINARY; PRT; 335 AA.
AC Q975Y7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adenylosuccinate synthetase (EC 6.3.4.4) (AMPase) (AdSS) (IMP--
DE aspartate ligase).
DE OrderedLocusNames=ST0291;
GN Sulfolobus tokodaii.
OS Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
CC -1- SIMILARITY: Belongs to the adenylosuccinate synthetase family.
DR EMBL; BA000023; BAB65261.1; -; Genomic DNA.


```

DR HSP; P12283; LCG3
DR GO; GO:0004019; F:adenylosuccinate synthase activity; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006164; F:purine nucleotide biosynthesis; IEA.
DR InterPro; IPR001114; Asucc synthase.
DR Pfam; PF00709; Adenylsucc_synth; 1.
DR Prodom; PD001188; Asucc synthase; 1.
DR PROSITE; PS01266; ADENYLOSUCCIN SYN_1; 1.
DR PROSITE; PS00300; SRP54; UNKNOWN 1.
KW Complete proteome; GTP-binding; Hypothetical protein; Ligase;
KW Magnesium; Metal-binding; Nucleotide-binding; Purine biosynthesis.
SQ SEQUENCE 335 AA; 7282 MW; 8A3739120C7BFCFB CRC64;

Query Match 72.7%; Score 40; DB 2; Length 335;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
|:| ||||
Db 180 LYHGEYPY 187

RESULT 22
Q9AJU2_9ACTO PRELIMINARY; PRT; 378 AA.
AC Q9AJU2;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE O-methyltransferase I.
GN Name=elmtI;
OS Streptomyces olivaceus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=47716;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21203889; PubMed=11306350; DOI=10.1016/S1074-5521(01)00010-2;
RA Blanco G., Patallo E.P., Brana A.F., Trefzer A., Bechthold A.,
RA Rohr J., Mendez C., Salas J.A.;
RT "Identification of a sugar flexible glycosyltransferase from
RT Streptomyces olivaceus, the producer of the antitumor polyketide
RT elloramyacin.";
RL J. Biol. Chem. Biol. 8:253-263(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21270205; PubMed=11376004; DOI=10.1074/jbc.M101225200;
RA Patallo E.P., Blanco G., Fischer C., Brana A.F., Rohr J., Mendez C.,
RA Salas J.A.;
RT "Deoxysugar methylation during biosynthesis of the antitumor
RT polyketide elloramyacin by Streptomyces olivaceus. Characterization of
RT three methyltransferase genes.";
RL J. Biol. Chem. 276:18765-18774 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Blanco G.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300305; CAD57139.1; -; Genomic DNA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
SQ SEQUENCE 378 AA; 41179 MW; 9D9D4EA7B46A0E3 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 378;
Best Local Similarity 85.7%; Pred. NO. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYP 7
|:| ||||
Db 328 LHHAEYP 334

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RESULT 23
Q86J75_DICDI PRELIMINARY; PRT; 587 AA.
AC Q86J75;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE Hypothetical protein (Oxalate/formate antiporter).
GN ORFNames=DOB0217281, DBO231384;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22097622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Baumgart C.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang B., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kernhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Murny D., Mouris T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Uruishihara H., Hernandez J., Rabinowitsch E., Steffen D., Tivey A.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauleky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
DR EMBL; AC116984; AA051438.1; -; Genomic DNA.
DR EMBL; AAF101000025; RAL70558.1; -; Genomic DNA.
DR EMBL; AAF101000023; RAL70815.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 587 AA; 65477 MW; E2970E90CC812977 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 587;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSYYPY 8
|:| ||||
Db 508 HHSYYPY 514

RESULT 24
HEPA_HCMVA STANDARD; PRT; 873 AA.
ID HEPA_HCMVA

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AC P16827; Q68286; Q7MG6F;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE DNA helicase/primase complex associated protein.
 GN Name=UL102;
 OS Human cytomegalovirus (strain AD169) (HHV-5) (Human herpesvirus 5).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10360;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=90269039; PubMed=2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horenell T., Hutchison C.A. III, Kourzarides T., Martignetti J.A.,
 RA Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "Analysis of the protein-coding content of the sequence of human
 cytomegalovirus strain AD169."
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENE] AND SEQUENCE REVISION.
 RX MEDLINE=95156603; PubMed=7853511;
 RA Smith J.A., Parf G.S.;
 RT "Human cytomegalovirus UL102 gene."
 RL J. Virol. 69:1734-1740(1995).
 RN [3]
 RP GENOME REANNOTATION.
 RX MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;
 RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
 RA Alexander D.J., McGeoch D.J., Hayward G.S.;
 RT "The human cytomegalovirus genome revisited: comparison with the
 chimpanzee cytomegalovirus genome."
 RL J. Gen. Virol. 84:17-28(2003).
 RN [4]
 RP ERRATUM.
 RA Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,
 RA Alexander D.J., McGeoch D.J., Hayward G.S.;
 RL J. Gen. Virol. 84:1053-1053(2003).
 CC 1- FUNCTION: Probable primase-associated factor (PAF) that is part of
 the helicase-primase complex and is required for viral origin-
 dependent DNA replication.
 CC 1- SUBUNIT: The helicase-primase complex is composed of the primase,
 the helicase and the primase-associated factor.
 CC 1- SIMILARITY: Belongs to the herpesviruses HEPA family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X17403; CAA35338.1; ALT_SEQ; Genomic_DNA.
 DR EMBL; U18289; AAA67889.1; -; mRNA.
 DR EMBL; BK000394; DAA00236.1; -; Genomic_DNA.
 DR PIR; S09867; S09867.
 DR InterPro: IPR004996; Herpes HEPA.
 DR Pfam; PF03324; Herpes_HEPA_1.
 KW DNA replication.
 FT CONFLICT 15 15 T -> A (in Ref. 2).
 FT CONFLICT 74 74 S -> T (in Ref. 2).
 FT CONFLICT 170 170 P -> S (in Ref. 2).
 FT CONFLICT 176 176 T -> A (in Ref. 2).
 FT CONFLICT 387 387 G -> S (in Ref. 2).
 FT CONFLICT 395 412 PLPRDDGGNNVVEVS -> RCRVTATVKTTSWKSAR
 (in Ref. 2).
 FT CONFLICT 493 493 S -> G (in Ref. 2).
 FT CONFLICT 525 525 Y -> C (in Ref. 2).
 FT CONFLICT 625 625 S -> G (in Ref. 2).
 FT CONFLICT 859 859 K -> R (in Ref. 2).
 SQ SEQUENCE 873 AA; 94050 MW; C2DB3734306FA4CB CRC64;
 Query Match 72.7%; Score 40; DB 1; Length 873;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LHHSEYPYT 9
 Db 7 LHHRHHPYT 15
 RESULT 25
 Q6RXD5_HCMV
 ID Q6RXD5_HCMV PRELIMINARY; PRT; 873 AA.
 AC Q6RXD5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE UL102
 GN Name=UL102; ORFName=HHV5gp095;
 OS Human cytomegalovirus (HHV-5) (Human herpesvirus 5).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Toledo;
 RA Brondke H., Schmitz B., Shenk T., Doerfler W.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY486477; AAS48988.1; -; Genomic_DNA.
 DR InterPro: IPR004996; Herpes HEPA.
 DR Pfam; PF03324; Herpes_HEPA_1.
 SQ SEQUENCE 873 AA; 94019 MW; 183E190C0691FAF0 CRC64;
 Query Match 72.7%; Score 40; DB 2; Length 873;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LHHSEYPYT 9
 Db 7 LHHRHHPYT 15
 RESULT 26
 Q6SW42_HCMV
 ID Q6SW42_HCMV PRELIMINARY; PRT; 873 AA.
 AC Q6SW42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE UL102.
 OS Human cytomegalovirus (HHV-5) (Human herpesvirus 5).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Merlin;
 RX PubMed=15105547; DOI=10.1099/vir.0.79888-0;
 RA Dolan A., Cunningham C., Hector R.D., Hassan-Walker A.F., Lee L.,
 RA Addison C., Dargan D.J., McGeoch D.J., Gatherer D., Emery V.C.,
 RA Griffiths P.D., Sinzger C., McSharry B.P., Wilkinson G.W.G.,
 RA Davison A.J.;
 RT "Genetic content of wild-type human cytomegalovirus."
 RL J. Gen. Virol. 85:1301-1312(2004).
 DR EMBL; AY446894; AAR31652.1; -; Genomic_DNA.
 DR InterPro: IPR004996; Herpes HEPA.
 DR Pfam; PF03324; Herpes_HEPA_1.
 SQ SEQUENCE 873 AA; 94080 MW; 844F50617EBB045F CRC64;
 Query Match 72.7%; Score 40; DB 2; Length 873;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LHHSEYPYT 9
 Db 7 LHHRHHPYT 15

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RESULT 27
Q80TD2_MOUSE PRELIMINARY; PRT; 1828 AA.
ID Q80TD2;
AC Q80TD2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MKTAA1455 protein (Fragment).
GN Name=Odz3; Synonyms=mKIAA1455;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
DR EMBL; AK122513; BAC65795.1; -; mRNA.
DR MGI; MGI:1345183; Odz3.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR006530; YD.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RHS repeat; 6.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR NON_TER 1
SQ SEQUENCE 1828 AA; 206341 MW; 5C2AAB91DC3DEB8C CRC64;

Query Match 72.7%; Score 40; DB 2; Length 1828;
Best Local Similarity 77.8%; Pred. No. 5.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 9 LHYSEYGT 17

RESULT 28
Q9JLC1_MOUSE PRELIMINARY; PRT; 2346 AA.
ID Q9JLC1;
AC Q9JLC1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ODZ3 (Fragment).
GN Name=Odz3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Ben-Zur T., Feige E., Motro B., Wides R.;
RA "The mammalian Odz gene family: Homologs of a Drosophila pair rule
RT gene with expression implying distinct yet overlapping developmental
RT roles.";
RL Dev. Biol. 117:107-120(2000).
DR EMBL; AF195418; AAF28316.1; -; mRNA.
DR HSP; P00750; ITPG.
DR MGI; MGI:1345183; Odz3.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR NON_TER 1
SQ SEQUENCE 2346 AA; 261700 MW; D761563C6ABDD735 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 2346;
Best Local Similarity 77.8%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 534 LHYSEYGT 542

RESULT 29
Q9WTS6_MOUSE PRELIMINARY; PRT; 2715 AA.
ID Q9WTS6;
AC Q9WTS6;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Ten-m3.
GN Name=Odz3; Synonyms=ten-m3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Brain;
RA Ohashi T., Zhou X., Peng K., Richter B., Moergelin M., Perez M.T.,
RA Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;
RT "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
RT proteins expressed in many tissues.";
RL J. Cell Biol. 0:0-0(1999).
DR EMBL; AB025412; BAA77398.1; -; mRNA.
DR HSP; P00750; ITPG.
DR Ensembl; ENSMUSG00000031561; Mus musculus.
DR MGI; MGI:1345183; Odz3.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR009471; Ten_N.
DR InterPro; IPR006530; YD.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RHS repeat; 6.
DR Pfam; PF06484; Ten_N; 1.
DR SMART; SM00181; EGF; 7.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR PROSITE; PS00022; EGF 1; 8.
DR PROSITE; PS01186; EGF 2; 7.
DR PROSITE; PS00026; EGF 3; 5.
DR PROSITE; PS00026; EGF 3; 5.
SQ SEQUENCE 2715 AA; 303063 MW; 598F46A77334C2E1 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 2715;
Best Local Similarity 77.8%; Pred. No. 8.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 896 LHYSEYGT 904

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DR InterPro; IPR001258; NHL.
DR InterPro; IPR006530; YD.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF01436; NHL; 6.
DR Pfam; PF05593; RHS repeat; 6.
DR SMART; SM00181; EGF; 7.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR PROSITE; PS00022; EGF 1; 8.
DR PROSITE; PS01186; EGF 2; 7.
DR PROSITE; PS00026; EGF 3; 4.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 2346 AA; 261700 MW; D761563C6ABDD735 CRC64;

Query Match 72.7%; Score 40; DB 2; Length 2346;
Best Local Similarity 77.8%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 534 LHYSEYGT 542

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RESULT 30
Q8EW8 SHEON
ID Q8EW8 SHEON PRELIMINARY; PRT; 111 AA.
AC Q8EW8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein S00338.
GN OrderedLocusNames=S00338;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imptaim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015481; AAN53423.1; -, Genomic_DNA.
DR TIGR; S00338; -.
KW Complete proteome.
SQ SEQUENCE 111 AA; 12407 MW; CC3A1605848DCD14 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 111;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYPT 8
Db 17 HHGQPY 23

RESULT 31
Q6LEMB MOUSE
ID Q6LEMB MOUSE PRELIMINARY; PRT; 112 AA.
AC Q6LEMB;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9;
RA HiFumi E., Mitsuda Y., Ohara K., Uda T.;
RT "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic
RT antibody light chain."
RL J. Immunol. Methods 269:283-298(2002).
DR EMBL; D85104; BAD00151.1; -, mRNA.
DR HSSP; P01820; 1A70.
DR SRS; Q6LEMB; 1-112.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.

RESULT 32
Q746U6 GEOSL
ID Q746U6 GEOSL PRELIMINARY; PRT; 202 AA.
AC Q746U6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU3422;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Ward M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Winn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR36812.1; -, Genomic_DNA.
DR TIGR; GSU3422; -.
DR InterPro; IPR005636; DTW.
DR Pfam; PF03942; DTW; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 202 AA; 22670 MW; CE758358026C6378 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 202;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 39 MHHREYPT 47

RESULT 33
Q5XKG4 MOUSE
ID Q5XKG4 MOUSE PRELIMINARY; PRT; 234 AA.
AC Q5XKG4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Mammary gland;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC031349; AAB31349.1; -; mRNA.
DR SMR: Q5XK24; 16-234..
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 234 AA; 25823 MW; 081C8E9982604DD CRC64;

Query Match 70.9%; Score 39; DB 2; Length 234;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 109 MQHLEYPT 117

RESULT 34
Q9A8R1 CAUCR
ID Q9A8R1 CAUCR PRELIMINARY; PRT; 240 AA.
AC Q9A8R1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CC1290.
GN OrderedLocusNames=CC1290;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

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RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolony J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005803; AAK23271.1; -; Genomic_DNA.
DR PIR: C87409; C87409.
DR TIGR: CC1290; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 240 AA; 25975 MW; B3D28CD377ED519E CRC64;

Query Match 70.9%; Score 39; DB 2; Length 240;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 230 VHSSELYPT 238

RESULT 35
Q8D5U2 VIBVU
ID Q8D5U2 VIBVU PRELIMINARY; PRT; 281 AA.
AC Q8D5U2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Small-conductance mechanosensitive channel.
GN OrderedLocusNames=VV20812;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE016810; AAO07737.1; -; Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR006685; MscS channel.
DR Pfam: PF00924; MS_channel; 1.
KW Complete proteome.
SQ SEQUENCE 281 AA; 32287 MW; 40152329E1A1CB76 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 281;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
: |||||
Db 142 LHHGQYHYT 150

RESULT 36
Q7MCW0 VIBVY
ID Q7MCW0 VIBVY PRELIMINARY; PRT; 281 AA.
AC Q7MCW0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Small-conductance mechanosensitive channel.
GN OrderedLocusNames=VVA1276;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; BA000038; BAC97302.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006685; Mscs_channel.
DR Pfam; PF00924; MS_channel; 1.
KW Complete proteome.
SQ SEQUENCE 281 AA; 32340 MW; 4015232951A1D1C6 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 281;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
||| :|||
Db 142 LHHGQYHYT 150

RESULT 37
Q87G78 VIBPA
ID Q87G78 VIBPA PRELIMINARY; PRT; 289 AA.
AC Q87G78
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VPA1439.
GN OrderedLocusNames=VPA1439;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; BA000032; BAC62782.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006685; Mscs_channel.
DR Pfam; PF00924; MS_channel; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 289 AA; 33369 MW; D20AD542C4DAF92B CRC64;

Query Match 70.9%; Score 39; DB 2; Length 289;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
||| :|||
Db 142 LHHGQYHYT 150

RESULT 38
Q9KMV5 VIBCH
ID Q9KMV5 VIBCH PRELIMINARY; PRT; 291 AA.
AC Q9KMV5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VCA0181.
GN OrderedLocusNames=VCA0181;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AB004358; AAF96094.1; -; Genomic_DNA.
DR PIR; D82491; D82491.
DR TIGR; VCA0181; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006685; Mscs_channel.
DR Pfam; PF00924; MS_channel; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 291 AA; 33046 MW; 0F1458B4360C44D8 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 291;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
||| :|||
Db 142 LHHGQYHYT 150

RESULT 39
Q7S199 NEUCR
ID Q7S199 NEUCR PRELIMINARY; PRT; 755 AA.
AC Q7S199
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU07521.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysisselis M., Mauceli E., Biele C., Rudd S., Frisman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000455; EAA29133.1; -; Genomic_DNA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR
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DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 3.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 4.
DR PROSITE; PS00082; WD_REPEATS_2; 5.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 755 AA; 82841 MW; F604F00B312B50E7 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 755;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8
Db 166 VHHGEYPP 173

RESULT 40
Q4WU9 ASPFU
ID Q4WU9 ASPFU PRELIMINARY; PRT; 860 AA.
AC Q4WU9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Plug protein.
GN ORFNames=Afu3g07140;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nieman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Guilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majores W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalba M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAH01000002; EAL32854.1; -; Genomic DNA.
SQ SEQUENCE 860 AA; 96527 MW; 7974ED7478B3BFA1 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 860;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
Db 298 LHHSEYPY 306

RESULT 41

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FLUG_EMENI
ID FLUG EMENI STANDARD; PRT; 865 AA.
AC P38094;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Protein flUG.
GN Name=flUG; Synonyms=acod;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC 26;
RX MEDLINE=95011568; PubMed=7926755;
RA Lee B., Adams T.H.;
RT "The Aspergillus nidulans flUG gene is required for production of an
extracellular developmental signal and is related to prokaryotic
glutamine synthetase I.";
RL Genes Dev. 8:641-651(1994).
CC -!- FUNCTION: May function as a GSI-related enzyme in synthesizing a
small diffusible factor that acts as an extracellular signal
directing asexual sporulation and perhaps other aspects of colony
growth. May be involved in brIA activation (an early
transcriptional regulator for conidiation specific gene).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the glutamine synthetase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; L27817; AAC37414.1; -; Genomic_DNA.
DR PIR; A53186; A53186.
DR InterPro; IPR006992; Amido_hydro_2.
DR InterPro; IPR008147; Gln_synt_beta.
DR InterPro; IPR008146; Gln_synt_C.
DR Pfam; PF04909; Amidohydro_2; 1.
DR Pfam; PF00120; Gln_synt_C; 1.
DR ProDom; PD001057; Gln_synt_C; 1.
KW Conidiation; Sporulation.
FT MUTAGEN 774 774 Y->N: Temperature-sensitive.
SQ SEQUENCE 865 AA; 96505 MW; D17F3BB83B8F1719 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 865;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
Db 296 LHHSEYPY 304

RESULT 42
Q51PK8 MAGGR
ID Q51PK8_MAGGR PRELIMINARY; PRT; 865 AA.
AC Q51PK8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=M300468.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

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RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Archuchi H., Armbruster J., Bachantseang P., Baldwin J., Barry A.,
RA Baychi T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collinmore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Duges A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Gnerre S.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat K., Kamyselis M., Karlsson E.,
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
RA Lana D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-Toh K., Liu X., Lokytas T., Lokytas Y., Lucien O.,
RA Lui A., Ma L.-J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Maucelli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mezes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'Donnell P., Okoawo O., O'leary S., Omotoho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Ruman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov N., Stavropoulos S.,
RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Valles D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe oryzae";
RL Submitted (OCT-2003) to the ENBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the ENBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the ENBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01001422; EAA48810.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 865 AA; 94167 MW; DFC932925EB6612 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 865;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LHHSEYPY 8
Db 645 IHPSEYPY 652
:|||||

RESULT 43
Q5B3R1 EMENI PRELIMINARY; PRT; 865 AA.
AC Q5B3R1,
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE FLUG_EMENI FLUG PROTEIN.

GN ORFNames=AN4819.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collinmore A., Cook A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans";
RL Submitted (JAN-2004) to the ENBL/GenBank/DBJ databases.
DR EMBL; AACD01000081; EAA60389.1; -; Genomic DNA.
DR GO; GO:0001760; F:aminocarboxymuconate-semialdehyde decarboxy. .; IEA.
DR GO; GO:0004356; P:glutamate-ammonia ligase activity; IEA.
DR GO; GO:0016874; P:ligase activity; IEA.
DR GO; GO:0006542; P:glutamine biosynthesis; IEA.
DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR InterPro; IPR006992; Amido_hydro_2.
DR InterPro; IPR008147; Gln_synth_beta.
DR InterPro; IPR008146; Gln_synth_C.
DR Pfam; PF04909; Amidohydro_2; 1.
DR Pfam; PF00120; Gln-synth C; 1.
SQ SEQUENCE 865 AA; 96505 MW; D17F3B883B8F1719 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 865;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LHHSEYPY 9
Db 296 LLHSSYPY 304
:|||||

RESULT 44
Q5PZ35 AJECA PRELIMINARY; PRT; 877 AA.
ID Q5PZ35 AJECA PRELIMINARY;
AC Q5PZ35;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE FLU1-I.
GN Name=FLU1;
OS Ajellomyces capsulata (Histoplasma capsulatum),
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Ajellomycetaceae; Ajellomyces.
OX NCBI_TaxID=5037;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G217B;
RX MEDLINE=22692911; PubMed=12808032; DOI=10.1091/mbc.E03-01-0027;
RA Hwang L., Hocking-Murray D., Bahrami A.K., Andersson M., Rine J.,
RA Sil A.;


```
RT "Identifying phase-specific genes in the fungal pathogen Histoplasma
RL capsulatum using a genomic shotgun microarray.";
RN Mol. Biol. Cell 14:2314-2326(2003).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G217B;
RA Sil A., Hwang L.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY816317; AAV67971.1; -; Genomic DNA.
DR GO; GO:0001760; F-aminocarboxymuconate-semialdehyde decarboxy. . . ; IEA.
DR GO; GO:0004356; F-glutamate-ammonia ligase activity; IEA.
DR GO; GO:0016874; F-ligase activity; IEA.
DR GO; GO:0008542; P-glutamine biosynthesis; IEA.
DR GO; GO:0006807; P-nitrogen compound metabolism; IEA.
DR InterPro; IPR006992; F-nitrogen compound metabolism; IEA.
DR InterPro; IPR008147; Gln synt beta.
DR InterPro; IPR008146; Gln synt C.
DR Pfam; PF04909; Amidohydro_2; I.
DR Pfam; PF00120; Gln-synt_C; 1.
DR ProDom; PD001057; Gln synt_C; 1.
SQ SEQUENCE 877 AA; 98674 MW; 80515E90BF292CD5 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 877;
Best Local Similarity 77.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSYPYPT 9
| | | | |
DB 298 LHSSYPYPT 306

RESULT 45
Q25265 LYMDI
ID Q25265 LYMDI PRELIMINARY; PRT; 1747 AA.
AC Q25265;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vitellogenin.
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hiremath S.T., Lehtoma K.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97468497; PubMed=9327584;
RX DOI=10.1002/(SICI)1520-6327(1997)36:3<151::AID-ARCH1>3.3.CO;2-7;
RA Hiremath S., Lehtoma K.;
RT "Structure of the gypsy moth vitellogenin gene.";
RL Arch. Insect Biochem. Physiol. 36:151-164(1997).
DR EMBL; U60186; AAB03336.1; -; mRNA.
DR PIR; T43162; T43162.
DR GO; GO:0005319; F-lipid transporter activity; IEA.
DR GO; GO:0006869; F-lipid transport; IEA.
DR InterPro; IPR001747; Lipid transport_N.
DR InterPro; IPR001846; VWF D.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00638; LPD_N; 1.
DR SMART; SM00216; VWD; 1.
SQ SEQUENCE 1747 AA; 198183 MW; 5FC70479C8FDF87 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 1747;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSYPYPT 9
| | | | |
DB 1012 LHSSVPYPS 1020

RESULT 47
Q9UKZ4 HUMAN
ID Q9UKZ4 HUMAN PRELIMINARY; PRT; 2725 AA.
AC Q9UKZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tenascin-M1.
GN Name=ODZ1; Synonyms=TNM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20025749; PubMed=10556288; DOI=10.1093/hmg/8.13.2407;
RA Brandau O., Schuster V., Weiss M., Hellebrand H., Fink F.M.,
RA Kreczy A., Friedrich W., Strahm B., Nieneyer C., Belohradsky B.H.,
RA Meindl A.;
RT "Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are
RT mutated in the SH2D1A gene, as are patients with X-linked
RT lymphoproliferative disease (XLP).";
RL Hum. Mol. Genet. 8:2407-2413(1999).
DR EMBL; AF100772; AAF04723.1; -; mRNA.
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```
DB 1012 LHSSVPYPS 1020

RESULT 46
Q25269 LYMDI
ID Q25269 LYMDI PRELIMINARY; PRT; 1747 AA.
AC Q25269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vitellogenin.
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hiremath S.T., Lehtoma K.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97468497; PubMed=9327584;
RX DOI=10.1002/(SICI)1520-6327(1997)36:3<151::AID-ARCH1>3.3.CO;2-7;
RA Hiremath S., Lehtoma K.;
RT "Structure of the gypsy moth vitellogenin gene.";
RL Arch. Insect Biochem. Physiol. 36:151-164(1997).
DR EMBL; U60186; AAB03336.1; -; mRNA.
DR PIR; T43162; T43162.
DR GO; GO:0005319; F-lipid transporter activity; IEA.
DR GO; GO:0006869; F-lipid transport; IEA.
DR InterPro; IPR001747; Lipid transport_N.
DR InterPro; IPR001846; VWF D.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00638; LPD_N; 1.
DR SMART; SM00216; VWD; 1.
SQ SEQUENCE 1747 AA; 198183 MW; 5FC70479C8FDF87 CRC64;

Query Match 70.9%; Score 39; DB 2; Length 1747;
Best Local Similarity 66.7%; Pred. No. 8.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSYPYPT 9
| | | | |
DB 1012 LHSSVPYPS 1020

RESULT 47
Q9UKZ4 HUMAN
ID Q9UKZ4 HUMAN PRELIMINARY; PRT; 2725 AA.
AC Q9UKZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tenascin-M1.
GN Name=ODZ1; Synonyms=TNM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20025749; PubMed=10556288; DOI=10.1093/hmg/8.13.2407;
RA Brandau O., Schuster V., Weiss M., Hellebrand H., Fink F.M.,
RA Kreczy A., Friedrich W., Strahm B., Nieneyer C., Belohradsky B.H.,
RA Meindl A.;
RT "Epstein-Barr virus-negative boys with non-Hodgkin lymphoma are
RT mutated in the SH2D1A gene, as are patients with X-linked
RT lymphoproliferative disease (XLP).";
RL Hum. Mol. Genet. 8:2407-2413(1999).
DR EMBL; AF100772; AAF04723.1; -; mRNA.
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DR	ENBL; AL031075; CAI42975.1; JOINED; Genomic_DNA.
DR	ENBL; Z81008; CAI42975.1; JOINED; Genomic_DNA.
DR	ENBL; Z83823; CAI42975.1; JOINED; Genomic_DNA.
DR	ENBL; Z85995; CAI42975.1; JOINED; Genomic_DNA.
DR	ENBL; AL022718; CAI43065.1; JOINED; Genomic_DNA.
DR	ENBL; AL023878; CAI43065.1; JOINED; Genomic_DNA.
DR	ENBL; Z81008; CAI43065.1; JOINED; Genomic_DNA.
DR	ENBL; Z83823; CAI43065.1; JOINED; Genomic_DNA.
DR	ENBL; Z85995; CAI43065.1; JOINED; Genomic_DNA.
DR	ENBL; AL022718; CAI42710.1; JOINED; Genomic_DNA.
DR	ENBL; AL023878; CAI42710.1; JOINED; Genomic_DNA.
DR	ENBL; AL031075; CAI42710.1; JOINED; Genomic_DNA.
DR	ENBL; Z83823; CAI42710.1; JOINED; Genomic_DNA.
DR	ENBL; Z85995; CAI42710.1; JOINED; Genomic_DNA.
DR	ENBL; AL022718; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; AL023878; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; AL031075; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; Z83823; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; Z81008; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; Z85995; CAI42721.1; JOINED; Genomic_DNA.
DR	ENBL; AL023878; CAI42154.1; JOINED; Genomic_DNA.
DR	ENBL; Z81008; CAI42154.1; JOINED; Genomic_DNA.
DR	ENBL; Z83823; CAI42154.1; JOINED; Genomic_DNA.
DR	ENBL; Z85995; CAI42154.1; JOINED; Genomic_DNA.
DR	HGNC; HGNC:8117; ODZ1.
GO	GO:0003735; F:structural constituent of ribosome; IEA.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR006209; EGF like.
DR	InterPro; IPR006210; IEGF.
DR	InterPro; IPR001258; NHL.
DR	InterPro; IPR000209; Pept_s8_S53.
DR	InterPro; IPR009471; Ten_N.
DR	Pfam; PF00008; EGF_2.
DR	Pfam; PF01436; NHS repeat; 5.
DR	Pfam; PF05593; RHS repeat; 6.
DR	Pfam; PF06484; Ten_N; 1.
DR	SMART; SM00181; EGF; 8.
DR	TIGRFAMs; TIGR01643; YD_repeat_2x; 5.
DR	PROSITE; PS00022; EGF_1; 8.
DR	PROSITE; PS01186; EGF-2; 7.
DR	PROSITE; PSS00026; EGF-3; 5.
DR	PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
KW	Ribosomal protein.
SQ	SEQUENCE 2725 AA; 305011 MW; 70P5C22BF3B58B7 CRC64;
Query Match	70.9%; Score 39; DB 2; Length 2725;
Best Local Similarity	66.7%; Pred. No. 1.3e+03;
Matches	6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy	1 LHSXPYPY 9 :
Db	909 LHSDYGYFT 917
RESULT 49	
Q9WTS4 MOUSE	
ID	Q9WTS4 MOUSE PRELIMINARY; PRT; 2731 AA.
AC	Q9WTS4;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DI	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Ten-mi.
GN	Name=Odz1; Synonyms=tan-mi;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.

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SQ SEQUENCE 235 AA; 26740 MW; A203BED60AF3AF2 CRC64;

Query Match          69.1%; Score 38; DB 2; Length 235;
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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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12	37	67.3	11	1	US-08-438-123-11
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21	36	65.5	128	2	US-09-012-097A-22
22	36	65.5	128	2	US-09-781-804-21
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24	36	65.5	397	2	US-09-270-767-46835
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55	34	61.8	107	2	US-09-647-468-147	Sequence 147, App
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152	32	58.2	566	2	US-09-514-245-21	Sequence 21, Appl	225	31	56.4	521	2	US-09-265-585C-97	Sequence 97, Appl
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402	30	54.5	314	2	US-09-270-767-50172	Sequence 50172, A	475	30	54.5	486	2	US-09-657-013-60	Sequence 60, Appl
403	30	54.5	315	1	US-08-253-155A-34	Sequence 34, Appl	476	30	54.5	486	2	US-09-657-013-62	Sequence 62, Appl
404	30	54.5	316	2	US-09-252-991A-19764	Sequence 19764, A	477	30	54.5	486	2	US-09-657-013-65	Sequence 65, Appl
405	30	54.5	316	2	US-09-674-529B-16	Sequence 16, Appl	478	30	54.5	486	2	US-09-657-013-68	Sequence 68, Appl
406	30	54.5	316	2	US-09-270-767-42663	Sequence 42663, A	479	30	54.5	486	2	US-09-657-013-72	Sequence 72, Appl
407	30	54.5	321	2	US-09-252-991A-20076	Sequence 20076, A	480	30	54.5	486	2	US-09-657-013-73	Sequence 73, Appl
408	30	54.5	325	2	US-09-107-532A-6786	Sequence 6786, Ap	481	30	54.5	486	2	US-09-657-013-74	Sequence 74, Appl
409	30	54.5	326	2	US-09-120-365-67	Sequence 67, Appl	482	30	54.5	487	2	US-09-949-016-10055	Sequence 10055, A
410	30	54.5	326	2	US-09-515-039-67	Sequence 67, Appl	483	30	54.5	492	2	US-09-489-039A-11838	Sequence 11838, A
411	30	54.5	337	2	US-09-585-645A-9	Sequence 9, Appl	484	30	54.5	497	1	US-08-336-235A-1	Sequence 1, Appl
412	30	54.5	337	2	US-09-585-645A-44	Sequence 44, Appl	485	30	54.5	497	1	US-08-649-432-1	Sequence 1, Appl
413	30	54.5	339	2	US-09-248-796A-14611	Sequence 14611, A	486	30	54.5	497	4	PCT-US95-14024-1	Sequence 1, Appl
414	30	54.5	341	2	US-09-328-352-6124	Sequence 6124, Ap	487	30	54.5	502	2	US-09-949-016-10209	Sequence 10209, A
415	30	54.5	343	2	US-09-120-365-71	Sequence 71, Appl	488	30	54.5	504	1	US-08-645-900A-1	Sequence 1, Appl
416	30	54.5	343	2	US-09-515-039-71	Sequence 71, Appl	489	30	54.5	504	1	US-08-882-238A-1	Sequence 1, Appl
417	30	54.5	346	2	US-09-543-681A-6716	Sequence 6716, Ap	490	30	54.5	504	1	US-08-667-790A-1	Sequence 1, Appl
418	30	54.5	349	2	US-09-438-185A-167	Sequence 167, App	491	30	54.5	504	2	US-09-220-659-1	Sequence 1, Appl
419	30	54.5	351	2	US-09-270-767-42647	Sequence 42647, A	492	30	54.5	504	2	US-08-938-668A-32	Sequence 32, Appl
420	30	54.5	359	2	US-09-543-681A-5431	Sequence 5431, Ap	493	30	54.5	504	2	US-08-846-568B-1	Sequence 1, Appl
421	30	54.5	360	2	US-09-116-498-8	Sequence 8, Appl	494	30	54.5	504	2	US-08-822-999-3	Sequence 3, Appl
422	30	54.5	360	2	US-09-116-498-10	Sequence 10, Appl	495	30	54.5	504	2	US-09-056-285A-8	Sequence 8, Appl
423	30	54.5	360	2	US-09-116-498-12	Sequence 12, Appl	496	30	54.5	504	2	US-09-306-828-32	Sequence 32, Appl
424	30	54.5	360	2	US-09-517-605-10	Sequence 10, Appl	497	30	54.5	504	2	US-09-952-464A-8	Sequence 8, Appl
425	30	54.5	360	2	US-09-170-496D-28	Sequence 28, Appl	498	30	54.5	507	2	US-09-134-000C-4961	Sequence 4961, Ap
426	30	54.5	360	2	US-09-170-496D-180	Sequence 180, App	499	30	54.5	508	2	US-09-583-110-5034	Sequence 5034, Ap
427	30	54.5	360	2	US-09-852-156-8	Sequence 8, Appl	500	30	54.5	520	2	US-09-270-767-45441	Sequence 45441, Ap
428	30	54.5	360	2	US-09-852-156-10	Sequence 10, Appl	501	30	54.5	541	2	US-10-104-047-2161	Sequence 2161, Ap
429	30	54.5	360	2	US-09-852-156-12	Sequence 12, Appl	502	30	54.5	594	2	US-09-107-433-4327	Sequence 4327, Ap
430	30	54.5	362	2	US-09-120-365-74	Sequence 74, Appl	503	30	54.5	607	2	US-09-252-991A-30814	Sequence 30814, A
431	30	54.5	362	2	US-09-515-039-74	Sequence 74, Appl	504	30	54.5	616	2	US-08-965-902A-2	Sequence 2, Appl
432	30	54.5	365	2	US-10-104-047-3671	Sequence 3671, Ap	505	30	54.5	626	2	US-09-134-001C-4342	Sequence 4342, Ap
433	30	54.5	367	2	US-09-464-035A-9	Sequence 9, Appl	506	30	54.5	628	2	US-09-270-767-35041	Sequence 35041, A
434	30	54.5	373	2	US-09-543-681A-6764	Sequence 6764, Ap	507	30	54.5	628	2	US-09-270-767-50258	Sequence 50258, A
435	30	54.5	374	2	US-09-540-236-2230	Sequence 2230, Ap	508	30	54.5	631	2	US-09-252-991A-18000	Sequence 18000, A
436	30	54.5	382	2	US-09-270-767-45405	Sequence 45405, A	509	30	54.5	637	2	US-09-107-433-3169	Sequence 3169, Ap
437	30	54.5	395	2	US-09-489-039A-8706	Sequence 8706, Ap	510	30	54.5	656	2	US-09-248-796A-20237	Sequence 20237, A
438	30	54.5	396	2	US-09-270-767-43587	Sequence 43587, A	511	30	54.5	671	2	US-09-421-321-16	Sequence 16, Appl
439	30	54.5	404	2	US-09-248-796A-18878	Sequence 18878, A	512	30	54.5	671	2	US-08-933-803A-16	Sequence 16, Appl
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441	30	54.5	408	1	US-08-742-440A-6	Sequence 6, Appl	514	30	54.5	682	2	US-09-949-016-11419	Sequence 11419, A
442	30	54.5	409	2	US-09-248-796A-16363	Sequence 16363, A	515	30	54.5	698	2	US-09-107-532A-5200	Sequence 5200, Ap
443	30	54.5	413	2	US-09-540-236-3672	Sequence 3672, Ap	516	30	54.5	734	2	US-09-583-110-4156	Sequence 4156, Ap
444	30	54.5	414	2	US-09-248-796A-15573	Sequence 15573, A	517	30	54.5	737	2	US-09-107-433-4728	Sequence 4728, Ap
445	30	54.5	423	2	US-09-976-594-19	Sequence 19, Appl	518	30	54.5	766	2	US-09-710-279-420	Sequence 420, App
446	30	54.5	423	2	US-09-919-039-19	Sequence 19, Appl	519	30	54.5	773	2	US-09-590-991-8	Sequence 8, Appl
447	30	54.5	430	2	US-09-252-991A-29287	Sequence 29287, A	520	30	54.5	775	2	US-09-308-179B-1	Sequence 1, Appl
448	30	54.5	433	2	US-10-104-047-3033	Sequence 3033, Ap	521	30	54.5	803	2	US-09-538-092-1026	Sequence 1026, Ap
449	30	54.5	438	2	US-09-270-767-34108	Sequence 34108, Ap	522	30	54.5	856	2	US-09-248-796A-16089	Sequence 16089, A
450	30	54.5	438	2	US-09-270-767-49325	Sequence 49325, A	523	30	54.5	876	1	US-08-785-429-2	Sequence 2, Appl
451	30	54.5	441	2	US-09-543-681A-5018	Sequence 5018, Ap	524	30	54.5	876	2	US-08-996-621-2	Sequence 2, Appl
452	30	54.5	441	2	US-09-492-709A-272	Sequence 272, App	525	30	54.5	888	2	US-09-134-001C-3032	Sequence 3032, Ap
453	30	54.5	442	2	US-09-134-000C-3610	Sequence 3610, Ap	526	30	54.5	902	2	US-09-193-562D-34	Sequence 34, Appl
454	30	54.5	448	2	US-09-543-681A-6749	Sequence 6749, Ap	527	30	54.5	902	2	US-10-055-412B-34	Sequence 34, Appl
455	30	54.5	448	2	US-10-104-047-3380	Sequence 3380, Ap	528	30	54.5	971	2	US-09-248-796A-19531	Sequence 19531, A
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457	30	54.5	456	1	US-08-819-013-1	Sequence 1, Appl	530	30	54.5	1038	2	US-09-752-639-151	Sequence 151, App
458	30	54.5	456	2	US-09-355-214-1	Sequence 1, Appl	531	30	54.5	1038	2	US-09-712-813-151	Sequence 151, App
459	30	54.5	457	2	US-09-355-214-5	Sequence 5, Appl	532	30	54.5	1038	2	US-09-700-354A-151	Sequence 151, App
460	30	54.5	462	2	US-09-489-039A-9508	Sequence 9508, Ap	533	30	54.5	1427	2	US-09-252-991A-27005	Sequence 27005, A
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462	30	54.5	474	2	US-09-252-991A-32449	Sequence 32449, A	535	30	54.5	1867	2	US-09-083-116-5	Sequence 5, Appl
463	30	54.5	476	2	US-09-657-013-75	Sequence 75, Appl	536	30	54.5	1867	2	US-09-134-016A-5	Sequence 5, Appl
464	30	54.5	477	1	US-08-453-956-25	Sequence 25, Appl	537	30	54.5	2035	1	US-08-479-537A-2	Sequence 2, Appl
465	30	54.5	477	1	US-08-086-631-25	Sequence 25, Appl	538	30	54.5	2035	2	US-09-083-116-2	Sequence 2, Appl

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540	30	54.5	2138	2	US-09-583-110-5274	Sequence 5274, Ap	613	29	52.7	113	1	US-08-672-345C-97	Sequence 97, Appl
541	30	54.5	2138	2	US-09-309-572-7	Sequence 7, Appli	614	29	52.7	113	2	US-09-214-095D-5	Sequence 5, Appli
542	30	54.5	2210	2	US-09-718-096-7	Sequence 760, Appl	615	29	52.7	113	2	US-09-214-095D-7	Sequence 7, Appli
543	30	54.5	2323	2	US-09-710-279-760	Sequence 1, Appli	616	29	52.7	113	2	US-09-214-095D-100	Sequence 100, App
544	30	54.5	2392	2	US-09-710-262E-1	Sequence 1, Appli	617	29	52.7	113	2	US-09-214-095D-112	Sequence 112, App
545	30	54.5	2404	2	US-09-134-001C-3464	Sequence 3464, Ap	618	29	52.7	113	2	US-09-710-279-1378	Sequence 1378, Ap
546	30	54.5	2763	2	US-08-496-944-2	Sequence 2, Appli	619	29	52.7	113	2	US-09-940-727B-5	Sequence 5, Appli
547	30	54.5	7831	2	US-09-902-540-12902	Sequence 12902, A	620	29	52.7	113	2	US-09-940-727B-7	Sequence 7, Appli
548	29.5	53.6	113	2	US-09-270-767-33394	Sequence 33394, A	621	29	52.7	113	2	US-09-940-727B-10	Sequence 10, App
549	29.5	53.6	113	2	US-09-270-767-48611	Sequence 48611, A	622	29	52.7	113	2	US-09-940-727B-112	Sequence 112, App
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552	29.5	53.6	132	2	US-09-270-767-40550	Sequence 40550, A	625	29	52.7	119	2	US-09-270-767-32694	Sequence 32694, A
553	29.5	53.6	132	2	US-09-270-767-55766	Sequence 55766, A	626	29	52.7	119	2	US-09-270-767-47911	Sequence 47911, A
554	29.5	53.6	132	2	US-09-248-796A-21355	Sequence 21355, A	627	29	52.7	120	1	US-08-917-456-4	Sequence 4, Appli
555	29.5	53.6	409	2	US-09-270-767-38540	Sequence 38540, A	628	29	52.7	120	2	US-09-229-804-4	Sequence 4, Appli
556	29.5	53.6	409	2	US-09-270-767-53757	Sequence 53757, A	629	29	52.7	121	2	US-09-471-276-1394	Sequence 1394, Ap
557	29.5	53.6	505	2	US-09-583-110-3179	Sequence 3179, Ap	630	29	52.7	125	2	US-09-134-001C-5285	Sequence 5285, Ap
558	29.5	53.6	505	2	US-09-769-787-120	Sequence 120, App	631	29	52.7	126	1	US-08-202-047-13	Sequence 13, Appl
559	29.5	53.6	511	2	US-09-107-433-4514	Sequence 4514, Ap	632	29	52.7	126	1	US-08-202-047-15	Sequence 15, Appl
560	29	52.7	9	1	US-08-672-345C-21	Sequence 21, Appl	633	29	52.7	126	1	US-08-202-047-17	Sequence 17, Appl
561	29	52.7	9	2	US-09-214-095D-21	Sequence 21, Appl	634	29	52.7	126	1	US-08-202-047-19	Sequence 19, Appl
562	29	52.7	9	2	US-09-518-046-46	Sequence 46, Appl	635	29	52.7	126	2	US-08-964-690-13	Sequence 13, Appl
563	29	52.7	9	2	US-09-518-046-71	Sequence 71, Appl	636	29	52.7	126	2	US-08-964-690-15	Sequence 15, Appl
564	29	52.7	9	2	US-09-518-046-145	Sequence 145, App	637	29	52.7	126	2	US-08-964-690-17	Sequence 17, Appl
565	29	52.7	9	2	US-09-257-069-10	Sequence 10, Appl	638	29	52.7	126	2	US-08-964-690-19	Sequence 19, Appl
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568	29	52.7	9	2	US-09-940-727B-21	Sequence 21, Appl	641	29	52.7	131	2	US-08-964-690-5	Sequence 5, Appli
569	29	52.7	9	2	US-09-650-371-46	Sequence 46, Appl	642	29	52.7	131	2	US-09-489-039A-10730	Sequence 10730, A
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571	29	52.7	9	2	US-09-650-371-145	Sequence 145, App	644	29	52.7	136	2	US-09-626-896-29	Sequence 29, Appl
572	29	52.7	63	2	US-09-513-999C-6458	Sequence 6458, Ap	645	29	52.7	136	2	US-09-841-730-29	Sequence 29, Appl
573	29	52.7	64	2	US-09-513-999C-5632	Sequence 5632, Ap	646	29	52.7	137	2	US-09-252-991A-32890	Sequence 32890, A
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575	29	52.7	68	2	US-09-270-767-34723	Sequence 34723, A	648	29	52.7	141	2	US-09-248-796A-24389	Sequence 24389, A
576	29	52.7	68	2	US-09-270-767-49940	Sequence 49940, A	649	29	52.7	146	2	US-09-732-210-575	Sequence 575, App
577	29	52.7	69	2	US-09-248-796A-28176	Sequence 28176, A	650	29	52.7	146	2	US-09-732-210-575	Sequence 575, App
578	29	52.7	72	2	US-09-248-796A-26147	Sequence 26147, A	651	29	52.7	147	2	US-09-107-532A-5303	Sequence 5303, Ap
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580	29	52.7	79	2	US-09-438-185A-487	Sequence 487, App	653	29	52.7	149	2	US-09-270-767-42968	Sequence 42968, A
581	29	52.7	86	2	US-09-640-211A-695	Sequence 695, App	654	29	52.7	153	2	US-09-634-238-385	Sequence 385, App
582	29	52.7	98	2	US-09-518-046-17	Sequence 17, Appl	655	29	52.7	153	2	US-09-270-767-32715	Sequence 32715, A
583	29	52.7	98	2	US-09-650-371-17	Sequence 17, Appl	656	29	52.7	153	2	US-09-270-767-47932	Sequence 47932, A
584	29	52.7	102	2	US-09-270-767-36545	Sequence 36545, A	657	29	52.7	157	2	US-09-378-238-31	Sequence 31, Appl
585	29	52.7	102	2	US-09-270-767-51762	Sequence 51762, A	658	29	52.7	157	2	US-09-626-896-27	Sequence 27, Appl
586	29	52.7	107	1	US-08-290-592E-20	Sequence 20, Appl	659	29	52.7	157	2	US-09-538-092-82	Sequence 82, Appl
587	29	52.7	107	1	US-08-290-592E-21	Sequence 21, Appl	660	29	52.7	157	2	US-09-841-730-27	Sequence 27, Appl
588	29	52.7	107	1	US-08-888-366-24	Sequence 24, Appl	661	29	52.7	158	1	US-08-917-456-2	Sequence 2, Appli
589	29	52.7	107	2	US-08-554-840-1	Sequence 1, Appli	662	29	52.7	158	2	US-09-229-804-2	Sequence 2, Appli
590	29	52.7	107	2	US-08-554-840-3	Sequence 3, Appli	663	29	52.7	162	2	US-08-992-176-9	Sequence 9, Appli
591	29	52.7	107	2	US-08-554-840-4	Sequence 4, Appli	664	29	52.7	162	2	US-09-489-039A-8176	Sequence 8176, Ap
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597	29	52.7	107	2	US-08-925-339-4	Sequence 4, Appli	670	29	52.7	186	2	US-08-205-049-1	Sequence 1, Appli
598	29	52.7	107	2	US-09-332-595-1	Sequence 1, Appli	671	29	52.7	197	2	US-09-270-767-35323	Sequence 35323, A
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601	29	52.7	107	2	US-09-332-595-4	Sequence 4, Appli	674	29	52.7	214	2	US-09-248-796A-15179	Sequence 15179, A
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603	29	52.7	107	4	PCT-US95-10053-17	Sequence 17, Appl	676	29	52.7	232	2	US-09-710-279-1700	Sequence 1700, Ap
604	29	52.7	107	4	PCT-US95-10053-18	Sequence 18, Appl	677	29	52.7	235	2	US-09-107-532A-5767	Sequence 5767, Ap
605	29	52.7	107	4	PCT-US96-09448-20	Sequence 20, Appl	678	29	52.7	236	2	US-09-248-796A-15388	Sequence 15388, A
606	29	52.7	107	4	PCT-US96-09448-21	Sequence 21, Appl	679	29	52.7	240	2	US-09-636-735A-2	Sequence 2, Appli
607	29	52.7	109	2	US-09-802-083-4	Sequence 4, Appli	680	29	52.7	240	2	US-09-134-001C-5190	Sequence 12, Appl
608	29	52.7	112	2	US-08-483-749A-4	Sequence 4, Appli	681	29	52.7	243	2	US-09-636-735A-12	Sequence 12, Appl
609	29	52.7	112	6	5206152-4	Patent No. 5206152	682	29	52.7	245	2	US-09-248-796A-17087	Sequence 17087, A
610	29	52.7	113	1	US-08-672-345C-5	Sequence 5, Appli	683	29	52.7	250	2	US-09-248-796A-24868	Sequence 24868, A
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697	29	52.7	273	2	US-09-134-000C-5235	Sequence 5235, App	770	29	52.7	454	2	US-09-805-694B-4	Sequence 4, Appli
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713	29	52.7	326	2	US-09-949-016-6679	Sequence 6679, Ap	786	29	52.7	506	2	US-09-877-476-42	Sequence 42, Appl
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717	29	52.7	342	2	US-10-104-047-2985	Sequence 2985, Ap	790	29	52.7	521	2	US-09-949-016-11081	Sequence 11081, A
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751	29	52.7	430	2	US-09-489-039A-7580	Sequence 7580, Ap	824	29	52.7	892	2	US-09-585-858-3	Sequence 3, Appli
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753	29	52.7	434	1	US-08-529-600D-2	Sequence 2, Appli	826	29	52.7	892	2	US-10-270-878-3	Sequence 3, Appli
754	29	52.7	434	1	US-08-973-275-4	Sequence 4, Appli	827	29	52.7	898	2	US-08-753-750B-10	Sequence 10, Appl
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833	29	52.7	903	2	US-10-270-595-18	Sequence 18, Appl	906	28	50.9	112	1	US-08-477-877B-88	Sequence 88, Appl
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843	29	52.7	1239	1	US-08-937-931-2	Sequence 2, Appli	916	28	50.9	115	2	US-10-115-123-160	Sequence 160, App
844	29	52.7	1239	2	US-09-285-502-2	Sequence 2, Appli	917	28	50.9	116	2	US-09-513-999C-6249	Sequence 6249, Ap
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847	29	52.7	1284	2	US-10-296-144-5	Sequence 5, Appli	920	28	50.9	127	1	US-08-646-981-8	Sequence 8, Appli
848	29	52.7	1478	2	US-09-487-558B-52	Sequence 52, Appl	921	28	50.9	128	2	US-09-513-999C-6248	Sequence 6248, Ap
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850	29	52.7	1781	1	US-08-477-451-11	Sequence 11, Appl	923	28	50.9	130	1	US-08-436-717-86	Sequence 86, Appl
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853	29	52.7	3457	1	US-08-416-603-4	Sequence 4, Appli	926	28	50.9	132	1	US-08-477-877B-84	Sequence 84, Appl
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855	28.5	51.8	139	2	US-10-126-273-13	Sequence 13, Appl	928	28	50.9	132	1	US-08-472-281A-84	Sequence 84, Appl
856	28.5	51.8	139	2	US-10-126-273-15	Sequence 15, Appl	932	28	50.9	132	1	US-08-472-281A-91	Sequence 91, Appl
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859	28.5	51.8	298	2	US-09-177-419C-4	Sequence 4, Appli	932	28	50.9	132	1	US-09-462-140D-92	Sequence 92, Appl
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861	28.5	51.8	383	2	US-10-286-606-15	Sequence 15, Appl	934	28	50.9	133	2	US-09-439-261-23	Sequence 23, Appl
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865	28	50.9	9	2	US-08-758-417A-216	Sequence 216, App	938	28	50.9	134	2	US-09-178-881-4	Sequence 4, Appli
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872	28	50.9	31	2	US-07-401-432-15	Sequence 15, Appl	945	28	50.9	142	2	US-09-248-796A-15390	Sequence 15390, A
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883	28	50.9	84	1	US-08-399-411-62	Sequence 62, Appl	956	28	50.9	156	2	US-09-270-767-41195	Sequence 41195, A
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886	28	50.9	84	2	US-09-528-706-62	Sequence 62, Appl	959	28	50.9	159	2	US-08-311-731A-343	Sequence 343, App
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893	28	50.9	103	2	US-09-621-976-6669	Sequence 6669, Ap	966	28	50.9	173	2	US-09-902-540-16193	Sequence 16193, A
894	28	50.9	104	2	US-08-881-037-38	Sequence 38, Appl	967	28	50.9	175	2	US-09-248-796A-16034	Sequence 16034, A
895	28	50.9	104	2	US-09-270-767-38303	Sequence 38303, A	968	28	50.9	180	2	US-09-252-991A-18500	Sequence 18500, A
896	28	50.9	104	2	US-09-270-767-53520	Sequence 53520, A	969	28	50.9	181	2	US-09-489-039A-14232	Sequence 14232, A
897	28	50.9	104	2	US-10-630-406-1	Sequence 1, Appli	970	28	50.9	182	1	US-08-721-925A-3	Sequence 3, Appli
898	28	50.9	106	2	US-09-710-279-178	Sequence 178, App	971	28	50.9	188	2	US-09-270-767-34999	Sequence 34999, A
899	28	50.9	106	2	US-09-710-279-1566	Sequence 1566, Ap	972	28	50.9	188	2	US-09-270-767-50216	Sequence 50216, A
900	28	50.9	108	2	US-09-065-059-3	Sequence 3, Appli	973	28	50.9	192	2	US-09-270-767-45356	Sequence 45356, A
901	28	50.9	108	2	US-08-913-555-3	Sequence 3, Appli	974	28	50.9	197	1	US-08-827-279-3	Sequence 3, Appli
902	28	50.9	108	2	US-08-913-555-21	Sequence 21, Appl	975	28	50.9	197	2	US-09-248-796A-26416	Sequence 26416, A
903	28	50.9	109	2	US-09-134-001C-4896	Sequence 4896, Ap	976	28	50.9	198	6	5240847-11	Patent No. 5240847

977 28 50.9 199 2 US-09-270-767-31722
978 28 50.9 199 2 US-09-270-767-46939
979 28 50.9 200 2 US-09-373-731-2
980 28 50.9 202 2 US-09-540-236-3054
981 28 50.9 213 2 US-09-270-767-46161
982 28 50.9 215 2 US-09-270-767-46501
983 28 50.9 215 2 US-09-902-540-15028
984 28 50.9 216 2 US-09-252-991A-24371
985 28 50.9 225 2 US-09-902-540-10010
986 28 50.9 226 2 US-09-270-767-59161
987 28 50.9 226 2 US-10-132-350-8
988 28 50.9 229 2 US-09-270-767-43214
989 28 50.9 232 2 US-10-132-350-6
990 28 50.9 235 2 US-09-949-016-11482
991 28 50.9 239 2 US-10-092-246-33
992 28 50.9 239 2 US-10-096-246A-33
993 28 50.9 240 2 US-10-092-246-36
994 28 50.9 240 2 US-10-092-246-37
995 28 50.9 240 2 US-10-096-246A-34
996 28 50.9 240 2 US-10-096-246A-35
997 28 50.9 240 2 US-10-096-246A-36
998 28 50.9 240 2 US-10-096-246A-37
999 28 50.9 240 2 US-10-630-406-8
1000 28 50.9 243 2 US-09-107-532A-6856

ALIGNMENTS

RESULT 1
US-09-155-106-6
; Sequence 6, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-6
Query Match 100.0%; Score 55; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 1 LHHSEYPYT 9

RESULT 2
US-09-155-106-22
; Sequence 22, Application US/09155106

Sequence 31722, A
Sequence 46939, A
Sequence 2, Appl1
Sequence 3054, Ap
Sequence 46161, A
Sequence 46501, A
Sequence 15028, A
Sequence 24371, A
Sequence 10010, A
Sequence 59161, A
Sequence 8, Appl1
Sequence 43214, A
Sequence 6, Appl1
Sequence 11482, A
Sequence 33, Appl1
Sequence 33, Appl1
Sequence 36, Appl1
Sequence 37, Appl1
Sequence 34, Appl1
Sequence 35, Appl1
Sequence 35, Appl1
Sequence 36, Appl1
Sequence 37, Appl1
Sequence 8, Appl1
Sequence 6856, Ap

; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22

Query Match 100.0%; Score 55; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 3
US-09-155-106-23
; Sequence 23, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23

Query Match 100.0%; Score 55; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 4

US-09-155-106-24
; Sequence 24, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 108 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-24

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 108;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 5

US-09-155-106-28
; Sequence 28, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 108 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-28

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 108;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 6

US-09-155-106-30

; Sequence 30, Application US/09155106

; Patent No. 6730300

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE

; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS

; NUMBER OF SEQUENCES: 45

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,106

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/04696

; FILING DATE: 19-MAR-1997

; APPLICATION NUMBER: US 60/013,708

; FILING DATE: 20-MAR-1996

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 108 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-155-106-30

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 108;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 7

US-09-698-705-5

; Sequence 5, Application US/09698705

; Patent No. 6824780

; GENERAL INFORMATION:

; APPLICANT: Devaux, B.

; APPLICANT: Keller, G.

; APPLICANT: Koepfen, H.

; APPLICANT: Lasky, L.

; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

; FILE REFERENCE: F1777R1

; CURRENT APPLICATION NUMBER: US/09/698,705

; CURRENT FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/162,558

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: US 60/182,872

; PRIOR FILING DATE: 2000-02-16

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 5

; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-698-705-5

Query Match 74.5%; Score 41; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 94 LQHLEYPYT 102

RESULT 8
US-09-698-705-10
; Sequence 10, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Laaky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P1777R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 10
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-10

Query Match 74.5%; Score 41; DB 2; Length 238;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 113 LQHLEYPYT 121

RESULT 9
US-09-328-352-7383
; Sequence 7383, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7383
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7383

Query Match 70.9%; Score 39; DB 2; Length 447;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYPYT 9
| | | | |

Db 28 HFSDPYPT 35

RESULT 10
US-08-435-925C-2
; Sequence 2, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCYTALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5646025o No. 5646025disk of No. 5646025th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,925C
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4429.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-925C-2

Query Match 69.1%; Score 38; DB 1; Length 717;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 426 IHRNKYPYT 434

RESULT 11
US-08-438-123-3
; Sequence 3, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123

;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/906,350
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: J.G. Mullins
;; REGISTRATION NUMBER: 33073
;; REFERENCE/DOCKET NUMBER: 149-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703 684 1111
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Polypeptide
US-08-438-123-3

Query Match 67.3%; Score 37; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
DB 1 LQHLEYPT 9

RESULT 12
US-08-438-123-11
; Sequence 11, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 149-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
US-08-438-123-11

Query Match 67.3%; Score 37; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 5.6;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 LHHSEYPYT 9
DB 1 LQHLEYPT 9

RESULT 13
US-08-438-123-7
; Sequence 7, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 149-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
US-08-438-123-7

Query Match 67.3%; Score 37; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
DB 114 LQHLEYPT 122

RESULT 14
US-09-248-796A-21229
; Sequence 21229, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

```
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21229
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21229

Query Match      67.3%; Score 37; DB 2; Length 274;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 HHSEYPY 8
Db      236 HHCKYPY 242

RESULT 15
US-09-248-796A-14372
; Sequence 14372, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14372
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14372

Query Match      67.3%; Score 37; DB 2; Length 309;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 HHSEYPY 8
Db      212 HHCKYPY 218

RESULT 16
US-08-758-621-6
; Sequence 6, Application US/08758621
; Patent No. 5846821
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou, and Eide, David J.
; TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,578
; FILING DATE: 29-MAY-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: DCI-099CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-758-621-6

Query Match      67.3%; Score 37; DB 1; Length 353;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LHHSEYPY 8
Db      122 LKHKEYPY 129

RESULT 17
US-09-107-858-6
; Sequence 6, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-6

Query Match      67.3%; Score 37; DB 2; Length 353;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LHHSEYPY 8
Db      122 LKHKEYPY 129

RESULT 18
US-09-579-174-6
; Sequence 6, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
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US-09-579-174-6

Query Match 67.3%; Score 37; DB 2; Length 353;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPY 8
Db 122 LKHSEYPY 129

RESULT 19

US-09-514-245-6

; Sequence 6, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-6

Query Match 67.3%; Score 37; DB 2; Length 567;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYP 7
Db 210 LHHSEYP 216

RESULT 20

US-08-936-165A-424

; Sequence 424, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/936,165A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,032
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 424:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-936-165A-424

Query Match 65.5%; Score 36; DB 2; Length 49;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 17 LHHSEHYVT 25

RESULT 21

US-09-012-097A-22

; Sequence 22, Application US/09012097A
; Patent No. 6187757
; GENERAL INFORMATION:
; APPLICANT: Clackson, Timothy
; APPLICANT: Gilman, Michael
; APPLICANT: Holt, Dennis
; APPLICANT: Keenan, Terence
; APPLICANT: Rozamus, Leonard
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: Regulation of Biological Events Using
; TITLE OF INVENTION: No. 6187757el Compounds
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,097A
; FILING DATE: 22-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berstein Esq., David L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: 374 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-494-0400
 TELEFAX: 617-494-0208
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-09-012-097A-22

Query Match 65.5%; Score 36; DB 2; Length 128;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHSEVPY 8
 |||||
 Db 4 HHHHPY 10

RESULT 22

US-09-781-804-21
 ; Sequence 21, Application US/09781804
 ; Patent No. 6649595
 ; GENERAL INFORMATION:
 ; APPLICANT: ARIAD Gene Therapeutics, Inc.
 ; TITLE OF INVENTION: Regulation of Biological Events Using No. 6649595el Compounds
 ; FILE REFERENCE: 374 USD1
 ; CURRENT APPLICATION NUMBER: US/09/781,804
 ; CURRENT FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 128
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: FKBP+His+HA epitopes
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)..(128)
 ; OTHER INFORMATION: FKBP+His+HA tags
 US-09-781-804-21

Query Match 65.5%; Score 36; DB 2; Length 128;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHSEVPY 8
 |||||
 Db 4 HHHHPY 10

RESULT 23

US-09-270-767-62464
 ; Sequence 62464, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 62464
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-62464

Query Match 65.5%; Score 36; DB 2; Length 176;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
 |||||:
 Db 83 LPHSEHPYS 91

RESULT 24

US-09-270-767-46835
 ; Sequence 46835, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 46835
 ; LENGTH: 397
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-46835

Query Match 65.5%; Score 36; DB 2; Length 397;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
 |||||:
 Db 304 LPHSEHPYS 312

RESULT 25

US-09-248-796A-19502
 ; Sequence 19502, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 19502
 ; LENGTH: 468
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-19502

Query Match 65.5%; Score 36; DB 2; Length 468;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HHSEVPY 8
 |||||
 Db 413 HHPNYPY 419

RESULT 26

US-09-328-352-4504

; Sequence 4504, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4504
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4504

Query Match 65.5%; Score 36; DB 2; Length 614;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHSEYPT 8
: : : : :
Db 476 HHNDYPT 482

RESULT 27
US-08-468-661-3
; Sequence 3, Application US/08468661
; Patent No. 5639621
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
; TITLE OF INVENTION: Preparation thereof and the Use thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,661
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/957,827
; FILING DATE: 08-OCT-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 35,694
; REFERENCE/DOCKET NUMBER: 05552-1227-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-661-3

Query Match 63.6%; Score 35; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHSEYPT 9
: : : : :
Db 92 MOHLEYPPT 100

RESULT 28
US-08-466-272A-3
; Sequence 3, Application US/08466272A
; Patent No. 5674994
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
; TITLE OF INVENTION: thereof and the Use Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,272A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/957,827
; FILING DATE: 08-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 02481-1227-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-272A-3

Query Match 63.6%; Score 35; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHSEYPT 9
: : : : :
Db 92 MOHLEYPPT 100

RESULT 29
US-08-478-857-3
; Sequence 3, Application US/08478857
; Patent No. 5695758
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard

```
;
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
; TITLE OF INVENTION: Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,857
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/957,827
; FILING DATE: 08-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugaisky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 02481-1227-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-478-857-3

Query Match 63.6%; Score 35; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db : |||||
92 MQHLEYPFT 100

RESULT 30
US-08-471-771-3
; Sequence 3, Application US/08471771
; Patent No. 5837824
; GENERAL INFORMATION:
; APPLICANT: Bossett, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,857
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,771
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1227-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-771-3

Query Match 63.6%; Score 35; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db : |||||
92 MQHLEYPFT 100

RESULT 31
US-09-130-783-3
; Sequence 3, Application US/09130783
; Patent No. 6030797
; GENERAL INFORMATION:
; APPLICANT: Bossett, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,783
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,771
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1227-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-771-3
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,771
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/957,827
; FILING DATE: 08-OCT-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1227-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-771-3

Query Match 63.6%; Score 35; DB 1; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db : |||||
92 MQHLEYPFT 100

RESULT 31
US-09-130-783-3
; Sequence 3, Application US/09130783
; Patent No. 6030797
; GENERAL INFORMATION:
; APPLICANT: Bossett, Klaus
; APPLICANT: Pfeleiderer, Peter
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Monoclonal Antibodies Against
; TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,783
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,771
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552-1227-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-771-3
```

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-783-3

Query Match 63.6%; Score 35; DB 2; Length 108;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
Db 92 MQHLEYPPT 100

RESULT 32
US-08-253-877C-10
Sequence 10, Application US/08253877C
Patent No. 5773001

GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-10

Query Match 63.6%; Score 35; DB 1; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
Db 114 MQHLEYPPT 122

RESULT 33
US-08-253-877C-28

Sequence 28, Application US/08253877C
Patent No. 5773001

GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-28

Query Match 63.6%; Score 35; DB 1; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
Db 114 MQHLEYPPT 122

RESULT 34
US-08-452-164A-10
Sequence 10, Application US/08452164A
Patent No. 5877296

GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany

; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-164A-10

Query Match 63.6%; Score 35; DB 1; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 114 MOHLEYPPT 122

RESULT 35
US-08-452-164A-28
; Sequence 28, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-164A-28

Query Match 63.6%; Score 35; DB 1; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 114 MOHLEYPPT 122

RESULT 36
US-08-603-024-4
; Sequence 4, Application US/08603024
; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
; TITLE OF INVENTION: ANTITUMOR AGENTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-603-024-4

Query Match 63.6%; Score 35; DB 2; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 114 MOHLEYPPT 122

RESULT 37
US-08-603-024-27
; Sequence 27, Application US/08603024

Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLRITRILIO
; TITLE OF INVENTION: ANTI-TUMOR AGENTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-603-024-27

Query Match 63.6%; Score 35; DB 2; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPT 9
: |||||
Db 114 MQHLEYPFT 122

RESULT 38
US-08-450-809-23
; Sequence 23, Application US/08450809
; Patent No. 6506881
; GENERAL INFORMATION:
; APPLICANT: Adair et al.
; TITLE OF INVENTION: Anti-HMG Antibodies and
; TITLE OF INVENTION: Procedures for their Production
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6506881ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,809
; FILING DATE:

CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/948,541B
; FILING DATE: 9/22/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Joanne Longo Feeney
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: CELL-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-809-23

Query Match 63.6%; Score 35; DB 2; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPT 9
: |||||
Db 114 MQHLEYPFT 122

RESULT 39
US-09-583-110-3045
; Sequence 3045, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3045
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3045

Query Match 63.6%; Score 35; DB 2; Length 219;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHSEYPT 7
: |||||
Db 111 HHQEYPT 116

RESULT 40
US-09-107-433-4852
; Sequence 4852, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

```

; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4852:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 221 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...221
; SEQUENCE DESCRIPTION: SEQ ID NO: 4852:
US-09-107-433-4852

Query Match 63.6%; Score 35; DB 2; Length 221;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYP 7
Db 113 HHQEYP 118

RESULT 41
US-08-157-101A-5
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSUROKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-5

Query Match 63.6%; Score 35; DB 1; Length 236;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHSEYP 7
Db 111 LHHNYP 117

RESULT 42
US-09-710-279-282
; Sequence 282, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-282

Query Match 63.6%; Score 35; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
Db 102 HSQVPY 107

RESULT 43
US-09-543-681A-6535
; Sequence 6535, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05

```

; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6535
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6535

Query Match 63.6%; Score 35; DB 2; Length 336;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPT 9
|||:|
Db 194 LHHQDIPWT 202

RESULT 44
US-09-134-001C-5155
; Sequence 5155, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5155
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5155

Query Match 63.6%; Score 35; DB 2; Length 338;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPT 8
|||:|
Db 106 HSQYPT 111

RESULT 45
US-09-543-681A-7363
; Sequence 7363, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7363
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7363

Query Match 63.6%; Score 35; DB 2; Length 569;
Best Local Similarity 62.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHSEYPT 9
|||:|
Db 26 HHNDYCYT 33

RESULT 46
US-09-991-258-3
; Sequence 3, Application US/09991258
; Patent No. 6783939
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Robert
; APPLICANT: Keith, Paula
; APPLICANT: Dryga, Sergey
; APPLICANT: Caley, Ian
; APPLICANT: Maughan, Maureen
; APPLICANT: Johnston, Robert
; APPLICANT: Davis, Nancy
; APPLICANT: Swanstrom, Ronald
; TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
; FILE REFERENCE: 01113.0001U3
; CURRENT APPLICATION NUMBER: US/09/991,258
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/902,537
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/216,995
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2492
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6783939e =
; OTHER INFORMATION: Synthetic construct
US-09-991-258-3

Query Match 63.6%; Score 35; DB 2; Length 2492;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHHSEYP 7
|||:|
Db 1147 LHHNEHP 1153

RESULT 47
US-09-647-468-138
; Sequence 138, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOMIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Amino acid sequence
; OTHER INFORMATION: of CDR3 of all versions of humanized L chain V region

US-09-647-468-138

Query Match 61.8%; Score 34; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 1 LQHGSPYT 9

RESULT 48

US-09-248-796A-24430
; Sequence 24430, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 24430

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-24430

Query Match 61.8%; Score 34; DB 2; Length 60;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 HHSEYPYT 9
| | | | |
Db 2 HHGSYSYT 9

RESULT 49

US-08-311-731A-243
; Sequence 243, Application US/08311731A
; Patent No. 6583266

; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS

; APPLICANT: MAO, JEN-I

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 411

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/311,731A

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: C0044/7125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 243:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 106 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEetical: YES

; ORIGINAL SOURCE:

; ORGANISM: Mycobacterium leprae

US-08-311-731A-243

Query Match 61.8%; Score 34; DB 2; Length 106;

Best Local Similarity 57.1%; Pred. No. 1.5e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYPYT 8

| | | | |

Db 95 HHTHYPT 101

RESULT 50

US-09-647-468-93

; Sequence 93, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOMIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 93

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid

; OTHER INFORMATION: sequence coding for version "a" of humanized L

; OTHER INFORMATION: chain V region

US-09-647-468-93

Query Match 61.8%; Score 34; DB 2; Length 107;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9

| | | | |

Db 89 LQHGSPYT 97

Search completed: May 11, 2006, 16:41:50

Job time : 27.9699 secs

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OM protein - protein search, using sw model

Run on: May 11, 2006, 16:38:41 ; Search time 67.8689 Seconds
(without alignments)
55.408 Million cell updates/sec

Title: US-10-808-538-6
Perfect score: 55
Sequence: 1 LHHSEYPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		DB	ID	Description
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1	55	100.0	9	3	US-09-155-106-6			Sequence 6, Appli
2	55	100.0	9	5	US-10-808-538-6			Sequence 6, Appli
3	55	100.0	108	3	US-09-155-106-22			Sequence 22, Appl
4	55	100.0	108	3	US-09-155-106-23			Sequence 23, Appl
5	55	100.0	108	3	US-09-155-106-24			Sequence 24, Appl
6	55	100.0	108	3	US-09-155-106-28			Sequence 28, Appl
7	55	100.0	108	3	US-09-155-106-30			Sequence 30, Appl
8	55	100.0	108	5	US-10-808-538-22			Sequence 22, Appl
9	55	100.0	108	5	US-10-808-538-23			Sequence 23, Appl
10	55	100.0	108	5	US-10-808-538-24			Sequence 24, Appl
11	55	100.0	108	5	US-10-808-538-28			Sequence 28, Appl
12	55	100.0	108	5	US-10-808-538-30			Sequence 30, Appl
13	43	78.2	976	4	US-10-263-929-121			Sequence 121, App
14	43	78.2	976	6	US-11-097-143-32997			Sequence 32997, A
15	42	76.4	508	6	US-11-097-143-40827			Sequence 40827, A
16	41	74.5	113	5	US-10-937-046-5			Sequence 5, Appli
17	41	74.5	238	5	US-10-937-046-10			Sequence 10, Appl
18	40	72.7	88	4	US-10-425-115-367833			Sequence 367833,
19	40	72.7	101	4	US-10-010-729-23			Sequence 23, Appl
20	40	72.7	108	4	US-10-010-729-43			Sequence 43, Appl
21	40	72.7	2346	4	US-10-072-012-491			Sequence 491, App
22	40	72.7	2715	4	US-10-042-865-52			Sequence 52, Appl
23	40	72.7	2715	4	US-10-029-020-51			Sequence 51, Appl
24	39	70.9	236	4	US-10-632-706-273			Sequence 273, App
25	39	70.9	236	4	US-10-038-591-48			Sequence 48, Appl
26	39	70.9	236	4	US-10-775-444A-48			Sequence 48, Appl
27	39	70.9	744	4	US-10-782-570-2			Sequence 2, Appli

28	39	70.9	2725	4	US-10-235-027-928			Sequence 928, App
29	39	70.9	2725	4	US-10-029-020-52			Sequence 52, Appl
30	39	70.9	2725	4	US-10-408-765A-1687			Sequence 1687, Ap
31	39	70.9	2725	5	US-10-723-860-4102			Sequence 4102, Ap
32	38	69.1	9	5	US-10-687-035-20			Sequence 20, Appl
33	38	69.1	18	4	US-10-685-898-82			Sequence 82, Appl
34	38	69.1	61	4	US-10-424-599-209690			Sequence 209690,
35	38	69.1	128	5	US-10-687-035-31			Sequence 31, Appl
36	38	69.1	247	4	US-10-437-963-195645			Sequence 195645,
37	38	69.1	254	4	US-10-767-701-36542			Sequence 36542, A
38	38	69.1	328	4	US-10-282-122A-42941			Sequence 42941, A
39	38	69.1	336	5	US-10-450-763-56327			Sequence 56327, A
40	38	69.1	717	4	US-10-815-495-14			Sequence 14, Appl
41	38	69.1	717	4	US-10-815-495-30			Sequence 30, Appl
42	38	69.1	1063	4	US-10-093-463-124			Sequence 124, App
43	38	69.1	1289	4	US-10-108-260A-2971			Sequence 2971, Ap
44	38	69.1	3003	4	US-10-093-463-126			Sequence 126, App
45	38	69.1	3361	4	US-10-093-463-128			Sequence 128, App
46	37	67.3	69	4	US-10-437-963-116249			Sequence 116249,
47	37	67.3	113	4	US-10-424-599-285574			Sequence 285574,
48	37	67.3	118	4	US-10-425-115-203113			Sequence 203113,
49	37	67.3	138	4	US-10-112-944-912			Sequence 912, App
50	37	67.3	139	4	US-10-264-049-4289			Sequence 4289, Ap
51	37	67.3	153	4	US-10-425-114-67502			Sequence 67502, A
52	37	67.3	250	4	US-10-333-235A-55			Sequence 55, Appl
53	37	67.3	262	4	US-10-744-572-78			Sequence 78, Appl
54	37	67.3	298	4	US-10-424-599-283396			Sequence 283396,
55	37	67.3	302	4	US-10-425-114-51114			Sequence 51114, A
56	37	67.3	368	4	US-10-333-235A-58			Sequence 58, Appl
57	37	67.3	385	4	US-10-136-728-56			Sequence 56, Appl
58	37	67.3	465	4	US-10-333-235A-59			Sequence 59, Appl
59	37	67.3	499	4	US-10-112-944-475			Sequence 475, App
60	37	67.3	519	4	US-10-108-260A-3767			Sequence 3767, Ap
61	37	67.3	567	4	US-10-682-420-6			Sequence 6, Appli
62	37	67.3	567	4	US-10-409-613-6			Sequence 6, Appli
63	37	67.3	567	4	US-10-442-180-6			Sequence 6, Appli
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65	37	67.3	567	5	US-10-775-337-6			Sequence 6, Appli
66	37	67.3	567	5	US-10-637-031-6			Sequence 6, Appli
67	37	67.3	567	6	US-11-007-798-6			Sequence 6, Appli
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69	37	67.3	616	4	US-10-430-011-44			Sequence 44, Appl
70	37	67.3	684	4	US-10-437-963-174682			Sequence 174682,
71	37	67.3	980	4	US-10-369-493-23214			Sequence 23214, A
72	36	65.5	9	4	US-10-632-706-135			Sequence 135, App
73	36	65.5	9	4	US-10-632-706-136			Sequence 136, App
74	36	65.5	9	4	US-10-632-706-137			Sequence 137, App
75	36	65.5	9	4	US-10-632-706-264			Sequence 264, App
76	36	65.5	9	4	US-10-632-706-270			Sequence 270, App
77	36	65.5	18	5	US-10-808-187-2361			Sequence 2361, Ap
78	36	65.5	18	5	US-10-807-807-2361			Sequence 2361, Ap
79	36	65.5	49	3	US-09-939-980-424			Sequence 424, App
80	36	65.5	81	4	US-10-006-593-53			Sequence 53, Appl
81	36	65.5	81	4	US-10-307-724-53			Sequence 53, Appl
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83	36	65.5	81	5	US-10-433-281-10			Sequence 10, Appl
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85	36	65.5	92	4	US-10-437-963-133943			Sequence 133943,
86	36	65.5	128	3	US-09-781-804-21			Sequence 21, Appl
87	36	65.5	128	4	US-10-716-062-21			Sequence 21, Appl
88	36	65.5	144	4	US-10-424-599-148912			Sequence 148912,
89	36	65.5	164	4	US-10-425-115-322680			Sequence 322680,
90	36	65.5	252	6	US-11-097-143-27273			Sequence 27273, A
91	36	65.5	252	6	US-11-097-143-28590			Sequence 28590, A
92	36	65.5	271	3	US-09-815-242-5851			Sequence 5851, Ap
93	36	65.5	271	3	US-09-815-242-12927			Sequence 12927, A
94	36	65.5	271	4	US-10-282-122A-44377			Sequence 44377, A
95	36	65.5	282	5	US-10-737-290-143			Sequence 143, App
96	36	65.5	294	4	US-10-282-122A-43959			Sequence 43959, A
97	36	65.5	2397	5	US-10-631-467-1518			Sequence 1518, Ap
98	35	63.6	9	4	US-10-632-706-267			Sequence 267, App
99	35	63.6	44	4	US-10-425-115-213974			Sequence 213974,
100	35	63.6	44	4	US-10-425-115-276058			Sequence 276058,

101	35	63.6	58	4	US-10-424-599-171823	Sequence 171823,	174	34	61.8	107	4	US-10-041-860-268	Sequence 268, App
102	35	63.6	58	4	US-10-424-599-235178	Sequence 235178,	175	34	61.8	107	4	US-10-041-860-303	Sequence 303, App
103	35	63.6	74	4	US-10-425-115-258526	Sequence 258526,	176	34	61.8	107	4	US-10-041-860-309	Sequence 309, App
104	35	63.6	83	4	US-10-425-115-361522	Sequence 361522,	177	34	61.8	107	4	US-10-041-860-316	Sequence 316, App
105	35	63.6	88	4	US-10-424-599-273214	Sequence 273214,	178	34	61.8	107	4	US-10-041-860-340	Sequence 340, App
106	35	63.6	96	6	US-11-097-143-33567	Sequence 33567, A	179	34	61.8	107	4	US-10-309-762-48	Sequence 48, Appl
107	35	63.6	98	4	US-10-425-115-300228	Sequence 300228,	180	34	61.8	107	4	US-10-309-762-52	Sequence 52, Appl
108	35	63.6	103	4	US-10-424-599-162229	Sequence 162229,	181	34	61.8	107	4	US-10-309-762-166	Sequence 166, App
109	35	63.6	105	4	US-10-437-963-159806	Sequence 159806,	182	34	61.8	107	4	US-10-462-062-93	Sequence 93, Appl
110	35	63.6	107	4	US-10-041-860-20	Sequence 20, Appl	183	34	61.8	107	4	US-10-462-062-99	Sequence 99, Appl
111	35	63.6	107	4	US-10-041-860-228	Sequence 228, App	184	34	61.8	107	4	US-10-462-062-101	Sequence 101, App
112	35	63.6	107	4	US-10-041-860-291	Sequence 291, App	185	34	61.8	107	4	US-10-462-062-107	Sequence 107, App
113	35	63.6	107	4	US-10-665-383-20	Sequence 20, Appl	186	34	61.8	107	4	US-10-462-062-109	Sequence 109, App
114	35	63.6	108	3	US-09-926-323-4	Sequence 4, Appl	187	34	61.8	107	4	US-10-462-062-147	Sequence 147, App
115	35	63.6	108	4	US-10-067-800-66	Sequence 66, Appl	188	34	61.8	107	4	US-10-462-062-148	Sequence 148, App
116	35	63.6	108	5	US-10-994-679-66	Sequence 66, Appl	189	34	61.8	107	4	US-10-660-357-18	Sequence 18, App
117	35	63.6	130	4	US-10-424-599-245762	Sequence 245762,	190	34	61.8	107	4	US-10-665-383-28	Sequence 28, Appl
118	35	63.6	141	4	US-10-425-115-259773	Sequence 259773,	191	34	61.8	107	4	US-10-665-383-32	Sequence 32, Appl
119	35	63.6	152	5	US-10-644-277-96	Sequence 96, Appl	192	34	61.8	107	4	US-10-665-383-36	Sequence 36, Appl
120	35	63.6	163	3	US-09-864-761-37390	Sequence 37390, A	193	34	61.8	107	4	US-10-665-383-52	Sequence 52, Appl
121	35	63.6	167	4	US-10-424-599-251450	Sequence 251450,	194	34	61.8	107	4	US-10-472-905A-82	Sequence 82, Appl
122	35	63.6	169	5	US-10-820-155-119	Sequence 119, App	195	34	61.8	107	4	US-10-472-905A-88	Sequence 88, Appl
123	35	63.6	207	4	US-10-282-122A-52891	Sequence 52891, A	196	34	61.8	107	4	US-10-472-905A-90	Sequence 90, Appl
124	35	63.6	219	4	US-10-474-776-372	Sequence 372, App	197	34	61.8	107	4	US-10-472-905A-96	Sequence 96, Appl
125	35	63.6	219	5	US-10-472-928-3738	Sequence 3738, Ap	198	34	61.8	107	4	US-10-472-905A-98	Sequence 98, Appl
126	35	63.6	221	5	US-10-617-320-4852	Sequence 4852, Ap	199	34	61.8	107	4	US-10-472-905A-100	Sequence 100, App
127	35	63.6	221	4	US-10-156-761-11067	Sequence 11067, A	200	34	61.8	107	5	US-10-727-155-64	Sequence 64, Appl
128	35	63.6	323	4	US-10-282-122A-53566	Sequence 53566, A	201	34	61.8	107	5	US-10-727-155-260	Sequence 260, App
129	35	63.6	338	4	US-10-724-972A-6761	Sequence 6761, Ap	202	34	61.8	107	5	US-10-727-155-274	Sequence 274, App
130	35	63.6	350	5	US-10-510-408-38	Sequence 38, Appl	203	34	61.8	107	5	US-10-727-155-307	Sequence 307, App
131	35	63.6	368	4	US-10-369-493-8643	Sequence 8643, Ap	204	34	61.8	108	6	US-11-010-797-6	Sequence 6, Appl
132	35	63.6	450	4	US-10-369-493-3595	Sequence 3595, Ap	205	34	61.8	109	4	US-10-437-963-117170	Sequence 117170,
133	35	63.6	450	4	US-10-343-650A-84	Sequence 84, Appl	206	34	61.8	110	4	US-10-437-963-170281	Sequence 170281,
134	35	63.6	451	6	US-11-097-143-30384	Sequence 30384, A	207	34	61.8	112	4	US-10-437-963-170281	Sequence 170281,
135	35	63.6	460	3	US-09-864-761-37089	Sequence 37089, A	208	34	61.8	112	6	US-11-054-041-2	Sequence 2, Appl
136	35	63.6	766	4	US-10-231-913-99	Sequence 99, Appl	209	34	61.8	113	4	US-10-364-743-47	Sequence 47, Appl
137	35	63.6	766	4	US-10-231-913-100	Sequence 100, App	210	34	61.8	113	5	US-10-452-593-47	Sequence 47, Appl
138	35	63.6	828	6	US-11-097-143-1896	Sequence 1896, Ap	211	34	61.8	115	4	US-10-437-963-163322	Sequence 163322,
139	35	63.6	924	4	US-10-467-252-2	Sequence 2, Appl	212	34	61.8	123	4	US-10-437-963-155157	Sequence 155157,
140	35	63.6	1131	5	US-10-450-763-42014	Sequence 42014, A	213	34	61.8	123	6	US-11-097-143-29049	Sequence 29049, A
141	35	63.6	1171	6	US-11-097-143-19953	Sequence 19953, A	214	34	61.8	127	4	US-10-462-062-162	Sequence 162, App
142	35	63.6	1413	6	US-11-097-143-9363	Sequence 9363, Ap	215	34	61.8	127	4	US-10-462-062-179	Sequence 179, App
143	35	63.6	1424	6	US-11-097-143-9354	Sequence 9354, Ap	216	34	61.8	127	4	US-10-462-062-127	Sequence 127, App
144	35	63.6	2492	3	US-09-991-258-3	Sequence 3, Appl	217	34	61.8	127	4	US-10-462-062-181	Sequence 181, App
145	35	63.6	2492	5	US-10-929-234-3	Sequence 3, Appl	218	34	61.8	127	4	US-10-462-062-182	Sequence 182, App
146	34.5	62.7	156	4	US-10-425-115-217583	Sequence 217583,	219	34	61.8	127	4	US-10-462-062-183	Sequence 183, App
147	34	61.8	9	4	US-10-462-062-138	Sequence 138, App	220	34	61.8	127	4	US-10-472-905A-104	Sequence 104, App
148	34	61.8	9	6	US-11-010-797-12	Sequence 12, Appl	221	34	61.8	127	4	US-10-472-905A-119	Sequence 119, App
149	34	61.8	125	4	US-10-293-086-125	Sequence 125, App	222	34	61.8	127	4	US-10-472-905A-120	Sequence 120, App
150	34	61.8	49	4	US-10-424-599-240936	Sequence 240936,	223	34	61.8	127	4	US-10-472-905A-121	Sequence 121, App
151	34	61.8	51	4	US-10-425-115-197178	Sequence 197178,	224	34	61.8	127	4	US-10-472-905A-122	Sequence 122, App
152	34	61.8	58	4	US-10-425-115-214197	Sequence 214197,	225	34	61.8	127	4	US-10-472-905A-123	Sequence 123, App
153	34	61.8	61	4	US-10-437-963-198673	Sequence 198673,	226	34	61.8	129	4	US-10-101-464A-609	Sequence 609, App
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158	34	61.8	96	4	US-10-080-170-257	Sequence 257, App	231	34	61.8	143	5	US-10-627-556-312	Sequence 312, App
159	34	61.8	96	4	US-10-468-356-257	Sequence 257, App	232	34	61.8	152	5	US-10-644-277-60	Sequence 60, Appl
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163	34	61.8	107	4	US-10-041-860-24	Sequence 24, Appl	236	34	61.8	163	5	US-10-452-593-20	Sequence 20, Appl
164	34	61.8	107	4	US-10-041-860-26	Sequence 26, Appl	237	34	61.8	182	3	US-09-764-864-1387	Sequence 1387, Ap
165	34	61.8	107	4	US-10-041-860-28	Sequence 28, Appl	238	34	61.8	212	3	US-09-764-864-951	Sequence 951, App
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[illegible]

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874	32	58.2	9	4	US-10-436-783-4	Sequence 4, Appl	947	32	58.2	132	4	US-10-424-599-225610	Sequence 225610, A
875	32	58.2	9	4	US-10-727-737-60	Sequence 60, Appl	948	32	58.2	142	4	US-10-425-115-247063	Sequence 247063, A
876	32	58.2	9	4	US-10-727-737-63	Sequence 63, Appl	949	32	58.2	145	4	US-10-219-220-173	Sequence 173, App
877	32	58.2	9	5	US-10-842-011-20	Sequence 20, Appl	950	32	58.2	149	4	US-10-437-963-102745	Sequence 102745, A
878	32	58.2	9	5	US-10-842-011-37	Sequence 37, Appl	951	32	58.2	153	4	US-10-424-599-226050	Sequence 226050, A
879	32	58.2	9	5	US-10-842-011-37	Sequence 37, Appl	952	32	58.2	160	4	US-10-108-260A-4018	Sequence 4018, App
880	32	58.2	9	6	US-11-004-795A-36	Sequence 36, Appl	953	32	58.2	171	5	US-10-739-930-6836	Sequence 6836, App
881	32	58.2	9	6	US-11-004-794A-36	Sequence 36, Appl	954	32	58.2	186	4	US-10-424-599-158815	Sequence 158815, A
882	32	58.2	34	3	US-09-864-761-37935	Sequence 37935, A	955	32	58.2	191	4	US-10-137-113-25	Sequence 25, Appl
883	32	58.2	35	4	US-10-425-115-194568	Sequence 194568, App	956	32	58.2	198	4	US-10-074-475-178	Sequence 178, App
884	32	58.2	38	4	US-10-424-599-18337	Sequence 18337, App	957	32	58.2	220	4	US-10-096-625-89	Sequence 89, Appl
885	32	58.2	38	4	US-10-424-599-206095	Sequence 206095, App	958	32	58.2	220	4	US-10-424-599-215299	Sequence 215299, App
886	32	58.2	43	4	US-10-425-115-341205	Sequence 341205, App	959	32	58.2	214	4	US-10-423-299-3	Sequence 3, Appl
887	32	58.2	44	4	US-10-437-963-113079	Sequence 113079, App	960	32	58.2	217	3	US-09-749-728B-21	Sequence 21, Appl
888	32	58.2	44	4	US-10-437-963-113079	Sequence 113079, App	961	32	58.2	220	3	US-09-972-211-89	Sequence 89, Appl
889	32	58.2	50	4	US-10-424-599-262317	Sequence 262317, App	962	32	58.2	220	4	US-10-096-625-89	Sequence 89, Appl
890	32	58.2	52	4	US-10-425-115-250861	Sequence 250861, App	963	32	58.2	225	4	US-10-424-599-182150	Sequence 182150, A
891	32	58.2	53	4	US-10-424-599-271304	Sequence 271304, App	964	32	58.2	226	4	US-10-156-761-12357	Sequence 12357, A
892	32	58.2	53	4	US-10-425-115-197616	Sequence 197616, App	965	32	58.2	229	4	US-10-425-115-199136	Sequence 199136, A
893	32	58.2	54	4	US-10-424-599-265299	Sequence 265299, App	966	32	58.2	255	4	US-10-424-599-220659	Sequence 220659, A
894	32	58.2	55	4	US-10-425-115-260253	Sequence 260253, App	967	32	58.2	256	4	US-10-282-122A-66274	Sequence 66274, A
895	32	58.2	57	3	US-09-864-761-46311	Sequence 46311, A	968	32	58.2	297	4	US-10-437-963-199300	Sequence 199300, A
896	32	58.2	57	3	US-09-864-761-47667	Sequence 47667, App	969	32	58.2	309	4	US-10-437-963-127826	Sequence 127826, A
897	32	58.2	59	4	US-10-437-963-130768	Sequence 130768, App	970	32	58.2	314	4	US-10-437-963-127826	Sequence 127826, A
898	32	58.2	61	4	US-10-425-115-236497	Sequence 236497, App	971	32	58.2	323	6	US-11-097-143-17625	Sequence 17625, A
899	32	58.2	63	4	US-10-424-599-231280	Sequence 231280, App	972	32	58.2	329	4	US-10-369-493-17435	Sequence 17443, A
900	32	58.2	64	4	US-10-425-115-186899	Sequence 186899, App	973	32	58.2	330	4	US-10-437-963-201358	Sequence 201358, A
901	32	58.2	66	4	US-10-424-599-249938	Sequence 249938, App	974	32	58.2	331	4	US-10-425-115-334637	Sequence 334637, A
902	32	58.2	68	3	US-09-864-408A-3408	Sequence 3408, App	975	32	58.2	339	3	US-09-791-489-2	Sequence 2, Appl
903	32	58.2	71	3	US-09-864-761-48042	Sequence 48042, App	976	32	58.2	339	4	US-10-369-493-2832	Sequence 2832, App
										341	3	US-09-800-770-4	Sequence 4, Appl

977 32 58.2 341 4 US-10-422-536-4 Sequence 4, Appli
978 32 58.2 341 6 US-11-011-880-4 Sequence 4, Appli
979 32 58.2 355 4 US-10-424-599-182151 Sequence 182151,
980 32 58.2 355 4 US-10-424-599-226051 Sequence 226051,
981 32 58.2 355 4 US-10-724-972A-6210 Sequence 6210, Ap
982 32 58.2 355 5 US-10-858-706-54 Sequence 54, Appl
983 32 58.2 362 4 US-10-437-963-123843 Sequence 123843,
984 32 58.2 370 4 US-10-365-742-100 Sequence 100, App
985 32 58.2 371 6 US-11-097-143-33840 Sequence 33840, A
986 32 58.2 378 4 US-10-770-668-36 Sequence 36, Appl
987 32 58.2 378 6 US-11-097-143-42897 Sequence 42897, A
988 32 58.2 381 4 US-10-424-599-247211 Sequence 247211,
989 32 58.2 387 5 US-10-483-505-23 Sequence 23, Appl
990 32 58.2 391 4 US-10-369-493-2338 Sequence 2338, Ap
991 32 58.2 395 5 US-10-741-849-7050 Sequence 7050, Ap
992 32 58.2 402 5 US-10-353-575A-35 Sequence 35, Appl
993 32 58.2 411 4 US-10-094-749-2243 Sequence 2243, Ap
994 32 58.2 413 4 US-10-437-963-195044 Sequence 195044,
995 32 58.2 416 3 US-09-769-734-52 Sequence 52, Appl
996 32 58.2 416 3 US-09-758-759-3 Sequence 3, Appli
997 32 58.2 416 4 US-10-107-431-229 Sequence 229, App
998 32 58.2 416 4 US-10-107-431-231 Sequence 231, App
999 32 58.2 416 6 US-11-021-825-3 Sequence 3, Appli
1000 32 58.2 444 4 US-10-425-115-199137 Sequence 199137,

ALIGNMENTS

RESULT 1
US-09-155-106-6
; Sequence 6, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/155.106
; FILING DATE: 19-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-808-538-6

Query Match 100.0%; Score 55; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 1 LHHSEYPT 9
|||||

RESULT 2
US-10-808-538-6
; Sequence 6, Application US/10808538
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/155.106
; FILING DATE: 19-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-155-106-6

Query Match 100.0%; Score 55; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 1 LHHSEYPT 9
|||||

RESULT 3
US-09-155-106-6
; Sequence 22, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/155.106
; FILING DATE: 19-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid

Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155.106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-808-538-6

Query Match 100.0%; Score 55; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 1 LHHSEYPT 9
|||||

RESULT 3
US-09-155-106-22
; Sequence 22, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/155.106
; FILING DATE: 19-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-22

Query Match      100.0%; Score 55; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 4
US-09-155-106-23
; Sequence 23, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-23

Query Match      100.0%; Score 55; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 5
US-09-155-106-24
; Sequence 24, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-24

Query Match      100.0%; Score 55; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 6
US-09-155-106-28
; Sequence 28, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-155-106-28

Query Match      100.0%; Score 55; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 7
US-09-155-106-30
; Sequence 30, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-155-106-30

Query Match 100.0%; Score 55; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 8

US-10-808-538-22
Sequence 22, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-10-808-538-22
Query Match 100.0%; Score 55; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 9

US-10-808-538-23
Sequence 23, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/808,538
FILING DATE: 25-Mar-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,106
FILING DATE: 17-NOV-1998
APPLICATION NUMBER: PCT/US97/04696
FILING DATE: 19-MAR-1997
APPLICATION NUMBER: US 60/013,708
FILING DATE: 20-MAR-1996
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-808-538-23

Query Match 100.0%; Score 55; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
Db 89 LHHSEYPYT 97

RESULT 10

US-10-808-538-24
Sequence 24, Application US/10808538
Publication No. US20050048053A1
GENERAL INFORMATION:
APPLICANT: Immunomedics, Inc.
TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

NUMBER OF SEQUENCES: 45
STREET: 300 American Road
CITY: Morris Plains
STATE: New Jersey
COUNTRY: USA
ZIP: 07950

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-808-538-24

Query Match 100.0%; Score 55; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

Qy 1 LHHSEYPYT 9
| | | | | | | |
Db 89 LHHSEYPYT 97

RESULT 11
US-10-808-538-28
; Sequence 28, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMERYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-808-538-28

Query Match 100.0%; Score 55; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

Qy 1 LHHSEYPYT 9
| | | | | | | |
Db 89 LHHSEYPYT 97

RESULT 12
US-10-808-538-30
; Sequence 30, Application US/10808538
; Publication No. US20050048053A1
; GENERAL INFORMATION:
; APPLICANT: Immunomedics, Inc.
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMERYONIC
; ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; STREET: 300 American Road
; CITY: Morris Plains
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07950
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/808,538
; FILING DATE: 25-Mar-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE: 17-NOV-1998
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-808-538-30

Query Match 100.0%; Score 55; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

Qy 1 LHHSEYPYT 9
| | | | | | | |
Db 89 LHHSEYPYT 97

RESULT 13
US-10-263-929-121
; Sequence 121, Application US/10263929
; Publication No. US20040067535A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; FILE REFERENCE: LSD-07417
; CURRENT APPLICATION NUMBER: US/10/263,929
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 121
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-263-929-121

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Query Match      78.2%; Score 43; DB 4; Length 976;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 296 LSHTEYPT 304

RESULT 14
US-11-097-143-32997
; Sequence 32997, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: 60/191,637
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32997
; LENGTH: 976
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32997

Query Match      78.2%; Score 43; DB 6; Length 976;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 296 LSHTEYPT 304

RESULT 15
US-11-097-143-40827
; Sequence 40827, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32997
; LENGTH: 976
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32997

Query Match      78.2%; Score 43; DB 6; Length 976;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 296 LSHTEYPT 304

RESULT 16
US-10-937-046-5
; Sequence 5, Application US/10937046
; Publication No. US20050036942A1
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: PL777R1D1
; CURRENT APPLICATION NUMBER: US/10/937,046
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 09/698,705
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-046-5

Query Match      74.5%; Score 41; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 94 LQHLEYPPT 102

RESULT 17
US-10-937-046-10
; Sequence 10, Application US/10937046
; Publication No. US20050036942A1
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
```

```
Query Match      76.4%; Score 42; DB 6; Length 508;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 8
Db 273 IHHSAYPT 280

RESULT 16
US-10-937-046-5
; Sequence 5, Application US/10937046
; Publication No. US20050036942A1
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: PL777R1D1
; CURRENT APPLICATION NUMBER: US/10/937,046
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 09/698,705
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-046-5

Query Match      74.5%; Score 41; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 94 LQHLEYPPT 102

RESULT 17
US-10-937-046-10
; Sequence 10, Application US/10937046
; Publication No. US20050036942A1
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
```

```
; FILE REFERENCE: P1777RID1
; CURRENT APPLICATION NUMBER: US/10/937,046
; PRIOR FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: US 09/698,705
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 10
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-10-937-046-10

Query Match          74.5%; Score 41; DB 5; Length 238;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEVPYT 9
| | | | |
Db 113 LOHLEPYT 121

RESULT 18
US-10-425-115-367833
; Sequence 367833, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 367833
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_98636C.1.pap
US-10-425-115-367833

Query Match          72.7%; Score 40; DB 4; Length 88;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHSEVPY 8
| | | | |
Db 22 HHLEVPY 28

RESULT 19
US-10-010-729-23
; Sequence 23, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
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; FILE REFERENCE: P1777RID1
; CURRENT APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-23

Query Match          72.7%; Score 40; DB 4; Length 101;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEVPYT 9
| | | | |
Db 91 HNEVPYT 97

RESULT 20
US-10-010-729-43
; Sequence 43, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-43

Query Match          72.7%; Score 40; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEVPYT 9
| | | | |
Db 91 HNEVPYT 97

RESULT 21
```

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US-10-072-012-491
; Sequence 491, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072.012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 491
; LENGTH: 2346
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-072-012-491

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Query Match 72.7%; Score 40; DB 4; Length 2346;
Best Local Similarity 77.8%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 LHHSEYPT 9
Db 534 LHYSEYGT 542

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RESULT 22
US-10-042-865-52
; Sequence 52, Application US/10042865
; Publication No. US20040029216A1

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```

; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Beha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-042-865-52

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```

Query Match 72.7%; Score 40; DB 4; Length 2715;
Best Local Similarity 77.8%; Pred. No. 9.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 1 LHHSEYPT 9
Db 896 LHYSEYGT 904

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```

RESULT 23
US-10-029-020-51
; Sequence 51, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704

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; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-020-51

Query Match 72.7%; Score 40; DB 4; Length 2715;
Best Local Similarity 77.8%; Pred. No. 9.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
|:|||||
DB 896 LHYSEGYT 904

RESULT 24
US-10-632-706-273
; Sequence 273, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-273

Query Match 70.9%; Score 39; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHSEYPYT 9
|:|||||
DB 2 HYSTPYT 9

RESULT 25
US-10-038-591-48
; Sequence 48, Application US/10038591
; Publication No. US20040086503A1

; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope B.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-48

Query Match 70.9%; Score 39; DB 4; Length 236;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
|:|||||
DB 111 LQHNSYPYT 119

RESULT 26
US-10-775-444A-48
; Sequence 48, Application US/10775444A
; Publication No. US20040202651A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Bedian, Vane
; APPLICANT: Obrocea, Mihail
; APPLICANT: Gomez-Navarro, Jesus
; APPLICANT: Cusmano, John D.
; APPLICANT: Wang, Huifen P.
; APPLICANT: Page, Kelly L.
; APPLICANT: Guyot, Deborah J.
; TITLE OF INVENTION: USES OF ANTI-INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: PC25232A
; CURRENT APPLICATION NUMBER: US/10/775,444A
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-444A-48

Query Match 70.9%; Score 39; DB 4; Length 236;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPYT 9
|:|||||
DB 111 LQHNSYPYT 119

RESULT 27
US-10-782-570-2
; Sequence 2, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.


```
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-2

Query Match      70.9%; Score 39; DB 4; Length 744;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LHHSEYPT 9
Db      25 IDHSEYPT 33

RESULT 28
US-10-295-027-928
; Sequence 928, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 928
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
```

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US-10-295-027-928

Query Match      70.9%; Score 39; DB 4; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYPT 9
Db      909 LHHSDYGT 917

RESULT 29
US-10-029-020-52
; Sequence 52, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-020-52

Query Match      70.9%; Score 39; DB 4; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYPT 9
Db      909 LHHSDYGT 917

RESULT 30
US-10-408-765A-1687
; Sequence 1687, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
```

; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1687
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1687

Query Match 70.9%; Score 39; DB 4; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEVPYT 9
|||:|:|
Db 909 LHSDYGT 917

RESULT 31
US-10-723-860-4102
; Sequence 4102, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataeha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4102
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4102

Query Match 70.9%; Score 39; DB 5; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEVPYT 9
|||:|:|
Db 909 LHSDYGT 917

RESULT 32
US-10-687-035-20
; Sequence 20, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albane, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 501.1 VL3 CDR

US-10-687-035-20

Query Match 69.1%; Score 38; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEVPYT 9
|||:|:|
Db 1 LHSDSPPT 9

RESULT 33
US-10-685-898-82
; Sequence 82, Application US/10685898
; Publication No. US20040121412A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: BETA SECRETASE EXOSITE BINDING PEPTIDES AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING BETA SECRETASE MODULATORS
; FILE REFERENCE: D0252 NP
; CURRENT APPLICATION NUMBER: US/10/685,898
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,679
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthesized Peptide
US-10-685-898-82

Query Match 69.1%; Score 38; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEVPY 8
||:|:|
Db 4 HHTHY 10

RESULT 34
US-10-424-599-209690
; Sequence 209690, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 209690
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31378C.1.pep
US-10-424-599-209690

Query Match 69.1%; Score 38; DB 4; Length 61;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HHSEVPY 8
||:|:|
Db 55 HHSDWPY 61

```
RESULT 35
US-10-687-035-31
; Sequence 31, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albano, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; FILE REFERENCE: CA 125/0772P AND METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: 6750-214-999
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 501.1 light chain polypeptide variable region (501.1L)
US-10-687-035-31

Query Match      69.1%; Score 38; DB 5; Length 128;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LHHSEYPYT 9
Db      111 LHHDESPFT 119

RESULT 36
US-10-437-963-195645
; Sequence 195645, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195645
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91574C.1.pep
US-10-437-963-195645

Query Match      69.1%; Score 38; DB 4; Length 247;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LHHSEYPYT 9
Db      6 VHHQAQYPPS 14

RESULT 37
US-10-767-701-36542
; Sequence 36542, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36542
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C95544_1.pep
US-10-767-701-36542

Query Match      69.1%; Score 38; DB 4; Length 254;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYPY 8
Db      42 LHHGDYFPW 49

RESULT 38
US-10-282-122A-42941
; Sequence 42941, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

;; CURRENT AFFILIATION NUMBER: 2004-03

APPLICANT:

APPLICANT:

APPLICANT:

; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 3003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-126

Query Match 69.1%; Score 38; DB 4; Length 3003;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
Db 2238 HSEYPY 2243
|||||

RESULT 45
US-10-093-463-128
; Sequence 128, Application US/10093463
; Publication No. US20030208039A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gusev, Vladimir
; APPLICANT: Pochart, Pascal
; APPLICANT: Zhong, Mei
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Pena, Carol
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gorman, Linda
; APPLICANT: Spaderna, Steven
; APPLICANT: Voss, Edward
; APPLICANT: Malyankar, Uriel
; APPLICANT: Anderson, David

; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; TITLE OF INVENTION: No. US20030208039A1el Antibodies that Bind to Antigenic Polypept
; FILE REFERENCE: 21402-290A (Cura 590AT)
; CURRENT APPLICATION NUMBER: US/10/093,463
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/283,675
; PRIOR FILING DATE: 2001-04-14
; PRIOR APPLICATION NUMBER: 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,101
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/287,424
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/299,027
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/309,198
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/281,194
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/330,380
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/275,235
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/288,342
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/275,578
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 3361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-093-463-128

Query Match 69.1%; Score 38; DB 4; Length 3361;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
Db 2596 HSEYPY 2601
|||||

RESULT 46
US-10-437-963-116249
; Sequence 116249, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

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; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 116249
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19768C.1.pep
US-10-437-963-116249

Query Match      67.3%; Score 37; DB 4; Length 69;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
   ||| |||:|
Db 32 LHRLEYPT 40

RESULT 47
US-10-424-599-285574
; Sequence 285574, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; Sequence 203113, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; Sequence 912, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
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; Sequence 4289, Application US/10264049
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; Publication No. US20040005579A1
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
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; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
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GenCore version 5.1.1.8
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	39	70.9	11 US-11-144-222-48	Sequence 48, Appl
5	39	70.9	11 US-11-182-343-48	Sequence 48, Appl
6	39	70.9	11 US-11-188-298-1519	Sequence 1519, Appl
7	39	70.9	11 US-11-113-424-52	Sequence 52, Appl
8	39	70.9	11 US-11-100-640-10	Sequence 10, Appl
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148	31	56.4	593	11	US-11-087-099-2140	Sequence 2140, Ap	221	30	54.5	136	11	US-11-182-343-2	Sequence 2, Appl
149	31	56.4	596	11	US-11-079-463-9928	Sequence 9928, Ap	222	30	54.5	168	9	US-10-714-887-68	Sequence 68, Appl
150	31	56.4	601	9	US-11-072-512-2541	Sequence 2541, Ap	223	30	54.5	193	11	US-11-087-099-9209	Sequence 9209, Ap
151	31	56.4	607	9	US-10-821-234-958	Sequence 958, App	224	30	54.5	198	11	US-11-188-298-11006	Sequence 11006, A
152	31	56.4	607	9	US-10-455-772-528	Sequence 528, App	225	30	54.5	205	9	US-10-995-561-796	Sequence 796, App
153	31	56.4	611	9	US-11-096-051-14	Sequence 14, Appl	226	30	54.5	213	11	US-11-188-298-1876	Sequence 1876, Ap
154	31	56.4	611	9	US-10-455-772-508	Sequence 508, App	227	30	54.5	214	11	US-11-188-298-14600	Sequence 14600, A
155	31	56.4	611	9	US-10-455-772-510	Sequence 510, App	228	30	54.5	234	9	US-11-188-298-1034	Sequence 1034, Ap
156	31	56.4	611	9	US-10-455-772-512	Sequence 512, App	229	30	54.5	234	11	US-10-793-626-1034	Sequence 626, Ap
157	31	56.4	611	9	US-10-455-772-514	Sequence 514, App	230	30	54.5	234	11	US-11-096-568A-7272	Sequence 7272, Ap
158	31	56.4	618	9	US-10-455-772-516	Sequence 516, App	231	30	54.5	235	11	US-11-096-568A-32343	Sequence 32343, A
159	31	56.4	618	9	US-10-455-772-506	Sequence 506, App	232	30	54.5	236	11	US-11-144-248-51	Sequence 51, Appl
160	31	56.4	618	9	US-10-455-772-506	Sequence 506, App	233	30	54.5	236	11	US-11-144-222-51	Sequence 51, Appl
161	31	56.4	675	9	US-10-204-639-6	Sequence 6, Appl	234	30	54.5	250	11	US-11-182-343-51	Sequence 51, Appl
162	31	56.4	816	9	US-10-455-772-490	Sequence 490, App	235	30	54.5	252	11	US-11-096-568A-7271	Sequence 7271, Ap
163	31	56.4	821	9	US-10-455-772-518	Sequence 518, App	236	30	54.5	255	11	US-11-079-463-8309	Sequence 8309, Ap
164	31	56.4	821	9	US-10-455-772-534	Sequence 534, App	237	30	54.5	256	9	US-11-087-099-7428	Sequence 7428, Ap
165	31	56.4	827	11	US-11-096-051-6	Sequence 6, Appl	238	30	54.5	264	11	US-10-517-696-130	Sequence 130, App
166	31	56.4	827	9	US-10-455-772-520	Sequence 520, App	239	30	54.5	264	11	US-11-264-096-306	Sequence 306, App
167	31	56.4	827	9	US-10-455-772-532	Sequence 532, App	240	30	54.5	265	9	US-10-454-437-352	Sequence 352, App
			827	9	US-10-455-772-536	Sequence 536, App		30	54.5	266	11	US-11-096-568A-7270	Sequence 7270, Ap

241	30	54.5	299	11	US-11-172-740-895	Sequence 895, App	314	30	54.5	517	9	US-10-517-696-144	Sequence 144, App
242	30	54.5	304	11	US-11-096-568A-3358	Sequence 3358, App	315	30	54.5	524	9	US-10-517-696-113	Sequence 113, App
243	30	54.5	305	11	US-11-087-099-5005	Sequence 5005, App	316	30	54.5	524	9	US-10-517-696-122	Sequence 122, App
244	30	54.5	307	9	US-10-401-386B-31	Sequence 31, Appl	317	30	54.5	524	11	US-11-096-568A-15787	Sequence 15787, A
245	30	54.5	309	9	US-10-524-647-110	Sequence 110, App	318	30	54.5	541	11	US-11-072-512-2161	Sequence 2161, App
246	30	54.5	309	9	US-10-524-972-98	Sequence 98, Appl	319	30	54.5	545	11	US-11-087-099-9173	Sequence 9173, App
247	30	54.5	309	9	US-10-524-971-6	Sequence 6, Appl	320	30	54.5	614	9	US-10-517-696-128	Sequence 128, App
248	30	54.5	314	11	US-11-096-568A-3357	Sequence 3357, App	321	30	54.5	635	9	US-10-821-234-1673	Sequence 1673, App
249	30	54.5	325	9	US-10-517-696-126	Sequence 126, App	322	30	54.5	668	11	US-11-188-298-17163	Sequence 17163, A
250	30	54.5	326	11	US-10-517-696-148	Sequence 148, App	323	30	54.5	710	11	US-11-045-004-818	Sequence 818, App
251	30	54.5	325	11	US-11-087-099-7835	Sequence 7835, App	324	30	54.5	717	11	US-11-079-463-6144	Sequence 6144, App
252	30	54.5	326	11	US-11-087-099-6841	Sequence 6841, App	325	30	54.5	728	9	US-10-517-696-112	Sequence 112, App
253	30	54.5	326	11	US-11-087-099-8724	Sequence 8724, App	326	30	54.5	763	11	US-11-045-004-2824	Sequence 2824, App
254	30	54.5	329	9	US-10-485-517-330	Sequence 330, App	327	30	54.5	766	9	US-10-793-626-420	Sequence 420, App
255	30	54.5	334	11	US-11-188-298-15542	Sequence 15542, A	328	30	54.5	769	11	US-11-079-463-8698	Sequence 8698, App
256	30	54.5	334	11	US-11-188-298-18112	Sequence 18112, A	329	30	54.5	981	11	US-11-079-463-6374	Sequence 6374, App
257	30	54.5	336	9	US-10-517-696-153	Sequence 153, App	330	30	54.5	1017	11	US-11-087-099-6494	Sequence 6494, App
258	30	54.5	350	9	US-10-517-696-125	Sequence 125, App	331	30	54.5	1190	9	US-10-506-454-1349	Sequence 1349, App
259	30	54.5	352	11	US-11-096-568A-3356	Sequence 3356, App	332	30	54.5	1214	11	US-11-024-959-483	Sequence 483, App
260	30	54.5	362	11	US-11-087-099-9198	Sequence 9198, App	333	30	54.5	1255	11	US-11-050-857-487	Sequence 487, App
261	30	54.5	362	11	US-11-188-298-8432	Sequence 8432, App	334	30	54.5	1255	11	US-11-043-806-398	Sequence 398, App
262	30	54.5	362	11	US-11-188-298-13127	Sequence 13127, A	335	30	54.5	1256	9	US-10-517-696-111	Sequence 111, App
263	30	54.5	363	11	US-11-188-298-10951	Sequence 10951, A	336	30	54.5	2323	9	US-10-793-626-760	Sequence 760, App
264	30	54.5	363	11	US-11-188-298-11263	Sequence 11263, A	337	29.5	53.6	184	9	US-10-506-454-1466	Sequence 1466, App
265	30	54.5	363	11	US-11-188-298-13316	Sequence 13316, A	338	29.5	53.6	346	11	US-11-087-099-944	Sequence 944, App
266	30	54.5	364	11	US-11-188-298-5584	Sequence 5584, App	339	29.5	53.6	346	11	US-11-087-099-2346	Sequence 2346, App
267	30	54.5	364	11	US-11-188-298-21352	Sequence 21352, A	340	29.5	53.6	505	9	US-10-873-528-120	Sequence 120, App
268	30	54.5	365	11	US-11-072-512-3671	Sequence 3671, App	341	29	52.7	9	US-10-981-356A-9	Sequence 9, Appl	
269	30	54.5	365	11	US-11-087-099-12419	Sequence 12419, App	342	29	52.7	9	US-11-096-046-9	Sequence 9, Appl	
270	30	54.5	366	11	US-11-087-099-4201	Sequence 4201, App	343	29	52.7	9	US-11-251-173-40	Sequence 40, Appl	
271	30	54.5	366	11	US-11-087-099-9353	Sequence 9353, App	344	29	52.7	10	US-10-982-357-74	Sequence 74, Appl	
272	30	54.5	366	11	US-11-087-099-936	Sequence 936, App	345	29	52.7	11	US-10-982-357-58	Sequence 58, Appl	
273	30	54.5	368	11	US-11-087-099-4522	Sequence 4522, App	346	29	52.7	58	11	US-11-188-298-13044	Sequence 13044, A
274	30	54.5	368	11	US-11-087-099-9713	Sequence 9713, App	347	29	52.7	76	9	US-10-925-366A-322	Sequence 322, App
275	30	54.5	368	11	US-11-087-099-11484	Sequence 11484, A	348	29	52.7	76	11	US-11-098-758-322	Sequence 322, App
276	30	54.5	370	9	US-10-330-773-446	Sequence 446, App	349	29	52.7	107	10	US-11-239-308-22	Sequence 22, Appl
277	30	54.5	372	9	US-10-517-696-129	Sequence 129, App	350	29	52.7	107	11	US-11-102-424-16	Sequence 16, Appl
278	30	54.5	375	11	US-11-087-099-3670	Sequence 3670, App	351	29	52.7	107	11	US-11-217-919-132	Sequence 132, App
279	30	54.5	377	11	US-11-079-463-8760	Sequence 8760, App	352	29	52.7	108	9	US-10-982-357-52	Sequence 52, Appl
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281	30	54.5	380	9	US-10-330-773-443	Sequence 443, App	354	29	52.7	113	9	US-10-793-626-1378	Sequence 1378, App
282	30	54.5	381	9	US-10-515-872-12	Sequence 12, Appl	355	29	52.7	117	11	US-11-096-568A-26856	Sequence 26856, A
283	30	54.5	385	9	US-10-501-035-210	Sequence 210, App	356	29	52.7	132	11	US-11-251-173-32	Sequence 32, Appl
284	30	54.5	387	11	US-11-096-568A-32342	Sequence 32342, A	357	29	52.7	136	11	US-11-051-267-29	Sequence 29, Appl
285	30	54.5	388	11	US-11-172-740-2131	Sequence 2131, App	358	29	52.7	143	11	US-11-188-298-13493	Sequence 13493, A
286	30	54.5	396	9	US-10-517-696-147	Sequence 147, App	359	29	52.7	143	11	US-11-096-568A-17233	Sequence 17233, A
287	30	54.5	398	9	US-10-517-696-136	Sequence 136, App	360	29	52.7	145	11	US-11-096-568A-26853	Sequence 26853, A
288	30	54.5	402	11	US-11-183-664-94	Sequence 94, Appl	361	29	52.7	150	11	US-11-267-310-9	Sequence 9, Appl
289	30	54.5	409	9	US-10-517-696-149	Sequence 149, App	362	29	52.7	150	11	US-11-267-191-9	Sequence 9, Appl
290	30	54.5	409	11	US-11-096-568A-32341	Sequence 32341, A	363	29	52.7	153	11	US-11-267-310-5	Sequence 5, Appl
291	30	54.5	417	11	US-11-188-298-15840	Sequence 15840, A	364	29	52.7	153	11	US-11-267-310-11	Sequence 11, Appl
292	30	54.5	420	9	US-10-517-696-141	Sequence 141, App	365	29	52.7	153	11	US-11-267-191-5	Sequence 5, Appl
293	30	54.5	423	9	US-10-995-561-794	Sequence 794, App	366	29	52.7	153	11	US-11-267-191-11	Sequence 11, Appl
294	30	54.5	423	9	US-10-995-561-795	Sequence 795, App	367	29	52.7	157	11	US-11-051-267-27	Sequence 27, Appl
295	30	54.5	433	11	US-11-072-512-3033	Sequence 3033, App	368	29	52.7	157	11	US-11-087-099-9732	Sequence 9732, App
296	30	54.5	435	9	US-10-517-696-123	Sequence 123, App	369	29	52.7	163	11	US-11-188-298-18890	Sequence 18890, A
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298	30	54.5	448	11	US-10-995-561-793	Sequence 793, App	371	29	52.7	168	11	US-11-096-568A-17232	Sequence 17232, A
299	30	54.5	448	11	US-11-072-512-3380	Sequence 3380, App	372	29	52.7	169	11	US-11-096-568A-14288	Sequence 14288, A
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302	30	54.5	475	9	US-10-501-035-309	Sequence 309, App	375	29	52.7	172	11	US-11-096-568A-17231	Sequence 17231, A
303	30	54.5	475	9	US-10-517-696-117	Sequence 117, App	376	29	52.7	178	11	US-11-072-512-3886	Sequence 3886, App
304	30	54.5	475	9	US-10-515-872-10	Sequence 10, Appl	377	29	52.7	182	11	US-11-087-099-4496	Sequence 4496, App
305	30	54.5	477	11	US-11-199-821-8	Sequence 8, Appl	378	29	52.7	186	11	US-11-188-298-14437	Sequence 14437, A
306	30	54.5	481	11	US-11-079-463-7050	Sequence 7050, App	379	29	52.7	187	11	US-11-096-568A-19658	Sequence 19658, A
307	30	54.5	483	9	US-10-517-696-132	Sequence 132, App	380	29	52.7	194	11	US-11-096-568A-17632	Sequence 17632, A
308	30	54.5	484	9	US-10-517-696-120	Sequence 120, App	381	29	52.7	197	11	US-11-188-298-6640	Sequence 6640, App
309	30	54.5	485	9	US-10-517-696-142	Sequence 142, App	382	29	52.7	204	11	US-11-219-145-1	Sequence 1, Appl
310	30	54.5	492	9	US-10-517-696-131	Sequence 131, App	383	29	52.7	207	11	US-11-087-099-770	Sequence 770, App
311	30	54.5	512	11	US-11-096-568A-15788	Sequence 15788, A	384	29	52.7	207	11	US-11-122-793-13	Sequence 13, Appl
312	30	54.5	515	9	US-10-517-696-114	Sequence 114, App	385	29	52.7	232	9	US-10-793-626-1700	Sequence 1700, App
313	30	54.5	515	11	US-11-233-510-20	Sequence 20, Appl	386	29	52.7	234	11	US-11-128-440-21	Sequence 21, Appl

387	29	52.7	251	11	US-11-045-004-535	Sequence 535, App	460	29	52.7	390	11	US-11-096-568A-30415	Sequence 30415, A
388	29	52.7	257	9	US-10-467-657-5054	Sequence 5054, Ap	461	29	52.7	392	11	US-11-096-568A-21694	Sequence 21694, A
389	29	52.7	257	11	US-11-087-099-328	Sequence 328, App	462	29	52.7	392	11	US-11-188-298-6024	Sequence 6024, Ap
390	29	52.7	262	11	US-11-054-281-89	Sequence 89, Appl	463	29	52.7	405	11	US-11-188-298-499	Sequence 499, App
391	29	52.7	265	11	US-11-079-463-5448	Sequence 5448, Ap	464	29	52.7	415	9	US-10-467-657-7774	Sequence 7774, Ap
392	29	52.7	266	11	US-11-054-281-88	Sequence 88, Appl	465	29	52.7	415	9	US-11-072-512-2624	Sequence 2624, Ap
393	29	52.7	269	11	US-11-188-298-5037	Sequence 5037, Ap	466	29	52.7	419	11	US-11-188-298-1381	Sequence 1381, Ap
394	29	52.7	274	11	US-11-172-740-1675	Sequence 1675, Ap	467	29	52.7	422	11	US-11-087-099-4279	Sequence 4279, Ap
395	29	52.7	279	11	US-11-188-298-22200	Sequence 22200, Ap	468	29	52.7	426	11	US-11-188-298-19735	Sequence 19735, A
396	29	52.7	280	11	US-11-096-568A-21696	Sequence 21696, A	469	29	52.7	427	11	US-11-188-298-19311	Sequence 19311, A
397	29	52.7	283	11	US-11-096-568A-32201	Sequence 32201, A	470	29	52.7	430	11	US-11-188-298-2034	Sequence 2034, Ap
398	29	52.7	283	11	US-11-188-298-17820	Sequence 17820, A	471	29	52.7	430	11	US-11-188-298-4693	Sequence 4693, Ap
399	29	52.7	287	11	US-11-096-568A-25788	Sequence 25788, A	472	29	52.7	431	11	US-11-096-568A-33761	Sequence 33761, A
400	29	52.7	293	11	US-11-096-568A-17631	Sequence 17631, A	473	29	52.7	432	11	US-11-188-298-5835	Sequence 5835, Ap
401	29	52.7	294	11	US-11-054-281-87	Sequence 87, Appl	474	29	52.7	434	11	US-11-188-298-4254	Sequence 4254, Ap
402	29	52.7	294	11	US-11-188-298-16929	Sequence 16929, A	475	29	52.7	436	11	US-11-188-298-8176	Sequence 8176, Ap
403	29	52.7	295	11	US-11-096-568A-21803	Sequence 21803, A	476	29	52.7	436	11	US-11-188-298-16401	Sequence 16401, A
404	29	52.7	297	11	US-11-096-568A-21802	Sequence 21802, A	477	29	52.7	436	11	US-11-188-298-17822	Sequence 17822, A
405	29	52.7	297	11	US-11-188-298-13624	Sequence 13624, A	478	29	52.7	436	11	US-11-188-298-20924	Sequence 20924, A
406	29	52.7	297	11	US-11-188-298-19279	Sequence 19279, A	479	29	52.7	440	11	US-11-045-004-2444	Sequence 2444, Ap
407	29	52.7	298	11	US-11-096-568A-25787	Sequence 25787, A	480	29	52.7	445	11	US-11-146-428-110	Sequence 110, App
408	29	52.7	298	11	US-11-188-298-18166	Sequence 18166, A	481	29	52.7	446	11	US-11-188-298-21999	Sequence 21999, A
409	29	52.7	298	11	US-11-188-298-20234	Sequence 20234, A	482	29	52.7	453	8	US-10-196-749-64	Sequence 64, Appl
410	29	52.7	299	11	US-11-096-568A-18196	Sequence 18196, A	483	29	52.7	453	9	US-10-793-626-804	Sequence 804, App
411	29	52.7	299	11	US-11-188-298-7502	Sequence 7502, Ap	484	29	52.7	453	9	US-10-194-487-64	Sequence 64, Appl
412	29	52.7	301	11	US-11-096-568A-18195	Sequence 18195, A	485	29	52.7	453	9	US-10-195-883-64	Sequence 64, Appl
413	29	52.7	301	11	US-11-096-568A-33763	Sequence 33763, A	486	29	52.7	453	9	US-10-195-888-64	Sequence 64, Appl
414	29	52.7	303	11	US-11-188-298-20394	Sequence 20394, A	487	29	52.7	453	9	US-10-195-889-64	Sequence 64, Appl
415	29	52.7	304	11	US-11-096-568A-17630	Sequence 17630, A	488	29	52.7	453	9	US-10-216-1614-103	Sequence 69, Appl
416	29	52.7	305	11	US-11-188-298-17917	Sequence 17917, A	489	29	52.7	454	11	US-11-037-243-103	Sequence 103, App
417	29	52.7	306	11	US-11-096-568A-33762	Sequence 33762, A	490	29	52.7	455	11	US-11-188-298-21623	Sequence 21623, A
418	29	52.7	307	11	US-11-188-298-22419	Sequence 22419, A	491	29	52.7	458	11	US-11-087-099-5414	Sequence 5414, Ap
419	29	52.7	310	11	US-11-096-568A-21801	Sequence 21801, A	492	29	52.7	459	11	US-11-087-099-2904	Sequence 2904, Ap
420	29	52.7	311	11	US-11-188-298-21052	Sequence 21052, A	493	29	52.7	459	11	US-11-087-099-10349	Sequence 10349, Ap
421	29	52.7	312	11	US-11-054-281-20	Sequence 20, Appl	494	29	52.7	477	11	US-11-096-568A-30414	Sequence 30414, A
422	29	52.7	312	11	US-11-054-281-86	Sequence 86, Appl	495	29	52.7	487	11	US-11-087-099-9898	Sequence 9898, Ap
423	29	52.7	313	11	US-11-188-298-5009	Sequence 5009, Ap	496	29	52.7	487	11	US-11-188-298-9143	Sequence 9143, Ap
424	29	52.7	315	11	US-11-096-568A-18194	Sequence 18194, A	497	29	52.7	489	11	US-11-096-568A-3438	Sequence 3438, Ap
425	29	52.7	316	11	US-11-079-463-7347	Sequence 7347, Ap	498	29	52.7	505	9	US-10-218-784-30	Sequence 30, Appl
426	29	52.7	316	11	US-11-188-298-3662	Sequence 3662, Ap	499	29	52.7	505	9	US-10-219-061-30	Sequence 30, Appl
427	29	52.7	316	11	US-11-188-298-9688	Sequence 9688, Ap	500	29	52.7	505	9	US-10-219-062-30	Sequence 30, Appl
428	29	52.7	316	11	US-11-188-298-22028	Sequence 22028, A	501	29	52.7	505	9	US-10-219-064-30	Sequence 30, Appl
429	29	52.7	317	11	US-11-188-298-1390	Sequence 1390, Ap	502	29	52.7	505	9	US-10-233-134-30	Sequence 30, Appl
430	29	52.7	317	11	US-11-188-298-19438	Sequence 19438, A	503	29	52.7	505	11	US-11-188-298-6263	Sequence 6263, Ap
431	29	52.7	320	9	US-10-455-772-694	Sequence 694, App	504	29	52.7	505	11	US-11-188-298-13370	Sequence 13370, A
432	29	52.7	323	11	US-11-072-175-152	Sequence 152, App	505	29	52.7	506	11	US-11-087-099-1457	Sequence 1457, Ap
433	29	52.7	323	11	US-11-288-493-2	Sequence 2, Appl1	506	29	52.7	506	11	US-11-087-099-10253	Sequence 10253, A
434	29	52.7	332	11	US-11-188-298-4963	Sequence 4963, Ap	507	29	52.7	507	11	US-11-188-298-15325	Sequence 15325, A
435	29	52.7	332	11	US-11-188-298-6666	Sequence 6666, Ap	508	29	52.7	509	11	US-11-087-099-2201	Sequence 2201, Ap
436	29	52.7	332	11	US-11-188-298-7946	Sequence 7946, Ap	509	29	52.7	522	8	US-10-505-928-543	Sequence 543, App
437	29	52.7	335	11	US-11-054-281-90	Sequence 90, Appl	510	29	52.7	528	11	US-11-096-568A-3064	Sequence 3064, Ap
438	29	52.7	337	11	US-11-045-004-1271	Sequence 1271, Ap	511	29	52.7	533	11	US-11-188-298-1282	Sequence 1282, Ap
439	29	52.7	341	11	US-11-096-568A-25786	Sequence 25786, A	512	29	52.7	551	11	US-11-096-568A-8457	Sequence 8457, Ap
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441	29	52.7	343	11	US-11-096-568A-33200	Sequence 33200, A	514	29	52.7	556	11	US-11-072-175-182	Sequence 182, App
442	29	52.7	345	11	US-11-188-298-12532	Sequence 12532, A	515	29	52.7	578	11	US-11-188-298-2140	Sequence 2140, Ap
443	29	52.7	345	11	US-11-188-298-16375	Sequence 16375, A	516	29	52.7	587	9	US-10-623-155-501	Sequence 501, App
444	29	52.7	350	11	US-11-096-568A-32199	Sequence 32199, A	517	29	52.7	609	11	US-11-096-568A-8456	Sequence 8456, Ap
445	29	52.7	356	9	US-10-506-454-753	Sequence 753, App	518	29	52.7	615	11	US-11-188-298-15175	Sequence 15175, A
446	29	52.7	359	11	US-11-037-243-114	Sequence 114, App	519	29	52.7	641	11	US-11-096-568A-28382	Sequence 28382, A
447	29	52.7	360	11	US-11-087-099-7607	Sequence 7607, Ap	520	29	52.7	656	11	US-11-079-463-7123	Sequence 7123, Ap
448	29	52.7	362	11	US-11-079-463-9498	Sequence 9498, Ap	521	29	52.7	659	9	US-10-467-657-6006	Sequence 6006, Ap
449	29	52.7	368	11	US-11-087-099-385	Sequence 385, App	522	29	52.7	661	11	US-11-096-568A-28381	Sequence 28381, A
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451	29	52.7	368	11	US-11-096-568A-32550	Sequence 32550, A	524	29	52.7	687	9	US-10-714-887-268	Sequence 268, App
452	29	52.7	369	11	US-11-188-298-8166	Sequence 8166, Ap	525	29	52.7	693	9	US-10-714-887-268	Sequence 268, App
453	29	52.7	373	11	US-11-188-298-4161	Sequence 4161, Ap	526	29	52.7	719	9	US-10-505-263-87	Sequence 87, Appl
454	29	52.7	374	11	US-11-079-463-8992	Sequence 8992, Ap	527	29	52.7	735	11	US-11-188-298-19249	Sequence 19249, A
455	29	52.7	377	11	US-11-096-568A-21695	Sequence 21695, A	528	29	52.7	745	11	US-11-096-568A-28380	Sequence 28380, A
456	29	52.7	383	11	US-11-087-099-4267	Sequence 4267, Ap	529	29	52.7	755	11	US-11-087-099-2677	Sequence 2677, Ap
457	29	52.7	383	11	US-11-188-298-3984	Sequence 3984, Ap	530	29	52.7	772	11	US-11-188-298-2937	Sequence 2937, Ap
458	29	52.7	384	11	US-11-087-099-5610	Sequence 5610, Ap	531	29	52.7	874	11	US-11-012-762-8	Sequence 8, Appl1
459	29	52.7	384	11	US-11-087-099-6149	Sequence 6149, Ap	532	29	52.7	882	11	US-11-012-762-34	Sequence 34, Appl1

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536	29	52.7	1401	11	US-11-188-298-13416	Sequence 13416, A	609	28	50.9	208	11	US-11-122-793-14	Sequence 14, Appl
537	29	52.7	1478	11	US-11-188-298-6040	Sequence 6040, Ap	610	28	50.9	212	11	US-11-096-568A-10374	Sequence 10374, A
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544	28.5	51.8	272	8	US-10-505-928-107	Sequence 107, App	617	28	50.9	229	9	US-10-524-647-104	Sequence 104, App
545	28.5	51.8	464	11	US-11-172-740-2137	Sequence 2137, Ap	618	28	50.9	229	9	US-10-524-972-88	Sequence 88, Appl
546	28.5	51.8	485	11	US-11-188-298-10345	Sequence 10345, A	619	28	50.9	231	11	US-11-172-740-858	Sequence 858, App
547	28	50.9	9	11	US-11-010-748A-321	Sequence 321, App	620	28	50.9	233	9	US-10-524-972-149	Sequence 149, App
548	28	50.9	9	11	US-11-010-748A-327	Sequence 327, App	621	28	50.9	236	11	US-11-079-463-8929	Sequence 8929, Ap
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552	28	50.9	9	11	US-11-009-873A-216	Sequence 216, App	625	28	50.9	241	9	US-10-902-546-6	Sequence 6, Appl
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556	28	50.9	9	11	US-11-009-769A-216	Sequence 216, App	629	28	50.9	245	11	US-11-045-004-1865	Sequence 1865, Ap
557	28	50.9	17	11	US-11-010-748A-319	Sequence 319, App	630	28	50.9	252	8	US-10-196-749-302	Sequence 302, App
558	28	50.9	32	9	US-10-467-657-1186	Sequence 1186, Ap	631	28	50.9	252	9	US-10-063-703-92	Sequence 92, Appl
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561	28	50.9	76	11	US-11-188-298-6252	Sequence 6252, Ap	634	28	50.9	252	9	US-10-195-888-302	Sequence 302, App
562	28	50.9	77	11	US-11-096-568A-2723	Sequence 2723, Ap	635	28	50.9	252	11	US-10-195-889-302	Sequence 302, App
563	28	50.9	78	11	US-11-000-463-421	Sequence 421, App	636	28	50.9	252	11	US-11-102-240-92	Sequence 92, Appl
564	28	50.9	78	11	US-11-000-463-893	Sequence 893, App	637	28	50.9	252	11	US-11-103-195-92	Sequence 92, Appl
565	28	50.9	83	11	US-11-079-463-5730	Sequence 5730, Ap	638	28	50.9	253	9	US-10-524-647-84	Sequence 84, Appl
566	28	50.9	92	11	US-11-102-476-15	Sequence 15, Appl	639	28	50.9	253	9	US-10-524-972-92	Sequence 92, Appl
567	28	50.9	106	9	US-10-793-626-178	Sequence 178, App	640	28	50.9	253	9	US-10-541-513-4	Sequence 4, Appl
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571	28	50.9	106	11	US-11-174-186-5	Sequence 5, Appl	644	28	50.9	262	9	US-10-714-887-14	Sequence 14, Appl
572	28	50.9	106	11	US-11-174-186-7	Sequence 7, Appl	645	28	50.9	262	9	US-10-524-972-90	Sequence 90, Appl
573	28	50.9	106	11	US-11-174-186-8	Sequence 8, Appl	646	28	50.9	262	11	US-10-541-513-2	Sequence 2, Appl
574	28	50.9	106	11	US-11-174-186-9	Sequence 9, Appl	647	28	50.9	262	11	US-11-096-568A-25092	Sequence 25092, A
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578	28	50.9	106	11	US-11-174-186-13	Sequence 13, Appl	651	28	50.9	273	11	US-11-264-728-22	Sequence 22, Appl
579	28	50.9	106	11	US-11-174-186-14	Sequence 14, Appl	652	28	50.9	275	11	US-11-079-463-9334	Sequence 9334, Ap
580	28	50.9	106	11	US-11-174-186-15	Sequence 15, Appl	653	28	50.9	275	11	US-11-172-740-897	Sequence 897, App
581	28	50.9	106	11	US-11-174-186-16	Sequence 16, Appl	654	28	50.9	286	11	US-11-096-568A-33425	Sequence 33425, A
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587	28	50.9	121	11	US-11-096-568A-14399	Sequence 14399, A	660	28	50.9	300	11	US-11-096-568A-20258	Sequence 20258, A
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591	28	50.9	133	11	US-11-264-096-1145	Sequence 1145, Ap	664	28	50.9	302	11	US-11-087-099-5607	Sequence 5607, Ap
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593	28	50.9	135	9	US-10-330-773-137	Sequence 137, App	666	28	50.9	302	11	US-11-172-740-1124	Sequence 1124, Ap
594	28	50.9	139	11	US-11-096-568A-3540	Sequence 3540, Ap	667	28	50.9	302	11	US-11-188-298-1627	Sequence 1627, Ap
595	28	50.9	143	11	US-11-096-568A-19896	Sequence 19896, A	668	28	50.9	302	11	US-11-188-298-16157	Sequence 16157, A
596	28	50.9	145	11	US-11-074-176-140	Sequence 140, App	669	28	50.9	303	11	US-11-087-099-4622	Sequence 4622, Ap
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600	28	50.9	163	9	US-10-793-626-2330	Sequence 2330, Ap	673	28	50.9	307	11	US-11-172-740-1118	Sequence 1118, App
601	28	50.9	170	11	US-11-096-568A-34157	Sequence 34157, A	674	28	50.9	308	11	US-11-172-740-1116	Sequence 1116, Ap
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603	28	50.9	183	9	US-10-455-772-682	Sequence 682, App	676	28	50.9	319	11	US-11-079-463-6073	Sequence 6073, Ap
604	28	50.9	186	11	US-11-087-099-11979	Sequence 11979, A	677	28	50.9	320	11	US-11-226-701-6	Sequence 6, Appl
605	28	50.9	187	11	US-11-096-568A-34155	Sequence 34155, A	678	28	50.9	320	11	US-11-188-298-8706	Sequence 8706, Ap

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680	28	50.9	320	11	US-11-188-298-12537	Sequence 12567, A	753	28	50.9	452	11	US-11-098-686-10203	Sequence 10203, A
681	28	50.9	320	11	US-11-188-298-12632	Sequence 12632, A	754	28	50.9	453	11	US-11-096-568A-2518	Sequence 2518, Ap
682	28	50.9	323	11	US-11-188-298-21790	Sequence 21790, A	755	28	50.9	458	11	US-11-087-099-11911	Sequence 11911, A
683	28	50.9	330	11	US-11-284-096-1189	Sequence 1189, Ap	756	28	50.9	464	11	US-11-096-568A-30210	Sequence 30210, A
684	28	50.9	333	9	US-10-821-234-1036	Sequence 1036, Ap	757	28	50.9	467	11	US-11-087-099-364	Sequence 364, App
685	28	50.9	333	11	US-11-188-298-1694	Sequence 1694, Ap	758	28	50.9	471	11	US-11-087-099-474	Sequence 474, App
686	28	50.9	335	11	US-11-087-099-5054	Sequence 5054, Ap	759	28	50.9	472	11	US-11-096-568A-29864	Sequence 29864, A
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697	28	50.9	361	11	US-11-087-099-9662	Sequence 9662, Ap	770	28	50.9	501	11	US-11-087-099-7328	Sequence 7328, Ap
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699	28	50.9	363	11	US-11-096-568A-5410	Sequence 5410, Ap	772	28	50.9	507	11	US-10-330-773-187	Sequence 187, App
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706	28	50.9	369	11	US-11-188-298-5175	Sequence 5175, Ap	779	28	50.9	530	11	US-11-096-568A-10341	Sequence 10341, A
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708	28	50.9	371	11	US-11-087-099-2219	Sequence 2219, Ap	781	28	50.9	543	11	US-11-072-512-2140	Sequence 2140, Ap
709	28	50.9	371	11	US-11-087-099-7215	Sequence 7215, Ap	782	28	50.9	545	11	US-11-096-568A-7463	Sequence 7463, Ap
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712	28	50.9	377	11	US-11-087-099-8199	Sequence 8199, Ap	785	28	50.9	560	11	US-11-096-568A-10340	Sequence 10340, A
713	28	50.9	377	11	US-11-096-568A-29768	Sequence 29768, A	786	28	50.9	561	11	US-11-072-512-2805	Sequence 2805, Ap
714	28	50.9	379	11	US-11-087-099-11045	Sequence 11045, A	787	28	50.9	575	11	US-11-072-512-3423	Sequence 3423, App
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ALIGNMENTS

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US-11-113-424-51
; Sequence 51, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR FILING DATE: 2000-12-19
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US-11-113-424-51

Query Match 72.7%; Score 40; DB 11; Length 2715;
Best Local Similarity 77.8%; Pred. No. 89;

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US-11-037-199-13
; Sequence 13, Application US/11037199
; Publication No. US20060030015A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes
; FILE REFERENCE: A251-01/PCT
; CURRENT APPLICATION NUMBER: US/11/037,199
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: JP 2002-211756
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; NUMBER OF SEQ ID NOS: 49
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RESULT 3
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; Sequence 48, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: AEX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-48

Query Match 70.9%; Score 39; DB 11; Length 236;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 111 LQHSYPYT 119

RESULT 4
US-11-144-222-48
; Sequence 48, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-48

Query Match 70.9%; Score 39; DB 11; Length 236;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 111 LQHSYPYT 119

RESULT 5
US-11-182-343-48
; Sequence 48, Application US/11182343
; Publication No. US20060018910A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce
; APPLICANT: Gualberto, Antonio
; APPLICANT: Melvin, Carrie
; APPLICANT: Roberts, Luisa M.
; TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
; FILE REFERENCE: PC32226A
; CURRENT APPLICATION NUMBER: US/11/182,343
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 60/588,721
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-343-48

Query Match 70.9%; Score 39; DB 11; Length 236;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 111 LQHSYPYT 119

RESULT 6
US-11-188-298-1519
; Sequence 1519, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1519
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Emericella nidulans
US-11-188-298-1519

Query Match 70.9%; Score 39; DB 11; Length 865;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
| | | | |
Db 296 LHHSSYPYT 304

RESULT 7
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52

Query Match 70.9%; Score 39; DB 11; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 LHHSEYPYT 9
    ||||:|
Db 909 LHHSYDGYFT 917

RESULT 8
US-11-100-640-10
; Sequence 10, Application US/11100640
; Publication No. US20060035244A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory J
; TITLE OF INVENTION: A Method for Distinguishing Follicular Thyroid Adenoma (FTA) from
; TITLE OF INVENTION: Follicular Thyroid Carcinoma (FTC)
; FILE REFERENCE: 000250.00021
; CURRENT APPLICATION NUMBER: US/11/100.640
; CURRENT FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: human
US-11-100-640-10

Query Match 70.9%; Score 39; DB 11; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
    ||||:|
Db 909 LHHSYDGYFT 917

RESULT 9
US-11-100-640-16
; Sequence 16, Application US/11100640
; Publication No. US20060035244A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory J
; TITLE OF INVENTION: A Method for Distinguishing Follicular Thyroid Adenoma (FTA) from
; TITLE OF INVENTION: Follicular Thyroid Carcinoma (FTC)
; FILE REFERENCE: 000250.00021
; CURRENT APPLICATION NUMBER: US/11/100.640
; CURRENT FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: human
US-11-100-640-16

Query Match 70.9%; Score 39; DB 11; Length 2725;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPYT 9
    ||||:|
Db 909 LHHSYDGYFT 917

RESULT 10
US-10-453-372-1072
; Sequence 1072, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1072
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
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; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1072
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1072

Query Match 69.1%; Score 38; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
    |||||
Db 258 HSEYPY 263

RESULT 11
US-10-453-372-1078
; Sequence 1078, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1078
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-453-372-1078

Query Match 69.1%; Score 38; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8
|||||
Db 258 HSEYPY 263

RESULT 12

US-10-453-372-1074
; Sequence 1074, Application US/10453372
; Publication No. US20060003323A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook, et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372

; CURRENT FILING DATE: 2003-06-03

; PRIOR APPLICATION NUMBER: 09/789390

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/185967

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/823187

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/195792

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 09/839446

; PRIOR FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 60/199476

; PRIOR FILING DATE: 2000-03-25

; PRIOR APPLICATION NUMBER: 09/863776

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: 60/208263

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/939398

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 60/227800

; PRIOR FILING DATE: 2000-08-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1609

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 1074

; LENGTH: 959

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-453-372-1074

Query Match 69.1%; Score 38; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8
|||||
Db 194 HSEYPY 199

RESULT 13

US-10-453-372-1076
; Sequence 1076, Application US/10453372
; Publication No. US20060003323A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook, et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-589 A

; CURRENT APPLICATION NUMBER: US/10/453,372

; CURRENT FILING DATE: 2003-06-03

; PRIOR APPLICATION NUMBER: 09/789390

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/185967

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1076
; LENGTH: 1021
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1076

Query Match 69.1%; Score 38; DB 9; Length 1021;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8

|||||

Db 256 HSEYPY 261

RESULT 14

US-10-453-372-1068

; Sequence 1068, Application US/10453372

; Publication No. US20060003323A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook, et al.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-589 A

; CURRENT APPLICATION NUMBER: US/10/453,372

; CURRENT FILING DATE: 2003-06-03

; PRIOR APPLICATION NUMBER: 09/789390

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/185967

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/823187

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/195792

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 09/839446

; PRIOR FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 60/199476

; PRIOR FILING DATE: 2000-03-25

; PRIOR APPLICATION NUMBER: 09/863776

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: 60/208263

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: 09/939398

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 60/227800

; PRIOR FILING DATE: 2000-08-25

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1609

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 1068

; LENGTH: 1025

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-453-372-1068

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Query Match      69.1%; Score 38; DB 9; Length 1025;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 HSEYPY 8
Db      258 HSEYPY 263

RESULT 15
US-10-453-372-1070
; Sequence 1070, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 1070
; LENGTH: 1025
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1070

Query Match      69.1%; Score 38; DB 9; Length 1025;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 HSEYPY 8
Db      258 HSEYPY 263

RESULT 16
US-10-453-372-1066
; Sequence 1066, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 1070
; LENGTH: 1025
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1070
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; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 1066
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1066

Query Match      69.1%; Score 38; DB 9; Length 1063;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 HSEYPY 8
Db      298 HSEYPY 303

RESULT 17
US-10-453-372-1080
; Sequence 1080, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 1080
; LENGTH: 3003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1080

Query Match      69.1%; Score 38; DB 9; Length 3003;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8
Db 2238 HSEYPY 2243

RESULT 18
US-10-453-372-1082
; Sequence 1082, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1082
; LENGTH: 3361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1082

Query Match 69.1%; Score 38; DB 9; Length 3361;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8
Db 2596 HSEYPY 2601

RESULT 19
US-11-188-298-10648
; Sequence 10648, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10648
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
US-11-188-298-10648

Query Match 67.3%; Score 37; DB 9; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Query Match 67.3%; Score 37; DB 11; Length 195;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LHHSEYP 7
Db 162 IHHEYPY 168

RESULT 20
US-11-188-298-287
; Sequence 287, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 287
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-188-298-287
```

```
Query Match 67.3%; Score 37; DB 11; Length 353;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 8
Db 122 LKHKEYPY 129
```

```
RESULT 21
US-10-718-264-6
; Sequence 6, Application US/10718264
; Publication No. US20040161410A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emmanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/718,264
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-718-264-6
```

```
Query Match 67.3%; Score 37; DB 9; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-11-176-667-6

Query Match      67.3%; Score 37; DB 11; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches      6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYP 7
        |||||
Db      210 LHHSPYP 216

RESULT 22
US-10-718-264-6
; Sequence 6, Application US/10718264
; Publication No. US20040161410A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/718,264
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-718-264-6

Query Match      67.3%; Score 37; DB 9; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches      6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYP 7
        |||||
Db      210 LHHSPYP 216

RESULT 23
US-11-176-667-6
; Sequence 6, Application US/11176667
; Publication No. US20060083756A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/11/176,667
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
```

```
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-11-176-667-6

Query Match      67.3%; Score 37; DB 11; Length 567;
Best Local Similarity 85.7%; Pred. No. 62;
Matches      6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LHHSEYP 7
        |||||
Db      210 LHHSPYP 216

RESULT 24
US-11-004-399-3054
; Sequence 3054, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3054
; LENGTH: 18
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-3054

Query Match      65.5%; Score 36; DB 11; Length 18;
Best Local Similarity 75.0%; Pred. No. 3;
Matches      6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 HHSEYPYT 9
        |||||
Db      3 HKIEYPYT 10

RESULT 25
US-11-030-313-1
; Sequence 1, Application US/11030313
; Publication No. US20050260698A1
; GENERAL INFORMATION:
; APPLICANT: Fromherz, Peter
; APPLICANT: Huebener, Gerd
; APPLICANT: Hinner, Marlon
; TITLE OF INVENTION: Selective Staining of Biomembranes Using Voltage-Sensitive Dyes
; FILE REFERENCE: 2923-684
; CURRENT APPLICATION NUMBER: US/11/030,313
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: EP 04 024 877.5
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: EP 04 000 268.5
; PRIOR FILING DATE: 2004-01-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasma membrane anchor containing regions from eukaryotic c-myc
; OTHER INFORMATION: protein, a bacterial cloning site and influenza hemagglutinin
```

US-11-030-313-1

Query Match 65.5%; Score 36; DB 11; Length 80;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HSEYPY 8
DB 5 HHHYPY 11

RESULT 26

US-10-793-626-282
; Sequence 282, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-282

Query Match 63.6%; Score 35; DB 9; Length 334;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HSEYPY 8
DB 102 HSQYPY 107

RESULT 27

US-11-239-308-8
; Sequence 8, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-8

Query Match 61.8%; Score 34; DB 10; Length 107;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
DB 111 LHHSEYPY 119

RESULT 30

DB 89 LQHNSYPWT 97

RESULT 28

US-11-239-308-10
; Sequence 10, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-10

Query Match 61.8%; Score 34; DB 10; Length 107;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
DB 89 LQHNSYPWT 97

RESULT 29

US-11-144-248-52
; Sequence 52, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-52

Query Match 61.8%; Score 34; DB 11; Length 236;
Best Local Similarity 55.6%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LHHSEYPY 9
DB 111 LQHNSYPWT 119


```

US-11-144-222-52
; Sequence 52, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-52
Query Match 61.8%; Score 34; DB 11; Length 236;
Best Local Similarity 55.6%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 111 LQHSYPT 119

RESULT 31
US-11-182-343-52
; Sequence 52, Application US/11182343
; Publication No. US20060018910A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce
; APPLICANT: Gualberto, Antonio
; APPLICANT: Melvin, Carrie
; APPLICANT: Roberts, Luisa M.
; TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
; FILE REFERENCE: PC32226A
; CURRENT APPLICATION NUMBER: US/11/182,343
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 60/588,721
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-343-52
Query Match 61.8%; Score 34; DB 11; Length 236;
Best Local Similarity 55.6%; Pred. No. 87;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 111 LQHSYPT 119

RESULT 32
US-11-045-004-267
; Sequence 267, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN

```

```

; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNNA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 267
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-267
Query Match 61.8%; Score 34; DB 11; Length 237;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 8
Db 156 LHHSIYAY 163

RESULT 33
US-10-506-454-289
; Sequence 289, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:

```

; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozhavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 289
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-289

Query Match 61.8%; Score 34; DB 9; Length 358;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYYP 8
| | | | |
Db 246 HEEYYP 251

RESULT 34
US-11-079-463-10293
; Sequence 10293, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10293
; LENGTH: 393
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10293

Query Match 61.8%; Score 34; DB 11; Length 393;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYYP 8
| | | | |
Db 196 LHHGYFPF 203

RESULT 35
US-11-072-512-2636
; Sequence 2636, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2636
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2636

Query Match 61.8%; Score 34; DB 11; Length 471;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYP 7
| | | | |
Db 320 LHHSEAP 326

RESULT 36
US-11-131-212-73
; Sequence 73, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: MOTOO YAMASAKI
; APPLICANT: NODUO HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-131-212-73

Query Match 61.8%; Score 34; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;

```
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
    |||||
Db 256 HSEYVYT 262

RESULT 37
US-11-218-473-73
; Sequence 73, Application US/11218473
; Publication No. US20060063254A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/218,473
; CURRENT FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-218-473-73

Query Match 61.8%; Score 34; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
    |||||
Db 256 HSEYVYT 262

RESULT 38
US-11-240-579-73
; Sequence 73, Application US/11240579
; Publication No. US20060064781A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/240,579
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73

Query Match 61.8%; Score 34; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
    |||||
Db 256 HSEYVYT 262

RESULT 39
US-11-287-324-73
; Sequence 73, Application US/11287324
; Publication No. US20060078990A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/287,324
; CURRENT FILING DATE: 2005-11-28
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-11-287-324-73

Query Match 61.8%; Score 34; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPYT 9
    |||||
Db 256 HSEYVYT 262

RESULT 40
US-11-287-359-73
; Sequence 73, Application US/11287359
; Publication No. US20060078991A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/287,359
; CURRENT FILING DATE: 2005-11-28
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2001-10-09
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; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Cricetus griseus
US-11-287-359-73

Query Match 61.8%; Score 34; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPT 9
|||: |||
Db 256 HSEYPT 262

RESULT 41

US-11-188-298-5169
; Sequence 5169, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 5169
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Podospora anserina
US-11-188-298-5169

Query Match 61.8%; Score 34; DB 11; Length 726;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
|||: |||
Db 431 IHKNVPT 439

RESULT 42

US-10-453-372-1210
; Sequence 1210, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 1210
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1210

Query Match 61.8%; Score 34; DB 9; Length 819;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 8
|||: |||
Db 430 LHNQPY 437

RESULT 43

US-11-087-099-1977
; Sequence 1977, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1977
; LENGTH: 1262
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-087-099-1977

Query Match 61.8%; Score 34; DB 11; Length 1262;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
|||: |||
Db 469 LHHKLPET 477

RESULT 44

US-10-507-662-40
; Sequence 40, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-40

```
Query Match      60.0%; Score 33; DB 9; Length 107;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
   | : |||
Db 89 LQYASYPY 97

RESULT 45
US-11-171-567-209
; Sequence 209, Application US/11171567
; Publication No. US20060057651A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhitter, John
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUKEMIA
; FILE REFERENCE: CELLS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR FILING DATE: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 110
; TYPE: PRT
; ORGANISM: murine
US-11-171-567-209

Query Match      60.0%; Score 33; DB 11; Length 110;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
   | : |||
Db 91 LQYDEFPY 99

RESULT 46
US-11-098-686-10824
; Sequence 10824, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10824
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10824
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Query Match      60.0%; Score 33; DB 11; Length 135;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LHHSEY 6
   | : |||
Db 2 LHHNEY 7

RESULT 47
US-11-087-099-6466
; Sequence 6466, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6466
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-6466

Query Match      60.0%; Score 33; DB 11; Length 175;
Best Local Similarity 57.1%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LHHSEYP 7
   | : |||
Db 137 MHEAHYP 143

RESULT 48
US-10-467-657-5122
; Sequence 5122, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5122
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5122

Query Match      60.0%; Score 33; DB 9; Length 187;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HSEYPY 8
   | : |||
Db 106 HREYPY 111

RESULT 49
US-11-137-253-16
; Sequence 16, Application US/11137253
; Publication No. US20060073159A1
; GENERAL INFORMATION:
```

; APPLICANT: Trustees of the University of Pennsylvania
; APPLICANT: Vonderheide, Robert H
; APPLICANT: Beatty, Gregory
; APPLICANT: Coughlin, Christina
; TITLE OF INVENTION: Human Anti-Cancer Immunotherapy
; FILE REFERENCE: 53893-5093-US1
; CURRENT APPLICATION NUMBER: US/11/137,253
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,017
; PRIOR FILING DATE: 2004-05-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-253-16

Query Match 60.0%; Score 33; DB 11; Length 390;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LHHSEYPT 9
Db 45 LHSQYPT 53

RESULT 50
US-11-096-568A-9175
; Sequence 9175, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9175
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(437)
; OTHER INFORMATION: Ceres Seq. ID no. 15169560
US-11-096-568A-9175

Query Match 60.0%; Score 33; DB 11; Length 437;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HHSEYP 7
Db 13 HHSPYP 18

Search completed: May 11, 2006, 16:50:46
Job time : 16.2131 secs

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